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ONLINE SEARCH REQUEST FORM  
\*\*\*\*\*USER Sheela Huff SERIAL NUMBER 08/012929  
ART UNIT 18010 PHONE 305-78060 DATE 3/11/97

Please give a detailed statement of requirements. Describe as specifically as possible the subject matter to be searched. Define any terms that may have special meaning. Give examples or relevant citations, authors, or keywords, if known.

You may include a copy of the broadest and or relevant claim(s).

Please search SCA ~~1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100~~

~~54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100~~

~~54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100~~

~~1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100~~

→ 2, 4, 11-28, and 53-56.

TXS-

Sheela

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FOR OFFICIAL USE ONLY  
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## STAFF USE ONLY

COMPLETED 3-19-97  
SEARCHER EEF x4391  
ONLINE TIME 6 TOTAL TIME 15  
(in minutes)  
NO. OF DATABASES 46SYSTEMS  
11aa ☐ CAS ONLINE  
13na ☐ DARC/QUESTEL  
☐ DIALOG  
☐ SDC  
☒ OTHER

Aladdin page 25

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WATERMAN

(TM)

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Release 2.1D John F. Collins, Biocomputing Research Unit.  
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Mar 18 10:16:58 1997; MasPar time 1.98 Seconds

Tabular output not generated. 57.292 Million cell updates/sec

Title: >US-08-612-929-26

Description: (1-11) from US08612929.pep

Perfect Score: 104

Sequence: 1 RETVFWYVDV 11

Scoring table: PAM 150

Gap 15

Searched: 88003 seqs, 10295656 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: a-geneseq25

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7

8:part8 9:part9 10:part10 11:part11 12:part12 13:part13

14:part14 15:part15 16:part16 17:part17 18:part18

Statistics: Mean 19.055; Variance 73.194; scale 0.260

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	104	100.0	11 13	R70200	MAB 3B9 heavy chain C	3.72e-03
2	104	100.0	140 13	R70190	Mouse MAB 3B9 heavy c	3.72e-03
3	104	100.0	141 13	R70191	Chimeric antibody 3B9	3.72e-03
4	104	100.0	141 13	R70192	Humanized antibody 3B	3.72e-03
5	73	70.2	10 12	R62884	Murine anti-human ath	3.13e+00
6	73	70.2	116 7	R38609	MCPC heavy chain.	3.13e+00
7	73	70.2	126 12	R62880	Murine anti-human ath	3.13e+00
8	73	70.2	126 12	R62879	Murine anti-human ath	3.13e+00
9	66	63.5	106 1	R04937	Sequence of human car	1.33e+01
10	66	63.5	121 18	R88846	Murine antibody 2CE-0	1.33e+01
11	66	63.5	122 16	R79878	Anti-EGFR antibody he	1.33e+01
12	66	63.5	122 1	P91382	Antibody heavy chain	1.33e+01

13	66	63.5	122 18	W02201	CDR switched variable	1.33e+01
14	66	63.5	123 16	R79877	Anti-EGFR antibody he	1.33e+01
15	66	63.5	140 1	P94780	2 H7 VH gene.	1.33e+01
16	66	63.5	140 2	P70627	Sequence encoded by t	1.33e+01
17	66	63.5	147 18	R99687	Monoclonal anti-idiot	1.33e+01
18	66	63.5	147 18	R98411	3H1 heavy chain varia	1.33e+01
19	66	63.5	151 4	P30252	Sequence of the leade	1.33e+01
20	66	63.5	239 12	R64812	ScFv anti-HCG.	1.33e+01
21	65	62.5	556 17	R96737	A. niger Bo-1 carboxy	1.63e+01
22	65	62.5	557 17	R96738	A. niger SFAG 2 carbo	1.63e+01
23	64	61.5	50 2	P70039	Secretory signal sequ	2.00e+01
24	64	61.5	491 9	R48059	Sequence of protease	2.00e+01
25	62	59.6	115 7	R34018	BW 835 VH.	3.00e+01
26	61	58.7	117 2	R07318	VH domain of antibody	3.66e+01
27	61	58.7	118 5	R29701	431/26 VH hum.	3.66e+01
28	61	58.7	119 3	P60335	Immunoglobulin heavy	3.66e+01
29	61	58.7	119 1	P81025	V region of H chain (	3.66e+01
30	61	58.7	147 6	R32542	C242 heavy chain vari	3.66e+01
31	61	58.7	148 6	R30455	C242:11 MAB heavy cha	3.66e+01
32	61	58.7	470 3	P60351	Sequence of novel mou	3.66e+01
33	61	58.7	470 3	P60351	Chimeric human-mouse	3.66e+01
34	61	58.7	909 10	R50092	Humanised anti-CEA sF	3.66e+01
35	60	57.7	110 4	R23903	RuBPCase small subuni	4.47e+01
36	60	57.7	4987 3	R10834	Rianodin receptor.	4.47e+01
37	60	57.7	5035 5	R25450	MH mutant porcine rya	4.47e+01
38	60	57.7	5072 2	R11510	Ryanodin receptor de	4.47e+01
39	59	56.7	58 15	R88965	Mutant serine proteas	5.45e+01
40	59	56.7	119 9	R47221	Antibody heavy chain	5.45e+01
41	59	56.7	120 16	R92089	Anti-RSV F glycoprote	5.45e+01
42	59	56.7	120 16	R92088	CDR-grafted anti-RSV	5.45e+01
43	59	56.7	139 12	R62678	CV1748RHA VH region.	5.45e+01
44	59	56.7	139 8	R43693	PB1.3/Humanised heavy	5.45e+01
45	59	56.7	139 8	R43689	PB1.3/Humanised heavy	5.45e+01

## ALIGNMENTS

RESULT	1
ID	R70200 standard; Protein; 11 AA.
AC	R70200;
DT	20-SEP-1995 (first entry)
DE	MAB 3B9 heavy chain CDR.
KW	Chimeric antibody; humanized antibody; antibody engineering;
KW	monoclonal antibody; MAB; interleukin-4; IL-4; allergy; CDR;
KW	complementarity determining region.
OS	Mus sp.
PN	W09507301-A.
PD	16-MAR-1995.
PF	07-SEP-1994; U10308.
PR	07-SEP-1993; US-117366.
PR	14-OCT-1993; US-136783.
PA	(SMIK ) SMITHKLINE BEECHAM CORP.
PA	(SMIK ) SMITHKLINE BEECHAM CORP.
PI	Gross MS, Holmes SD, Sylvester DR;
DR	WPI; 95-123387/16.
PT	Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived
PT	from high affinity mAbs - useful in treatment of IL-4-mediated
PT	and IgE-mediated allergic conditions
PS	Disclosure; Page 58; 97pp; English.
CC	Spleen cells from mice immunized with human IL-4 were used to prepare
CC	hybridomas, which were screened for anti-IL-4 MAb secretion. Only
CC	clone 3B9 was positive. cDNA clones of the 3B9 light and heavy
CC	chains were cloned into pCEM7f+ and transformed into E. coli
CC	DH5-alpha. A heavy chain cDNA clone was sequenced (Q83491) that



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3

CC encoded the protein given in R70190. 3 CDRs (R70198-200) were  
CC identified.  
SQ Sequence 11 AA;

Query Match 100.0%; Score 104; DB 13; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.72e-03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 retvfywyfdv 11  
|||||  
QY 1 RETVFWYFDV 11

## RESULT 2

ID R70190 standard; Protein; 140 AA.  
AC R70190;  
DT 20-SEP-1995 (first entry)  
DE Mouse MAb 3B9 heavy chain.  
KW Chimeric antibody; humanized antibody; antibody engineering;  
KW monoclonal antibody; MAb; interleukin-4; IL-4; allergy.  
OS Mus sp.

FH Key Location/Qualifiers  
FT Peptide 1..19  
FT /label= Sig\_peptide  
FT Region 50..56  
FT /label= CDR  
FT /note= "complementarity determining region"  
FT Region 71..86  
FT /label= CDR  
FT /note= "complementarity determining region"  
FT Region 119..129  
FT /label= CDR  
FT /note= "complementarity determining region"  
PN W09507301-A.

PF 07-SEP-1994; U10308.  
PR 07-SEP-1993; US-117366.  
PR 14-OCT-1993; US-136783.  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
PA (SMIK ) SMITHKLINE BEECHAM PLC.  
PI Gross MS, Holmes SD, Sylvester DR;  
DR WPI; 95-123387/16.  
DR N-PSDB; Q83491.  
PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived  
PT from high affinity mAbs - useful in treatment of IL-4-mediated  
PT and IgE-mediated allergic conditions  
PS Disclosure; Fig.2; 97pp; English.  
CC Spleen cells from mice immunized with human IL-4 were used to prepare  
CC hybridomas, which were screened for anti-IL-4 MAb secretion. Only  
CC clone 3B9 was positive. cDNA clones of the 3B9 light and heavy  
CC chains were cloned into pGEM7ft and transformed into E. coli  
CC DH5-alpha. The clones were sequenced (Q83490-91), and used for  
CC antibody engineering.  
SQ Sequence 140 AA;

Query Match 100.0%; Score 104; DB 13; Length 140;  
Best Local Similarity 100.0%; Pred. No. 3.72e-03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 119 retvfywyfdv 129  
|||||  
QY 1 RETVFWYFDV 11

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4

## RESULT 3

ID R70191 standard; Protein; 141 AA.  
AC R70191;  
DT 20-SEP-1995 (first entry)  
DE Chimeric antibody 3B9 heavy chain.  
KW Chimeric antibody; antibody engineering; monoclonal antibody;  
KW MAb; interleukin-4; IL-4; allergy.  
OS Homo sapiens; Mus sp.

FH Key Location/Qualifiers  
FT Peptide 1..19  
FT /label= Sig\_peptide  
FT Region 51..57  
FT /label= CDR  
FT /note= "complementarity determining region"  
FT Region 72..87  
FT /label= CDR  
FT /note= "complementarity determining region"  
FT Peptide 120..130  
FT /label= CDR  
FT /note= "complementarity determining region"  
PN W09507301-A.

PD 16-MAR-1995.  
PF 07-SEP-1994; U10308.  
PR 07-SEP-1993; US-117366.  
PR 14-OCT-1993; US-136783.  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
PA (SMIK ) SMITHKLINE BEECHAM PLC.  
PI Gross MS, Holmes SD, Sylvester DR;  
DR WPI; 95-123387/16.  
DR N-PSDB; Q83492.  
PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived  
PT from high affinity mAbs - useful in treatment of IL-4-mediated  
PT and IgE-mediated allergic conditions  
PS Disclosure; Fig.3; 97pp; English.  
CC A human/mouse chimeric antibody heavy chain variable region was  
CC constructed (given in R70191) that contained the mouse anti-human  
CC IL-4 MAb 3B9 variable region including 3 CDRs (R70198-200) and a  
CC human antibody signal peptide (R70193). The construct was used  
CC for humanized antibody production.  
SQ Sequence 141 AA;

Query Match 100.0%; Score 104; DB 13; Length 141;  
Best Local Similarity 100.0%; Pred. No. 3.72e-03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 120 retvfywyfdv 130  
|||||  
QY 1 RETVFWYFDV 11

## RESULT 4

ID R70192 standard; Protein; 141 AA.  
AC R70192;  
DT 20-SEP-1995 (first entry)  
DE Humanized antibody 3B9 heavy chain.  
KW Humanized antibody; antibody engineering; monoclonal antibody;  
KW MAb; interleukin-4; IL-4; allergy.  
OS Homo sapiens.

FH Key Location/Qualifiers  
FT Peptide 1..19  
FT /label= Sig\_peptide  
FT Region 51..57  
FT /label= CDR  
FT /note= "complementarity determining region"

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FT Region 72..87
FT /label= CDR
FT /note= "complementarity determining region"
FT Region 120..130
FT /label= CDR
FT /note= "complementarity determining region"
PN W09507301-A.
PD 16-MAR-1995.
PF 07-SEP-1994; U10308.
PR 07-SEP-1993; US-117366.
PR 14-OCT-1993; US-136783.
PA (SMIK ) SMITHKLINE BEECHAM CORP.
PA (SMIK ) SMITHKLINE BEECHAM PLC.
PI Gross MS, Holmes SD, Sylvester DR;
PI WPI; 95-123387/16.
DR N-PSDB; Q83493.
PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived
PT from high affinity mAbs - useful in treatment of IL-4-mediated
PT and IgE-mediated allergic conditions
PS Disclosure; Fig.4; 97pp; English.
CC A humanized antibody heavy chain variable region and signal
CC sequence is given in R70192. The signal sequence is also
CC provided in R70193. The CDR sequences of the construct are
CC identical to the native CDRs of mouse anti-human IL-4 mAb
CC 3B9 (R70198-200).
SQ Sequence 141 AA;

Query Match 100.0%; Score 104; DB 13; Length 141;
Best Local Similarity 100.0%; Pred. No. 3.72e-03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 120 retvfywyfdv 130
   |||||
QY 1 RETVFWYFDV 11

RESULT 5
ID R62884 standard; peptide; 10 AA.
AC R62884;
DE 18-JUL-1995 (first entry)
DE Murine anti-human atherosclerotic plaque MAb Z2D3 VH CDR3.
KW Atherosclerosis; atherosclerotic plaque; anti-hydroxysteroid antibody;
KW murine monoclonal antibody; heavy chain variable region: CDR3;
KW complementarity determining region; imaging; plaque ablation.
OS Mus musculus.
FH Key Location/Qualifiers
FT Region 1..10
FT /label= CDR3
FN W09425053-A.
PD 10-NOV-1994.
PF 26-APR-1994; U04641.
PR 26-APR-1993; US-053451.
PA (SCOT-) SCOTGEN BIOPHARMACEUTICALS INC.
PI Calenoff E, Chen FW, Ditlow CC;
DR WPI; 94-357904/44.
DR N-PSDB; Q78738.
PT New antigen comprising hydroxy:steroid and quat. ammonium salt -
PT and related antibodies, useful e.g. for imaging, ablating or
PT treating atherosclerotic plaque, and detecting plaque specific
PT antibodies
PS Claim 199; Page 149; 288pp; English.
CC Mice were immunised with an extract of human atherosclerotic plaque,
CC then spleen cells were fused with SP2/O1-Ag-14 myeloma cells.
CC Hybrids were screened by ELISA for reactivity with the immunogen
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CC and clone Z2D3 was isolated. The Z2D3 antibody reacts specifically
CC with atherosclerotic tissue; it recognises a non-protein antigen
CC containing cholesterol (or similar steroid that is a substrate for
CC cholesterol oxidase) and a quaternary ammonium salt (pref. a
CC phosphatidylcholine or related compound that is a substrate for
CC phospholipase C). The CDR sequences for the heavy and light chains
CC of Z2D3 were determined; peptides comprising the CDRs are claimed,
CC including chimeric (CDR-grafted) murine-human antibodies.
SQ Sequence 10 AA;

Query Match 70.2%; Score 73; DB 12; Length 10;
Best Local Similarity 85.7%; Pred. No. 3.13e+00;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 4 yywyfdv 10
   :|
QY 5 FYWYFDV 11

RESULT 6
ID R38609 standard; peptide; 116 AA.
AC R38609;
DT 28-OCT-1993 (first entry)
DE MCPC heavy chain.
KW Antibody; variable domain; light; L; heavy; H; consensus;
KW affinity; antigen; immunogenicity; humanisation; framework.
OS Homo sapiens.
PN W09311794-A.
PD 24-JUN-1993.
PF 14-DEC-1992; U10906.
PR 13-DEC-1991; US-808464.
PA (XOMA ) XOMA CORP.
PI Fishwild DM, Kohn FR, Little RG, Studnicka GW;
DR WPI; 93-213827/26.
PT Antibodies prepn. used for treatment of auto-immune diseases - by
PT replacement of critical residues to reduce immunogenicity but
PT retain binding affinity, etc.
PS Disclosure; Fig 1B; 160pp; English.
CC The amino acid sequences of the light and heavy chains of the
CC variable domains from antibodies HYH [HYHEL-10 Fab-lysosyme complex]
CC (R38601 and R38608, respectively), MCPC [IgA Fab MCPC603-phosphocholine
CC complex] (R38602-03 and R38609-10, respectively), NEMM [Ig Fab' NEMM
CC (R38604-05 and R38611, respectively) and KOL [IgG1 KOL] (R38606-07 and
CC R38612, respectively) may be used to determine an alignment from which
CC appropriate changes may be made.
CC Unlike other methods of humanisation, which advocate the
CC replacement of entire antibody framework regions with those of human
CC antibodies, this method involves only the introduction of human
CC residues into those positions not critical for antigen binding.
CC This ensures that the binding properties of the modified antibody
CC are not diminished.
SQ Sequence 116 AA;

Query Match 70.2%; Score 73; DB 7; Length 116;
Best Local Similarity 85.7%; Pred. No. 3.13e+00;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 99 yywyfdv 105
   :|
QY 5 FYWYFDV 11

RESULT 7
ID R62880 standard; protein; 126 AA.
```

AC R62880;  
 DT 18-JUL-1995 (first entry)  
 DE Murine anti-human atherosclerotic plaque MAb 22D3 VH sequence.  
 KW Atherosclerosis; atherosclerotic plaque; anti-hydroxysteroid antibody;  
 KW murine monoclonal antibody; heavy chain variable region;  
 KW imaging; plaque ablation.  
 OS Mus musculus.  
 FH Key Location/Qualifiers  
 FT Misc difference 2  
 FT /note= "lys at this position in R62879 and  
 FT Gln at this position in R62880; also, the  
 FT first 8 amino acids are dictated by the  
 FT oligonucleotides used in the PCR and are  
 FT not necessarily identical to those of the  
 FT murine antibody"  
 FT Region 30..34  
 FT /label= CDR1  
 FT Region 49..65  
 FT /label= CDR2  
 FT Region 98..107  
 FT /label= CDR3  
 FT Region 120..126  
 FT /label= CH1  
 FT /note= "start of constant region"  
 PN W09425053-A.  
 PD 10-NOV-1994.  
 PE 26-APR-1994; U04641.  
 PR 26-APR-1993; US-053451.  
 PA (SCOT-) SCOTGEN BIOPHARMACEUTICALS INC.  
 PI Calenoff E, Chen FW, Dittlow CC;  
 DR WPI; 94-357904/44.  
 DR N-PSDB; Q78730.  
 PT New antigen comprising hydroxy:steroid and quat. ammonium salt -  
 PT and related antibodies, useful e.g. for imaging, ablating or  
 PT treating atherosclerotic plaque, and detecting plaque specific  
 PT antibodies  
 PS Claim 194; Page 145; 288pp; English.  
 CC Mice were immunised with an extract of human atherosclerotic plaque,  
 CC then spleen cells were fused with SP2/01-Ag-14 myeloma cells.  
 CC Hybridomas were screened by ELISA for reactivity with the immunogen  
 CC and clone 22D3 was isolated. The 22D3 antibody reacts specifically  
 CC with atherosclerotic tissue; it recognises a non-protein antigen  
 CC containing cholesterol (or similar steroid that is a substrate for  
 CC cholesterol oxidase) and a quaternary ammonium salt (pref. a  
 CC phosphatidylcholine or related compound that is a substrate for  
 CC phospholipase C).  
 SQ Sequence 126 AA;  
 Query Match 70.2%; Score 73; DB 12; Length 126;  
 Best Local Similarity 85.7%; Pred. No. 3.13e+00;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Db 101 ywyfdiv 107  
 :|||||  
 QY 5 FYWYFDV 11  
 RESULT 8  
 ID R62879 standard; protein; 126 AA.  
 AC R62879;  
 DT 18-JUL-1995 (first entry)  
 DE Murine anti-human atherosclerotic plaque MAb 22D3 VH sequence.  
 KW Atherosclerosis; atherosclerotic plaque; anti-hydroxysteroid antibody;  
 KW murine monoclonal antibody; heavy chain variable region;

KW imaging; plaque ablation.  
 OS Mus musculus.  
 FH Key Location/Qualifiers  
 FT Misc difference 2  
 FT /note= "lys at this position in R62879 and  
 FT Gln at this position in R62880; also, the  
 FT first 8 amino acids are dictated by the  
 FT oligonucleotides used in the PCR and are  
 FT not necessarily identical to those of the  
 FT murine antibody"  
 FT Region 30..34  
 FT /label= CDR1  
 FT Region 49..65  
 FT /label= CDR2  
 FT Region 98..107  
 FT /label= CDR3  
 FT Region 120..126  
 FT /label= CH1  
 FT /note= "start of constant region"  
 PN W09425053-A.  
 PD 10-NOV-1994.  
 PE 26-APR-1994; U04641.  
 PR 26-APR-1993; US-053451.  
 PA (SCOT-) SCOTGEN BIOPHARMACEUTICALS INC.  
 PI Calenoff E, Chen FW, Dittlow CC;  
 DR WPI; 94-357904/44.  
 DR N-PSDB; Q78730.  
 PT New antigen comprising hydroxy:steroid and quat. ammonium salt -  
 PT and related antibodies, useful e.g. for imaging, ablating or  
 PT treating atherosclerotic plaque, and detecting plaque specific  
 PT antibodies  
 PS Claim 194; Page 145; 288pp; English.  
 CC Mice were immunised with an extract of human atherosclerotic plaque,  
 CC then spleen cells were fused with SP2/01-Ag-14 myeloma cells.  
 CC Hybridomas were screened by ELISA for reactivity with the immunogen  
 CC and clone 22D3 was isolated. The 22D3 antibody reacts specifically  
 CC with atherosclerotic tissue; it recognises a non-protein antigen  
 CC containing cholesterol (or similar steroid that is a substrate for  
 CC cholesterol oxidase) and a quaternary ammonium salt (pref. a  
 CC phosphatidylcholine or related compound that is a substrate for  
 CC phospholipase C).  
 SQ Sequence 126 AA;  
 Query Match 70.2%; Score 73; DB 12; Length 126;  
 Best Local Similarity 85.7%; Pred. No. 3.13e+00;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Db 101 ywyfdiv 107  
 :|||||  
 QY 5 FYWYFDV 11  
 RESULT 9  
 ID R04937 standard; protein; 106 AA.  
 AC R04937;  
 DT 10-MAR-1993 (revised)  
 DT 28-SEP-1990 (first entry)  
 DE Sequence of human carcinoembryonic heavy chain antigen (CEA).  
 KW Carcinoembryonic antigen; CEA; Chelate-specific antigen; CEA;  
 KW tumor; cancer; serum sickness.  
 OS Homo sapiens.  
 PN EP-369566-A.  
 PD 23-MAY-1990.  
 PF 8-MAR-1989; 302313.

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US-08-612-929-26 tag

9

PR 17-NOV-1988; US-274105.  
 PA (HYBR-) Hybritech Inc.  
 PI Johnson MJ, Phelps JL;  
 DR WPI; 90-157695/21.  
 DR N-PSDB; Q04593.  
 PT Bifunctional chimeric antibodies -  
 PT having variable regions which recognise different antigens and  
 PT metal chelates and human constant regions.  
 PS Claim 1; Page 24; 40pp; English.  
 CC CEA heavy chain antigen, useful in generating chimeric monoclonal  
 CC antibody binding to CEA at a tumour site and a metal chelate bonded  
 CC to say a toxin or other drug.  
 SQ Sequence 106 AA;

Query Match 63.5%; Score 66; DB 1; Length 106;  
 Best Local Similarity 100.0%; Pred. No. 1.33e+01;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 89 ywyfdv 94  
 |||||  
 QY 6 YWYFDV 11

RESULT 10

ID R88846 standard; Protein; 121 AA.  
 AC R88846;  
 DT 10-OCT-1996 (first entry)  
 DE Murine antibody ZCE-025 heavy chain variable region.  
 KW Heavy chain; variable region; murine; tumour antigen; antibody;  
 KW ZCE-025; construction; CDR switched variable light chain region;  
 KW kappa-body fragment; in vitro; in vivo; diagnosis; therapy;  
 KW naked antibody; radioimmunotherapy; radioimmunodiagnosis;  
 KW radioimmunometric assays; ELISA; immunohistochemical;  
 KW complementarity determining region.  
 OS Mus musculus.  
 PN W09606625-A1.  
 PD 07-MAR-1996.  
 PF 25-AUG-1995; U10791.  
 PR 26-AUG-1994; US-296625.  
 PA (ELIL) LILLY & CO ELI.  
 PI Ill CR, Ludwig JR, Rathnachalam R;  
 DR WPI; 96-160137/16.  
 DR N-PSDB; T12813.  
 PT Recombinant antibody comprising CDR-switched light chain variable  
 PT region - having VL domain framework and VH domain CDRs, useful in  
 PT radioimmunotherapy, ELISA assays, etc.  
 PS Example 1; Page 61; 162pp; English.  
 CC The present sequence is the heavy chain variable (HL) region  
 CC of the murine anti-ZCE-025 tumour antigen antibody (Ab). ZCE-025,  
 CC which was used in the construction of a CDR switched light chain  
 CC variable (VL) region (CSVL) Ab, or kappa-body fragment. A CSVL  
 CC comprises at least 1 VL region with 3 CDR, where 1 or more of the  
 CC CDR is derived from the corresponding CDR of a VH region of 1  
 CC (donor) Ab, and 4 framework (FW) regions where 1 or more of the  
 CC regions is derived from the corresponding FW region(s) from the VL  
 CC region of the same or different (acceptor) Ab.  
 CC The CSVL Ab, or kappa-body fragment can be used in in vitro and  
 CC in vivo diagnostic and therapeutic applications, including naked Ab  
 CC therapy, radioimmunotherapy (i.e. when fused to a chelating peptide  
 CC incorporating Yttrium-90 as the therapeutic radioion), in vivo  
 CC radioimmunodiagnosis, in vitro radioimmunometric assays, ELISA  
 CC and immunohistochemical applications.  
 SQ Sequence 121 AA;

Mar 18 10:15

US-08-612-929-26 tag

10

Query Match 63.5%; Score 66; DB 18; Length 121;  
 Best Local Similarity 100.0%; Pred. No. 1.33e+01;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 105 ywyfdv 110  
 |||||  
 QY 6 YWYFDV 11

RESULT 11

ID R79878 standard; Protein; 122 AA.  
 AC R79878;  
 DT 24-MAY-1996 (first entry)  
 DE Anti-EGFR antibody heavy chain variable region (Clone L2 8C).  
 KW Single chain antibody; antibody; epidermal growth factor receptor;  
 KW EGFR; tumour; cancer; glioma; melanoma; carcinoma; diagnosis;  
 KW assessment; phage antibody library.  
 OS Mus musculus.  
 FH Key Location/Qualifiers  
 FT Region 1..30  
 FT /label= Framework region 1.  
 FT Region 31..35  
 FT /label= CDR1.  
 FT Region 36..49  
 FT /label= Framework region 2.  
 FT Region 50..65  
 FT /label= CDR2.  
 FT Region 66..97  
 FT /label= Framework region 3.  
 FT Region 98..111  
 FT /label= CDR3.  
 FT Region 112..122  
 FT /label= Framework region 4.  
 PN W09525167-A1.  
 PD 21-SEP-1995.  
 PF 16-MAR-1995; E00978.  
 PR 17-MAR-1994; EP-104160.  
 PR 02-DEC-1994; EP-118970.  
 PA (MERE) MERCK PATENT GMBH.  
 PI Adan J, Ansell KH, Bendig MM, Blasco F, Guesow D;  
 PI Kettleborough AC, Mitjans F, Piulats J, Rosell E;  
 DR WPI; 95-336972/43.  
 PT Anti-EGFR antibodies and single chain Fv antibody fragments -  
 PT obtained from phage-antibody libraries, useful for diagnosis and  
 PT therapy of tumours  
 PS Disclosure; Figure 1A; 93pp; English.  
 CC Anti-epidermal growth factor receptor (EGFR) single chain antibodies  
 CC and antibodies constructed from anti-EGFR antibody fragments can be  
 CC used for diagnosis of tumours and assessment of tumour growth in  
 CC vitro and in vivo. They may also be used in a pharmaceutical  
 CC composition for the therapy of e.g. melanomas, gliomas and carcinomas.  
 CC The antibodies and fragments are derived from mice but are humanised  
 CC so as to cause minimum reaction against them. They are produced  
 CC using the phage antibody library. (See T04011-T04026 and  
 CC R79858-R79873)  
 SQ Sequence 122 AA;

Query Match 63.5%; Score 66; DB 16; Length 122;  
 Best Local Similarity 100.0%; Pred. No. 1.33e+01;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 106 ywyfdv 111  
 |||||  
 QY 6 YWYFDV 11

Mar 18 10:15

US-08-612-929-26.rag

11

RESULT 12  
ID P91382 standard; protein; 122 AA.  
AC P91382;  
DT 10-MAR-1993 (revised)  
DE Antibody heavy chain variable region against carcinoembryonic antigen.  
KW Carcinoembryonic antigen; immunogen; tumour; chimeric antibody.  
OS Murine (mouse) hybridoma CEM 231.6.7 (ATCC HB 9620).  
PN EP-332424-A.  
PD 13-SEP-1989.  
PF 08-MAR-1989; 302312.  
PR 09-MAR-1988; US-272577.  
PA (HYBR) Hybritech Inc.  
PI Beidler CB, Johnson MJ, Ludwig JR, Carlo DJ, David GS;  
DR WPI; 89-265635/37.  
DR N-PSDB; P91382.  
PT DNA constructs encoding light or heavy chain variable regions  
PT - chimeric monoclonal antibody, specific for human  
PT carcinoembryonic antigen, useful for diagnosis, imaging and  
PT treatment of tumours.  
PS Claim 6; page 18; 32pp; English.  
CC This region is encoded in a DNA construct with light chain variable  
CC and constant regions, heavy chain constant region, and 2 eukaryotic  
CC leader sequences. The chimeric monoclonal antibodies thus formed  
CC can be directed against CEA for immunoassay, and imaging and  
CC treatment of tumours, eg colorectal or breast carcinoma. The  
CC constant regions are human-derived and so are less immunogenic  
CC than entirely murine Abs.  
SQ Sequence 122 AA;

Query Match 63.5%; Score 66; DB 1; Length 122;  
Best Local Similarity 100.0%; Pred. No. 1.33e+01;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 105 ywyfdv 110  
|||||  
QY 6 YWYFDV 11

RESULT 13  
ID W02201 standard; Protein; 122 AA.  
AC W02201;  
DT 10-OCT-1996 (first entry)  
DE CDR switched variable light chain region kappa-body fragment.  
KW Variable region; murine; human; tumour antigen; plasmacytoma;  
KW antibody; ZCE-025; IM9; construction; in vitro; in vivo;  
KW CDR switched variable light chain region; kappa-body fragment;  
KW diagnosis; therapy; naked antibody; radioimmunotherapy;  
KW radioimmunodiagnosics; radioimmunometric assays; ELISA;  
KW immunohistochemical; complementarity determining region.  
OS Synthetic.  
PN W0960625-A1.  
PD 07-MAR-1996.  
PF 25-AUG-1995; U10791.  
PR 26-AUG-1994; US-296625.  
PA (ELIL) LILLY & CO ELI.  
PI ILL CR, Ludwig JR, Rathnachalam R;  
DR WPI; 96-160137/16.  
PT Recombinant antibody comprising CDR-switched light chain variable  
PT region - having VL domain framework and VH domain CDRs, useful in  
PT radioimmunotherapy, ELISA assays, etc.  
PS Example 7; Page 92; 162pp; English.

Mar 18 10:15

US-08-612-929-26.rag

12

CC The present sequence is a CDR switched light chain variable (VL)  
CC region (CSVL) kappa fragment, constructed using the heavy chain  
CC variable (VH) region of the murine anti-ZCE-025 tumour antigen  
CC antibody (Ab), ZCE-025, and the VL region of the human plasmacytoma  
CC cell line IM9 Ab, IM9. A CSVL comprises at least 1 VL region  
CC with 3 CDR, where 1 or more of the CDR is derived from the  
CC corresponding CDR of a heavy chain variable (VH) region of 1  
CC (donor) Ab, and 4 framework (FW) regions where 1 or more of the  
CC regions is derived from the corresponding FW region(s) from the VL  
CC region of the same or different (acceptor) Ab.  
CC The CSVL Ab, or kappa-body fragment can be used in vitro and  
CC in vivo diagnostic and therapeutic applications, including naked Ab  
CC therapy, radioimmunotherapy (i.e. when fused to a chelating peptide  
CC incorporating Yttrium-90 as the therapeutic radioion), in vivo  
CC radioimmunodiagnosics, in vitro radioimmunometric assays, ELISA  
CC and immunohistochemical applications.  
SQ Sequence 122 AA;

Query Match 63.5%; Score 66; DB 18; Length 122;  
Best Local Similarity 100.0%; Pred. No. 1.33e+01;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 106 ywyfdv 111  
|||||  
QY 6 YWYFDV 11

RESULT 14  
ID R79877 standard; Protein; 123 AA.  
AC R79877;  
DT 24-MAY-1996 (first entry)  
DE Anti-EGFR antibody heavy chain variable region (Clone L2 1C).  
KW Single chain antibody; antibody; epidermal growth factor receptor;  
KW EGFR; tumour; cancer; glioma; melanoma; carcinoma; diagnosis;  
KW assessment; phage antibody library.  
OS Mus musculus.

FH Key Location/Qualifiers  
FT Region 1..30  
FT /label= Framework region 1.  
FT Region 31..35  
FT /label= CDR1.  
FT Region 36..49  
FT /label= Framework region 2.  
FT Region 50..66  
FT /label= CDR2.  
FT Region 67..98  
FT /label= Framework region 3.  
FT Region 99..112  
FT /label= CDR3.  
FT Region 113..123  
FT /label= Framework region 4.  
PN W09525167-A1.  
PD 21-SEP-1995.  
PF 16-MAR-1995; E00978.  
PR 17-MAR-1994; EP-104160.  
PR 02-DEC-1994; EP-118970.  
PA (MERE) MERCK PATENT GMBH.  
PI Adan J, Ansell KH, Bendig MM, Blasco F, Guessow D;  
PI Kettleborough AC, Mitjans F, Piulats J, Rosell E;  
DR WPI; 95-336972/43.  
PT Anti-EGFR antibodies and single chain Fv antibody fragments -  
PT obtained from phage-antibody libraries, useful for diagnosis and  
PT therapy of tumours  
PS Disclosure; Figure 1A; 93pp; English.

Mar 18 10:15

13

US-08-612-929-26.rag

CC Anti-epidermal growth factor receptor (EGFR) single chain antibodies  
CC and antibodies constructed from anti-EGFR antibody fragments can be  
CC used for diagnosis of tumours and assessment of tumour growth in  
CC vitro and in vivo. They may also be used in a pharmaceutical  
CC composition for the therapy of e.g. melanomas, gliomas and carcinomas.  
CC The antibodies and fragments are derived from mice but are humanised  
CC so as to cause minimum reaction against them. They are produced  
CC using the phage antibody library. (See T04011-T04026 and  
CC R79858-R79873)  
SQ Sequence 123 AA;

Query Match 63.5%; Score 66; DB 16; Length 123;  
Best Local Similarity 100.0%; Pred. No. 1.33e+01;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 107 ywyfdv 112  
|||||  
Qy 6 YWYFDV 11

#### RESULT 15

ID P94780 standard; protein; 140 AA.  
AC P94780;  
DT 06-JUL-1990 (first entry)  
DE 2 H7 VH gene.  
KW Antibodies; passive immunisation; pH3-12a; ss.  
OS Synthetic.  
FH Key Location/Qualifiers  
FT Peptide 1..19  
FT /label=Leader: peptide.  
FT Domain 20..49  
FT /label=FR1.  
FT Domain 50..54  
FT /label=CDR1  
FT Domain 55..68  
FT /label=FR2  
FT Domain 69..85  
FT /label=CDR2.  
FT Domain 86..117  
FT /label=FR3.  
FT Domain 118..130  
FT /label=CDR3.  
FT Domain 131..140  
FT /label=FR4.  
FT Domain 108..123  
FT /label=JK2  
PN W08900999-A.  
PD 9-FEB-1989.  
PF 25-JUL-1988; 02514.  
PR 24-JUL-1987; US-077528.  
PA (ITGE-) Int Genetic Eng Inc.  
PI Robinson RR, Liu AY, Horwitz AH, Wall R, Better M;  
DR WPI; 89-061144/08.  
DR N-PSDB; N91146.  
PT Polynucleotide(s) encoding immunoglobulin molecules -  
PT used for efficient prodn. of chimeric human or non-human or  
PT class switched antibodies.  
PS Dielosure; 7pp; English.  
CC Sequence carries the variable region of the chimeric immunoglobulin  
CC sequence. The antibodies are useful in passive immunisation avoiding  
CC negative immune reactions. They are also useful in assaying and in vitro  
CC imaging.  
SQ Sequence 140 AA;

Mar 18 10:15

US-08-612-929-26.rag

14

Query Match 63.5%; Score 66; DB 1; Length 140;  
Best Local Similarity 100.0%; Pred. No. 1.33e+01;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Db 125 ywyfdv 130  
|||||  
Qy 6 YWYFDV 11

Search completed: Tue Mar 18 10:17:10 1997  
Job time : 12 secs.

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WQSNL (TM)

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MPerch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Mar 18 10:17:27 1997; MasPar time 1.76 Seconds  
Tabular output not generated. 94.634 Million cell updates/sec

Title: >US-08-612-929-28  
Description: (1-9) from US08612929.pep  
Perfect Score: 60  
Sequence: 1 QQSNEPPR 9

Scoring table: PAM 150  
Gap 15

Searched: 52205 seqs, 18531385 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: swiss-prot33  
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10

Statistics: Mean 20.411; Variance 22.437; scale 0.910

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	47	78.3	277	5 J11_HCMVA	HYPOTHETICAL PROTEIN	5.76e-01
2	44	73.3	514	5 MP11_MOUSE	M-PHASE INDUCER PHOSP	2.89e+00
3	44	73.3	525	6 NCAP_MEASI	NUCLEOCAPSID PROTEIN.	2.89e+00
4	44	73.3	823	2 CRYW_BACTA	130 KD CRYSTAL PROTEI	2.89e+00
5	44	73.3	1189	2 CRYT_BACTE	134 KD CRYSTAL PROTEI	2.89e+00
6	43	71.7	111	5 KV3M_MOUSE	IG KAPPA CHAIN V-III	4.87e+00
7	43	71.7	111	5 KV3Q_MOUSE	IG KAPPA CHAIN V-III	4.87e+00
8	43	71.7	111	5 KV3H_MOUSE	IG KAPPA CHAIN V-III	4.87e+00
9	43	71.7	111	5 KV3L_MOUSE	IG KAPPA CHAIN V-III	4.87e+00
10	43	71.7	111	5 KV3N_MOUSE	IG KAPPA CHAIN V-III	4.87e+00
11	43	71.7	111	5 KV3O_MOUSE	IG KAPPA CHAIN V-III	4.87e+00
12	43	71.7	132	5 KV3F_MOUSE	IG KAPPA CHAIN PRECUR	4.87e+00
13	42	70.0	194	10 YPE4_NFVLD	HYPOTHETICAL 20.6 KD	8.14e+00

14	42	70.0	847	10 YAF6_YEAST	HYPOTHETICAL 95.1 KD	8.14e+00
15	41	68.3	268	5 MIND_BACSU	SEPTUM SITE-DETERMINI	1.35e+01
16	41	68.3	295	6 MYRA_MICGR	MYCINAMICIN-RESISTANC	1.35e+01
17	40	66.7	111	5 KV3K_MOUSE	IG KAPPA CHAIN V-III	2.21e+01
18	40	66.7	111	5 KV3J_MOUSE	IG KAPPA CHAIN V-III	2.21e+01
19	40	66.7	131	5 KV3I_MOUSE	IG KAPPA CHAIN PRECUR	2.21e+01
20	40	66.7	497	5 LMP2_EBV	GENE TERMINAL PROTEIN	2.21e+01
21	40	66.7	914	1 AZF1_YEAST	ASPARAGINE-RICH ZINC	2.21e+01
22	40	66.7	1431	9 TOP2_SCHPO	DNA TOPOISOMERASE II	2.21e+01
23	39	65.0	109	10 YCKK_HAEIN	HYPOTHETICAL PROTEIN	3.59e+01
24	39	65.0	207	6 NEF_HVIND	NEGATIVE FACTOR (F-PR	3.59e+01
25	39	65.0	347	5 MAGP_HUMAN	MELANOMA-ASSOCIATED A	3.59e+01
26	39	65.0	367	5 IPOU_DROME	INHIBITORY POU PROTEI	3.59e+01
27	39	65.0	375	3 DEK_HUMAN	DEK PROTEIN.	3.59e+01
28	39	65.0	414	7 PRS3_CAEEL	PROBABLE 26S PROTEASE	3.59e+01
29	39	65.0	416	3 FILA_HUMAN	FILAGGRIN PRECURSOR (	3.59e+01
30	39	65.0	446	10 YCAJ_HAEIN	HYPOTHETICAL PROTEIN	3.59e+01
31	39	65.0	472	5 IN14_HUMAN	INTERFERON-INDUCED 54	3.59e+01
32	39	65.0	509	10 YB19_YEAST	HYPOTHETICAL 57.1 KD	3.59e+01
33	39	65.0	581	7 PRIM_ECOLI	DNA PRIMASE (EC 2.7.7	3.59e+01
34	39	65.0	584	4 GUND_GLOCE	ENDOGALACTINASE D PRECU	3.59e+01
35	39	65.0	590	9 VG28_HSV11	HYPOTHETICAL GENE 28	3.59e+01
36	39	65.0	648	1 BGLR_RAT	BETA-GLUCURONIDASE PR	3.59e+01
37	39	65.0	648	1 BGLR_MOUSE	BETA-GLUCURONIDASE PR	3.59e+01
38	39	65.0	730	3 ERG7_YEAST	LANOSTEROL SYNTHASE (	3.59e+01
39	39	65.0	1260	6 NEU_RAT	NEU ONCOGENE PRECURSO	3.59e+01
40	38	63.3	78	6 MULI_NORMO	MAJOR OUTER MEMBRANE	5.78e+01
41	38	63.3	160	5 MAX_HUMAN	MAX PROTEIN.	5.78e+01
42	38	63.3	200	10 YM62_CAEEL	HYPOTHETICAL 23.2 KD	5.78e+01
43	38	63.3	273	4 GVPL_HALSA	GVPL PROTEIN.	5.78e+01
44	38	63.3	983	5 KHEK_HUMAN	TYROSINE-PROTEIN KINA	5.78e+01
45	38	63.3	983	5 KEK4_MOUSE	TYROSINE-PROTEIN KINA	5.78e+01

## ALIGNMENTS

RESULT	1	STANDARD;	PRT;	277 AA.
ID	J11_HCMVA			
AC	P09711;			
DT	01-MAR-1989 (REL. 10, CREATED)			
DT	01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)			
DT	01-FEB-1991 (REL. 17, LAST ANNOTATION UPDATE)			
DE	HYPOTHETICAL PROTEIN HKREX (J11).			
OS	HUMAN CYTOMEALOVIRUS (STRAIN AD169).			
OC	VIRIDAE; DS-DNA ENVELOPED VIRUSES; HERPESVIRIDAE; BETAHERPESVIRINAE.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE; 87169717.			
RA	WESTON K., BARRELL B.G.;			
RL	J. MOL. BIOL. 192:177-208 (1986).			
RN	[2]			
RP	COMPLETE GENOME.			
RX	MEDLINE; 90269039.			
RA	CHEE M.S., BANKIER A.T., BECK S., BOHNI R., BROWN C.M., CERNY R.,			
RA	HORSNELL T., HUTCHISON C.A. III, KOUZARIDES T., MARTIGNETTI J.A.,			
RA	PREDDIE E., SATCHWELL S.C., TOMLINSON P., WESTON K.M., BARRELL B.G.;			
RL	CURR. TOP. MICROBIOL. IMMUNOL. 154:125-169 (1990).			
DR	EMBL; X17403; -; NOT ANNOTATED_CDS.			
DR	EMBL; X04650; E3275; ALT_SEQ.			
DR	PIR; B26078; QQBEC2.			
KW	HYPOTHETICAL PROTEIN.			
FT	CARBOHYD 50 50			POTENTIAL.
FT	CARBOHYD 233 233			POTENTIAL.
SQ	SEQUENCE 277 AA; 29115 MW; 1B1F5DCB CRC32;			

Mar 18 10:15

US-08-612-929-28.rsp

3

Query Match 78.3%; Score 47; DB 5; Length 277;  
Best Local Similarity 77.8%; Pred. No. 5.76e-01;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 97 qhsledppr 105  
:|:|||||  
Qy 1 QQSNEPPR 9

RESULT 2

ID MP11\_MOUSE STANDARD; PRT; 514 AA.  
AC P48964;  
DT 01-FEB-1996 (REL. 33, CREATED)  
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)  
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)  
DE M-PHASE INDUCER PHOSPHATASE 1 (EC 3.1.3.48).  
GN CDC25A OR CDC25M3.  
OS MUS MUSCULUS (MOUSE).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; RODENTIA.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 95361758.  
RA WICKRAMASINGHE D., BECKER S., ERNST M.K., RESNICK J.L.,  
RA CANTIANI J.M., TESSAROLLO L., GRABEL L.B., DONOVAN P.J.;  
RL DEVELOPMENT 121:2047-2056(1995).  
CC -!- FUNCTION: THIS PROTEIN FUNCTIONS AS A DOSAGE-DEPENDENT INDUCER IN  
CC MITOTIC CONTROL. IT IS A TYROSINE PROTEIN PHOSPHATASE REQUIRED FOR  
CC PROGRESSION OF THE CELL CYCLE. IT MAY DIRECTLY DEPHOSPHORYLATE  
CC P34(CDC2) AND ACTIVATE THE P34(CDC2) KINASE ACTIVITY.  
CC -!- CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)O =  
CC PROTEIN TYROSINE + ORTHOPHOSPHATE.  
CC -!- SIMILARITY: STRONG, TO OTHER SPECIES M-PHASE INDUCER PHOSPHATASE  
CC AND IN GENERAL TO PROTEIN-TYROSINE PHOSPHATASES.  
DR EMBL; U73233; G862992; -.  
KW CELL DIVISION; MITOSIS; HYDROLASE; MULTIGENE FAMILY.  
FT ACT SITE 421 421 BY SIMILARITY.  
SQ SEQUENCE 514 AA; 57758 MW; EDECB85C CRC32;

Query Match 73.3%; Score 44; DB 5; Length 514;  
Best Local Similarity 55.6%; Pred. No. 2.89e+00;  
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 269 drsheeppr 277  
:|:|||||  
Qy 1 QQSNEPPR 9

RESULT 3

ID NCAP\_MEASI STANDARD; PRT; 525 AA.  
AC P26029;  
DT 01-MAY-1992 (REL. 22, CREATED)  
DT 01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)  
DT 01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)  
DE NUCLEOCAPSID PROTEIN.  
GN NP OR N.  
OS MEASLES VIRUS (STRAIN IP-3-CA) (SUBACUTE SCLEROSE PANENCEPHALITIS  
OS VIRUS).  
OC VIRIDAE; SS-RNA ENVELOPED VIRUSES; NEGATIVE-STRAND; PARAMYXOVIRIDAE;  
OC MORBILLIVIRUSES.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 92263801.

Mar 18 10:15

US-08-612-929-28.rsp

4

RA SCHMID A., SPIELHOFER P., CATTANEO R., BACZKO K., TER MEULEN V.,  
RA BILLETTER M.A.;  
RL VIROLOGY 188:910-915(1992).  
CC -!- FUNCTION: MOST ABUNDANT PROTEIN IN THE VIRION AND AN IMPORTANT  
CC ELEMENT CONFERRING HELICAL SYMMETRY ON THE NUCLEOPROTEIN CORE AS  
CC WELL AS INTERACTING WITH M PROTEIN DURING VIRION FORMATION.  
CC -!- SIMILARITY: TO OTHER PARAMYXOVIRUSES NUCLEOCAPSID PROTEINS.  
DR EMBL; X16566; G60539; -.  
KW NUCLEOCAPSID.  
SQ SEQUENCE 525 AA; 58206 MW; 80A2FA0D CRC32;

Query Match 73.3%; Score 44; DB 6; Length 525;  
Best Local Similarity 55.6%; Pred. No. 2.89e+00;  
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 423 dgseneppr 431  
:|:|||||  
Qy 1 QQSNEPPR 9

RESULT 4

ID CRYW\_BACTA STANDARD; PRT; 823 AA.  
AC P10327;  
DT 01-MAR-1989 (REL. 10, CREATED)  
DT 01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)  
DT 01-MAY-1991 (REL. 18, LAST ANNOTATION UPDATE)  
DE 130 KD CRYSTAL PROTEIN (DELTA ENDOTOXIN) (CRYSTALLINE ENTOMOCIDAL  
DE PROTOXIN) (FRAGMENT).  
OS BACILLUS THURINGIENSIS (SUBSP. AIZAWAI).  
OC PROKARYOTA; FIRMICUTES; ENDOSPORE-FORMING RODS AND COCCI; BACILLACEAE.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=7-29;  
RX MEDLINE; 89343627.  
RA SANCHIS V., LERECHUS D., MENOUE M., CHAUFAX J., GUO S., LECADET M.M.;  
RL MOL. MICROBIOL. 3:229-238(1989).  
CC -!- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT  
CC EPITHELIAL CELLS OF INSECTS.  
CC -!- TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE N-TERMINUS.  
CC -!- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING  
CC SPOULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART  
CC OF THE SPORE COAT.  
DR EMBL; X13620; G40356; -.  
DR PIR; S04181; S04181.  
DR HSSP; P07130; IDUC.  
KW TOXIN; SPOULATION.  
FT NON TER 823 823  
SQ SEQUENCE 823 AA; 92854 MW; B17D932D CRC32;

Query Match 73.3%; Score 44; DB 2; Length 823;  
Best Local Similarity 44.4%; Pred. No. 2.89e+00;  
Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 344 reangeppr 352  
:|:|||||  
Qy 1 QQSNEPPR 9

RESULT 5

ID CRYT\_BACTE STANDARD; PRT; 1189 AA.  
AC P05518;  
DT 01-NOV-1988 (REL. 09, CREATED)  
DT 01-NOV-1988 (REL. 09, LAST SEQUENCE UPDATE)  
DT 01-MAY-1991 (REL. 18, LAST ANNOTATION UPDATE)



DE 134 KD CRYSTAL PROTEIN (DELTA ENDOTOXIN) (CRYSTALLINE ENTOMOCIDAL  
 DE PROTOXIN).  
 OS BACILLUS THURINGIENSIS (SUBSP. ENTOMOCIDUS).  
 OC PROKARYOTA; FIRMICUTES; ENDOSPORE-FORMING RODS AND COCCI; BACILLACEAE.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=60.5;  
 RX MEDLINE; 88289380.  
 RA HONEE G., VAN DER SALT T.P.M., VISSER B.;  
 RL NUCLEIC ACIDS RES. 16:6240-6240(1988).  
 CC -!- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT  
 CC EPITHELIAL CELLS OF SPIDOPTERA SPECIES.  
 CC -!- TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE N-TERMINUS.  
 CC -!- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING  
 CC SPOULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART  
 CC OF THE SPORE COAT.  
 DR EMBL; X07518; G40294; -.  
 DR PIR; S00944; S00944.  
 DR HSP; P07130; IDIC.  
 KW TOXIN; SPOULATION.  
 SQ SEQUENCE 1189 AA; 134836 MW; 30C5D51C CRC32;

Query Match 73.3%; Score 44; DB 2; Length 1189;  
 Best Local Similarity 44.4%; Pred. No. 2.89e+00;  
 Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 344 reanqppr 352  
 QY :::::||||  
 1 QQSNEPDR 9

RESULT 6  
 ID KV3M MOUSE STANDARD; PRT; 111 AA.  
 AC P01655;

DT 21-JUL-1986 (REL. 01, CREATED)  
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)  
 DE IG KAPPA CHAIN V-III REGION (PC 7043).  
 OS MUS MUSCULUS (MOUSE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; RODENTIA.  
 RN [1]  
 RP SEQUENCE.

RX MEDLINE; 79073152.  
 RA WEIGERT M., GATMAITAN L., LOH E., SCHILLING J., HOOD L.E.;  
 RL NATURE 276:785-790(1978).  
 DR PIR; A01937; KWS43.  
 DR HSP; P01679; ICGB.

KW IMMUNOGLOBULIN V REGION.  
 FT DOMAIN 1 23  
 FT DOMAIN 24 38  
 FT DOMAIN 39 53  
 FT DOMAIN 54 60  
 FT DOMAIN 61 92  
 FT DOMAIN 93 101  
 FT DOMAIN 102 111  
 FT DISULFID 23 92  
 FT NON TER 111 111  
 SQ SEQUENCE 111 AA; 12002 MW; ADC728CA CRC32;

Query Match 71.7%; Score 43; DB 5; Length 111;  
 Best Local Similarity 100.0%; Pred. No. 4.87e+00;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 93 qgsnedp 99  
 QY :::::||||  
 1 QQSNEPDR 7

RESULT 7  
 ID KV3Q MOUSE STANDARD; PRT; 111 AA.  
 AC P01659;  
 DT 21-JUL-1986 (REL. 01, CREATED)  
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)  
 DE IG KAPPA CHAIN V-III REGION (PC 7769).  
 OS MUS MUSCULUS (MOUSE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; RODENTIA.  
 RN [1]  
 RP SEQUENCE.

RX MEDLINE; 79073152.  
 RA WEIGERT M., GATMAITAN L., LOH E., SCHILLING J., HOOD L.E.;  
 RL NATURE 276:785-790(1978).  
 DR PIR; E01937; KWS69.  
 DR HSP; P01679; IACY.

KW IMMUNOGLOBULIN V REGION.  
 FT DOMAIN 1 23  
 FT DOMAIN 24 38  
 FT DOMAIN 39 53  
 FT DOMAIN 54 60  
 FT DOMAIN 61 92  
 FT DOMAIN 93 101  
 FT DOMAIN 102 111  
 FT DISULFID 23 92  
 FT NON TER 111 111  
 SQ SEQUENCE 111 AA; 12011 MW; 9CB705B9 CRC32;

Query Match 71.7%; Score 43; DB 5; Length 111;  
 Best Local Similarity 100.0%; Pred. No. 4.87e+00;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 93 qgsnedp 99  
 QY :::::||||  
 1 QQSNEPDR 7

RESULT 8  
 ID KV3H MOUSE STANDARD; PRT; 111 AA.  
 AC P01660;  
 DT 21-JUL-1986 (REL. 01, CREATED)  
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)  
 DE IG KAPPA CHAIN V-III REGION (PC 3741 AND TEPC 111).  
 OS MUS MUSCULUS (MOUSE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; RODENTIA.  
 RN [1]  
 RP SEQUENCE (PC 3741).  
 RX MEDLINE; 79073152.

RX WEIGERT M., GATMAITAN L., LOH E., SCHILLING J., HOOD L.E.;  
 RL NATURE 276:785-790(1978).  
 DR PIR; E01937; KWS69.  
 DR HSP; P01679; IACY.

KW IMMUNOGLOBULIN V REGION.  
 FT DOMAIN 1 23  
 FT DOMAIN 24 38  
 FT DOMAIN 39 53  
 FT DOMAIN 54 60  
 FT DOMAIN 61 92  
 FT DOMAIN 93 101  
 FT DOMAIN 102 111  
 FT DISULFID 23 92  
 FT NON TER 111 111  
 SQ SEQUENCE 111 AA; 12002 MW; ADC728CA CRC32;

Query Match 71.7%; Score 43; DB 5; Length 111;  
 Best Local Similarity 100.0%; Pred. No. 4.87e+00;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DR PIR; A01934; KWSG37.  
DR HSP; P01679; ICGB.  
KW IMMUNOGLOBULIN V REGION.  
FT DOMAIN 1 23  
FT DOMAIN 24 38  
FT DOMAIN 39 53  
FT DOMAIN 54 60  
FT DOMAIN 61 92  
FT DOMAIN 93 101  
FT DOMAIN 102 111  
FT DISULFID 23 92  
FT NON TER 111 111  
SQ SEQUENCE 111 AA; 12099 MW; 7650289 CRC32;

Query Match 71.7%; Score 43; DB 5; Length 111;  
Best Local Similarity 100.0%; Pred. No. 4.87e+00;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 93 qgsndp 99  
|||||||  
Qy 1 QQSNDP 7

## RESULT 9

ID KV3L MOUSE STANDARD; PRT; 111 AA.  
AC P01664;  
DT 21-JUL-1986 (REL. 01, CREATED)  
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)  
DE IG KAPPA CHAIN V-III REGION (CBPC 101).  
OS MUS MUSCULUS (MOUSE).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; RODENTIA.  
RN [1]  
RP SEQUENCE.  
RX MEDLINE; 79012520.  
RA MCKEAN D.J., BELL M., POTTER M.;  
RL PROC. NATL. ACAD. SCI. U.S.A. 75:3913-3917(1978).  
CC -I- THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.  
DR PIR; A01936; KWSG1.  
DR HSP; P01679; ICGB.  
KW IMMUNOGLOBULIN V REGION.  
FT DOMAIN 1 23  
FT DOMAIN 24 38  
FT DOMAIN 39 53  
FT DOMAIN 54 60  
FT DOMAIN 61 92  
FT DOMAIN 93 101  
FT DOMAIN 102 111  
FT DISULFID 23 92  
FT NON TER 111 111  
SQ SEQUENCE 111 AA; 11964 MW; A2AC84C7 CRC32;

Query Match 71.7%; Score 43; DB 5; Length 111;  
Best Local Similarity 100.0%; Pred. No. 4.87e+00;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 93 qgsndp 99  
|||||||  
Qy 1 QQSNDP 7

## RESULT 10

ID KV3N\_MOUSE STANDARD; PRT; 111 AA.

AC P01666;  
DT 21-JUL-1986 (REL. 01, CREATED)  
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)  
DE IG KAPPA CHAIN V-III REGION (PC 7183).  
OS MUS MUSCULUS (MOUSE).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; RODENTIA.  
RN [1]  
RP SEQUENCE.  
RX MEDLINE; 79073152.  
RA WEIGERT M., GATWALTAN L., LOH E., SCHILLING J., HOOD L.E.;  
RL NATURE 276:785-790(1978).  
DR PIR; B01937; KWSG83.  
DR HSP; P01679; ICGB.  
KW IMMUNOGLOBULIN V REGION.  
FT DOMAIN 1 23  
FT DOMAIN 24 38  
FT DOMAIN 39 53  
FT DOMAIN 54 60  
FT DOMAIN 61 92  
FT DOMAIN 93 101  
FT DOMAIN 102 111  
FT DISULFID 23 92  
FT NON TER 111 111  
SQ SEQUENCE 111 AA; 11952 MW; 041902B8 CRC32;

Query Match 71.7%; Score 43; DB 5; Length 111;  
Best Local Similarity 100.0%; Pred. No. 4.87e+00;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 93 qgsndp 99  
|||||||  
Qy 1 QQSNDP 7

## RESULT 11

ID KV3O MOUSE STANDARD; PRT; 111 AA.  
AC P01667;  
DT 21-JUL-1986 (REL. 01, CREATED)  
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)  
DE IG KAPPA CHAIN V-III REGION (PC 6308).  
OS MUS MUSCULUS (MOUSE).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; RODENTIA.  
RN [1]  
RP SEQUENCE.  
RX MEDLINE; 79073152.  
RA WEIGERT M., GATWALTAN L., LOH E., SCHILLING J., HOOD L.E.;  
RL NATURE 276:785-790(1978).  
DR PIR; C01937; KWSG08.  
DR HSP; P01679; ICGB.  
KW IMMUNOGLOBULIN V REGION.  
FT DOMAIN 1 23  
FT DOMAIN 24 38  
FT DOMAIN 39 53  
FT DOMAIN 54 60  
FT DOMAIN 61 92  
FT DOMAIN 93 101  
FT DOMAIN 102 111  
FT DISULFID 23 92  
FT NON TER 111 111  
SQ SEQUENCE 111 AA; 12071 MW; F7865271 CRC32;

Query Match 71.7%; Score 43; DB 5; Length 111;  
Best Local Similarity 100.0%; Pred. No. 4.87e+00;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 93 qgsnedp 99  
:|||||  
Qy 1 QQSNEDP 7

RESULT 12  
ID KV3F MOUSE STANDARD; PRT; 132 AA.  
AC P01658;  
DT 21-JUL-1986 (REL. 01, CREATED)  
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)  
DE IG KAPPA CHAIN PRECURSOR V-III REGION (MOPC 321).  
OS MUS MUSCULUS (MOUSE).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; RODENTIA.  
RN [1]  
RP SEQUENCE OF 1-37.  
RX MEDLINE; 78235887.  
RA BURSTEIN Y., SCHECHTER I.;  
RL BIOCHEMISTRY 17:2392-2400(1978).  
RN [2]  
RP SEQUENCE OF 21-132.  
RX MEDLINE; 73140224.  
RA MCKEAN D.J., POTTER M., HOOD L.E.;  
RL BIOCHEMISTRY 12:749-759(1973).  
CC -/- THE PARTIAL SEQUENCE OF THE C REGION OF THIS BENCE-JONES PROTEIN  
CC WAS ALSO DETERMINED. IT DIFFERS FROM THAT REPORTED FOR MOUSE  
CC MOPC 21 ONLY IN THE TRANSPOSITION OF TWO NEARBY RESIDUES.  
DR PIR; A01933; KVM632.  
DR HSP; P01679; IGB.  
RW IMMUNOGLOBULIN V REGION; BENCE-JONES PROTEIN; SIGNAL.  
FT SIGNAL 1 20  
FT CHAIN 21 132 IG KAPPA CHAIN V-III REGION (MOPC 321).  
FT DOMAIN 21 43 FRAMEWORK 1.  
FT DOMAIN 44 58 COMPLEMENTARITY-DETERMINING 1.  
FT DOMAIN 59 73 FRAMEWORK 2.  
FT DOMAIN 74 80 COMPLEMENTARITY-DETERMINING 2.  
FT DOMAIN 81 112 FRAMEWORK 3.  
FT DOMAIN 113 121 COMPLEMENTARITY-DETERMINING 3.  
FT DOMAIN 122 131 FRAMEWORK 4.  
FT DISULFID 43 112 BY SIMILARITY.  
FT NON\_TER 132 132  
SQ SEQUENCE 132 AA; 14523 MW; E57F824 CRC32;

Query Match 71.7%; Score 43; DB 5; Length 132;  
Best Local Similarity 28.6%; Pred. No. 4.87e+00;  
Matches 2; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 113 zzezbzp 119  
:|||||  
Qy 1 QQSNEDP 7

RESULT 13  
ID YPE4 NPVLD STANDARD; PRT; 194 AA.  
AC P36868;  
DT 01-JUN-1994 (REL. 29, CREATED)  
DT 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)  
DT 01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)

DE HYPOTHETICAL 20.6 KD PROTEIN IN PE 3' REGION (ORF 4).  
OS LYMANTRIA DISPAR MULTICAPSID NUCLEAR POLYHEDROSIS VIRUS (LDMNPV).  
OC VIRIDAE; DS-DNA ENVELOPED VIRUSES; BACULOVIRIDAE; EUBACULOVIRINAE.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 92300345.  
RA BJORNSEN R.M., ROHRMANN G.F.;  
RL J. GEN. VIROL. 73:1499-1504(1992).  
DR EMBL; D10836; E55473; -.  
DR PIR; JQ1560; JQ1560.  
RW HYPOTHETICAL PROTEIN.  
SQ SEQUENCE 194 AA; 20578 MW; F21E7B9A CRC32;

Query Match 70.0%; Score 42; DB 10; Length 194;  
Best Local Similarity 50.0%; Pred. No. 8.14e+00;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 172 qgrdeppr 179  
:|||||  
Qy 2 QSNEDPPR 9

RESULT 14  
ID YAF6 YEAST STANDARD; PRT; 847 AA.  
AC P39717; P39716;  
DT 01-FEB-1995 (REL. 31, CREATED)  
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)  
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)  
DE HYPOTHETICAL 95.1 KD PROTEIN IN CNEL-ACSI INTERGENIC REGION.  
GN YAL056W.  
OS SACCAROMYCES CEREVISIAE (BAKER'S YEAST).  
OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOCYCETES.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-S288C / AB972;  
RX MEDLINE; 95249563.  
RA BUSSEY H., KABACK D.B., ZHONG W., VO D.T., CLARK M.W., FORTIN N.,  
RA HALL J., OUELLETTE B.F.F., KENG T., BARTON A.B., SU Y., DAVIES C.K.,  
RA STORMS R.K.;  
RL PROC. NATL. ACAD. SCI. U.S.A. 92:3809-3813(1995).  
DR EMBL; U12980; G623256; -.  
KW HYPOTHETICAL PROTEIN.  
SQ SEQUENCE 847 AA; 95108 MW; 666443E9 CRC32;

Query Match 70.0%; Score 42; DB 10; Length 847;  
Best Local Similarity 37.5%; Pred. No. 8.14e+00;  
Matches 3; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 772 enddeppr 779  
:|||||  
Qy 2 QSNEDPPR 9

RESULT 15  
ID MIND BACSU STANDARD; PRT; 268 AA.  
AC Q01464;  
DT 01-JUL-1993 (REL. 26, CREATED)  
DT 01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)  
DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)  
DE SEPTUM SITE-DETERMINING PROTEIN MIND.  
GN MIND OR DIVIVB.  
OS BACILLUS SUBTILIS.  
OC PROKARYOTA; FIRMICUTES; ENDOSPORE-FORMING RODS AND COCCI; BACILLACEAE.  
RN [1]

RP SEQUENCE FROM N.A.  
RC STRAIN=168;  
RX MEDLINE; 93015732.  
RA VARLEY A.W., STEWART G.C.;  
RL J. BACTERIOL. 174:6729-6742(1992).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=168;  
RX MEDLINE; 93211302.  
RA LEE S., PRICE C.W.;  
RL MOL. MICROBIOL. 7:601-610(1993).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 93015731.  
RA LEVIN P.A., MARGOLIS P.S., SETLOW P., LOSICK R., SUN D.;  
RL J. BACTERIOL. 174:6717-6728(1992).  
CC -!- FUNCTION: MEMBRANE ATPASE REQUIRED FOR THE CORRECT PLACEMENT  
CC OF THE DIVISION SITE. CELL DIVISION INHIBITORS MINC AND MIND ACT  
CC IN CONCERT TO FORM AN INHIBITOR CAPABLE OF BLOCKING FORMATION OF  
CC THE CELL DIVISION SEPTUM AT ALL POTENTIAL SITES. FTSZ SEEMS TO BE  
CC THE TARGET OF MINCD. MIND PLAYS AN ACCESSORY ROLE, ENHANCING THE  
CC INHIBITORY EFFECT OF MINC AND ALLOWING INTERACTION WITH MINE.  
CC -!- SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED.  
DR EMBL; M95582; G143216; -.  
DR EMBL; Z15113; G580893; -.  
DR EMBL; M96343; G142859; -.  
DR PIR; S31205; S31205.  
DR PIR; G45239; G45239.  
DR PIR; F45240; F45240.  
DR SUBTILIST; BG10330; MIND.  
KW CELL DIVISION; SEPTATION; ATP-BINDING; MEMBRANE.  
FT NP BIND 10 17 ATP (POTENTIAL).  
SQ SEQUENCE 268 AA; 29407 MW; 122E55F1 CRC32;

Query Match 68.3%; Score 41; DB 5; Length 268;  
Best local Similarity 55.6%; Pred.No. 1.35e+01;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 162 qeenleppr 170  
|: | :|||  
Qy 1 QQSNEPPR 9

Search completed: Tue Mar 18 10:17:36 1997  
Job time : 9 secs.

\*\*\*\*\*

WATERMAN

(TM)

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MPerch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Mar 18 10:17:54 1997; MasPar time 3.14 Seconds

Tabular output not generated. 73.712 Million cell updates/sec

Title: >US-08-612-929-28

Description: (1-9) from US08612929, pep

Perfect Score: 60

Sequence: 1 QQSNEPPR 9

Scoring table: PAM 150

Gap 15

Searched: 82182 seqs, 25727515 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: pir48

1:ann1 2:ann2 3:ann3 4:unann1 5:unann2 6:unann3 7:unann4  
8:unann5 9:unann6 10:unann7 11:unann8 12:unann9 13:unann  
14:unrev

Statistics: Mean 19.758; Variance 27.311; scale 0.723

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	49	81.7	209	6	JQ2347	hypothetical 23.6K p 1.53e+00
2	47	78.3	112	5	S19971	Ig kappa chain V reg 3.83e+00
3	47	78.3	131	5	PH1226	Ig kappa chain V reg 3.83e+00
4	47	78.3	277	3	QQBEC2	HKRFX protein - huma 3.83e+00
5	44	73.3	643	12	A43423	dysen 74K chain, cy 1.45e+01
6	44	73.3	823	6	S04181	parasporal crystal p 1.45e+01
7	44	73.3	1176	6	A48970	insecticidal crystal p 1.45e+01
8	44	73.3	1189	6	S00944	parasporal crystal p 1.45e+01
9	43	71.7	65	12	C38601	Ig kappa chain V reg 2.24e+01
10	43	71.7	81	12	S42193	Ig kappa chain V reg 2.24e+01
11	43	71.7	85	12	S42189	Ig kappa chain V reg 2.24e+01
12	43	71.7	87	12	S42190	Ig kappa chain V reg 2.24e+01

13	43	71.7	88	12	S42194	Ig kappa chain V reg 2.24e+01
14	43	71.7	90	12	S42187	Ig kappa chain V reg 2.24e+01
15	43	71.7	96	12	B49442	Ig light chain V reg 2.24e+01
16	43	71.7	107	5	S26344	Ig kappa chain V reg 2.24e+01
17	43	71.7	107	5	S26343	Ig kappa chain V reg 2.24e+01
18	43	71.7	111	2	KVMS31	Ig kappa chain V reg 2.24e+01
19	43	71.7	111	5	S09966	Ig kappa chain V-J r 2.24e+01
20	43	71.7	111	2	KVMS08	Ig kappa chain V reg 2.24e+01
21	43	71.7	111	2	KVMS83	Ig kappa chain V reg 2.24e+01
22	43	71.7	111	5	A33936	Ig kappa chain V reg 2.24e+01
23	43	71.7	111	2	KVMS43	Ig kappa chain V reg 2.24e+01
24	43	71.7	111	2	KVMS37	Ig kappa chain V reg 2.24e+01
25	43	71.7	111	2	KVMS69	Ig kappa chain V reg 2.24e+01
26	43	71.7	132	2	KVMS32	Ig kappa chain V reg 2.24e+01
27	42	70.0	67	5	PH1081	Ig light chain V reg 3.43e+01
28	42	70.0	194	6	JQ1560	hypothetical 20.6K p 3.43e+01
29	42	70.0	303	12	A40807	membrane glycoprotein 3.43e+01
30	42	70.0	847	9	S51965	hypothetical protein 3.43e+01
31	41	68.3	268	8	G45239	septum placement det 5.21e+01
32	41	68.3	306	12	S59863	polyA binding protei 5.21e+01
33	40	66.7	65	12	B38601	Ig kappa chain V reg 7.87e+01
34	40	66.7	93	12	A38601	Ig kappa chain V reg 7.87e+01
35	40	66.7	102	5	PH1078	Ig light chain V reg 7.87e+01
36	40	66.7	111	12	D45722	anti-glycoprotein H 7.87e+01
37	40	66.7	131	2	KVMSW6	Ig kappa chain V reg 7.87e+01
38	40	66.7	497	3	WMBELM	membrane protein IMP 7.87e+01
39	40	66.7	715	12	A53209	adseverin - bovine 7.87e+01
40	40	66.7	914	14	S61671	hypothetical protein 7.87e+01
41	40	66.7	914	9	S46593	asparagine-rich zinc 7.87e+01
42	40	66.7	1431	1	ISZPT2	DNA topoisomerase (A 7.87e+01
43	39	65.0	509	10	S45413	probable membrane pr 1.18e+02
44	39	65.0	648	4	A32576	beta-glucuronidase ( 1.18e+02
45	39	65.0	731	10	A57741	lanosterol synthase 1.18e+02

## ALIGNMENTS

RESULT 1  
ENTRY JQ2347 #type complete  
TITLE hypothetical 23.6K protein - turkey herpesvirus  
ALTERNATE\_NAMES ORF2 protein  
ORGANISM #formal name turkey herpesvirus  
DATE 30-Sep-1993 #sequence\_revision 20-Aug-1994 #text\_change 20-Aug-1994  
ACCESSION JQ2347  
REFERENCE JQ2346  
#authors Zelnik, V.; Dartell, R.; Audonnet, J.C.; Smith, G.D.; Riviere, M.; Pastorek, J.; Ross, L.J.N.  
#journal J. Gen. Virol. (1993) 74:2151-2162  
#title The complete sequence and gene organization of the short unique region of herpesvirus of turkeys.  
#accession JQ2347  
##molecule type DNA  
##residues 1-209 ##label ZEL  
##cross-references EMBL:X68653  
##experimental source strain FC126  
SUMMARY #length 209 #molecular-weight 23610 #checksum 68  
Query Match 81.7%; Score 49; DB 6; Length 209;  
Best Local Similarity 75.0%; Pred. No. 1.53e+00;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 112 qnneppr 119  
|:|:|:|

Mar 18 10:16

US-08-612-929-28 rpr

3

QY 2 QSQSDPP 9

RESULT 2  
ENTRY  
TITLE Ig kappa chain V region (CD4 mAb clone M-T310 and others) - mouse (fragment)  
ORGANISM #formal\_name Mus musculus #common\_name house mouse  
DATE 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 01-Dec-1995  
ACCESSIONS S19971; S19973  
REFERENCE S19963  
#authors Weissenhorn, W.; Riethmüller, G.; Weiss, E.M.; Rieber, E.P.  
#submission submitted to the EMBL Data Library, March 1992  
#description Structural characterization of CD4 mAb.  
#accession S19971  
##molecule\_type mRNA  
##residues 1-112 #label WEI  
##cross-references EMBL:X65091  
##experimental\_source clone M-T310  
#accession S19973  
##molecule\_type mRNA  
##residues 1-112 #label WEW  
##cross-references EMBL:X65092  
##experimental\_source M-T404  
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology  
SUMMARY #length 112 #checksum 4782

Query Match 78.3%; Score 47; DB 5; Length 112;  
Best Local Similarity 87.5%; Pred. No. 3.83e+00;  
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 93 qsqsdpp 100  
|||||  
QY 1 QSQSDPP 8

RESULT 3  
ENTRY  
TITLE Ig kappa chain precursor V region (M-T310) - human (fragment)  
ORGANISM #formal\_name Homo sapiens #common\_name man  
DATE 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 30-Apr-1995  
ACCESSIONS PH1226  
REFERENCE PH1224  
#authors Weissenhorn, W.; Scheuer, W.; Kaluza, B.; Schwirzke, M.; Reiter, C.; Flieger, D.; Lenz, H.; Weiss, E.H.; Rieber, E.P.; Riethmüller, G.; Weidle, U.H.  
#journal Gene (1992) 121:271-278  
#title Combinatorial functions of two chimeric antibodies directed to human CD4 and one directed to the alpha-chain of the human interleukin-2 receptor.  
#accession PH1226  
##molecule\_type mRNA  
##residues 1-131 #label WEI  
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology  
KEYWORDS immunoglobulin  
FEATURE 1-20  
21-131 #domain signal sequence #status predicted #label SIG  
#product Ig light chain V region #status predicted  
#label MAT  
#length 131 #checksum 4648

Query Match 78.3%; Score 47; DB 5; Length 131;

Mar 18 10:16

US-08-612-929-28 rpr

4

Best Local Similarity 87.5%; Pred. No. 3.83e+00;  
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 113 qsqsdpp 120  
|||||  
QY 1 QSQSDPP 8

RESULT 4  
ENTRY  
TITLE QQBEC2 #type complete  
ORGANISM HKRFX protein - human cytomegalovirus (strain AD169)  
DATE 30-Sep-1989 #sequence\_revision 30-Sep-1989 #text\_change 08-Apr-1994  
ACCESSIONS B26078  
REFERENCE A92935  
#authors Weston, K.; Barrell, B.G.  
#journal J. Mol. Biol. (1986) 192:177-208  
#title Sequence of the short unique region, short repeats, and part of the long repeats of human cytomegalovirus.  
#cross-references MUID:87169717  
#accession B26078  
##molecule\_type DNA  
##residues 1-277 #label WES

COMMENT The DNA sequence was obtained from EMBL, release 13.

GENETICS  
#gene HKRFX  
CLASSIFICATION #superfamily cytomegalovirus HKRFX protein  
SUMMARY #length 277 #molecular-weight 29115 #checksum 4671

Query Match 78.3%; Score 47; DB 3; Length 277;  
Best Local Similarity 77.8%; Pred. No. 3.83e+00;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 97 qheledpp 105  
|||||  
QY 1 QSQSDPP 9

RESULT 5  
ENTRY  
TITLE A43423 #type complete  
ORGANISM dynein 74K chain, cytosolic - rat  
DATE 10-Jun-1993 #sequence\_revision 18-Nov-1994 #text\_change 19-Oct-1995  
ACCESSIONS A43423; S26608  
REFERENCE A43423

#authors Paschal, B.M.; Mikami, A.; Pfister, K.K.; Vallee, R.B.  
#journal J. Cell Biol. (1992) 118:1133-1143  
#title Homology of the 74-kD cytoplasmic dynein subunit with a flagellar dynein polypeptide suggests an intracellular targeting function.

#cross-references MUID:92381100  
#accession A43423  
##status preliminary  
##molecule\_type mRNA  
##residues 1-643 #label PAS  
##cross-references NCBI:111952; NCBI:111953  
##experimental\_source brain  
#note sequence extracted from NCBI backbone  
REFERENCE S26608  
#authors Paschal, B.M.; Mikami, A.; Pfister, K.K.; Vallee, R.B.  
#submission submitted to the EMBL Data Library, June 1992  
#description Molecular cloning of a cytoplasmic dynein subunit: homology

Mar 18 10:16

US-08-612-929-28 mpr

5

with a flagellar dynein polypeptide.

```
#accession      S26608
##status        preliminary
##molecule_type mRNA
##residues      1-643 ##label PAS2
##cross-references EMBL:X66845
SUMMARY         #length 643 #molecular-weight 72754 #checksum 8108
```

```
Query Match      73.3%; Score 44; DB 12; Length 643;
Best Local Similarity 55.6%; Pred. No. 1.45e+01;
Matches          5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
Db      204 qetkeappr 212
      |:~:~:~|
Qy      1 QQSNEDPPR 9
```

```
RESULT      6
ENTRY       S04181 #type fragment
TITLE       parasporal crystal protein - Bacillus thuringiensis (strain
            aizawai 7.29) (fragment)
ALTERNATE_NAMES
ORGANISM     delta-endotoxin
            #formal name Bacillus thuringiensis
DATE         07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change
            30-Sep-1993
ACCESSIONS   S04181
REFERENCE    S04181
#authors     Sanchis, V.; Lereclus, D.; Menou, G.; Chaufaux, J.; Guo, S.;
            Lecadet, M.M.
#journal     Mol. Microbiol. (1989) 3:229-238
#title       Nucleotide sequence and analysis of the N-terminal coding
            region of the Spodoptera-active delta-endotoxin gene of
            Bacillus thuringiensis aizawai 7.29.
#cross-references MUID:89343627
#accession   S04181
##molecule_type DNA
##residues   1-823 ##label SAN
##cross-references EMBL:X13620
```

```
GENETICS     bta
#gene        #superfamily parasporal crystal protein
CLASSIFICATION #length 823 #checksum 803
SUMMARY
```

```
Query Match      73.3%; Score 44; DB 6; Length 823;
Best Local Similarity 44.4%; Pred. No. 1.45e+01;
Matches          4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
```

```
Db      344 reangeppr 352
      |:~:~:~|
Qy      1 QQSNEDPPR 9
```

```
RESULT      7
ENTRY       A48970 #type complete
TITLE       insecticidal crystal toxin CryIC(b) - Bacillus thuringiensis
ORGANISM     #formal name Bacillus thuringiensis
DATE         19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change
            12-Apr-1995
ACCESSIONS   A48970
REFERENCE    A48970
#authors     Kalman, S.; Kiehne, K.L.; Libs, J.L.; Yamamoto, T.
#journal     Appl. Environ. Microbiol. (1993) 59:1131-1137
#title       Cloning of a novel cryIC-type gene from a strain of Bacillus
            thuringiensis subsp. galleriae.
```

Mar 18 10:16

US-08-612-929-28 mpr

6

```
#cross-references MUID:93236401
#accession      A48970
##status        preliminary
##molecule_type nucleic acid
##residues      1-1176 ##label KAL
##cross-references NCBI:129672; NCBI:129675
##experimental_source subsp. galleriae HD29
##note          #sequence extracted from NCBI backbone
CLASSIFICATION #superfamily parasporal crystal protein
SUMMARY         #length 1176 #molecular-weight 132867 #checksum 6917
```

```
Query Match      73.3%; Score 44; DB 6; Length 1176;
Best Local Similarity 44.4%; Pred. No. 1.45e+01;
Matches          4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
```

```
Db      344 reangeppr 352
      |:~:~:~|
Qy      1 QQSNEDPPR 9
```

```
RESULT      8
ENTRY       S00944 #type complete
TITLE       parasporal crystal protein - Bacillus thuringiensis (strain
            entomocidus 60.5)
ORGANISM     #formal name Bacillus thuringiensis
DATE         31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change
            18-Nov-1994
ACCESSIONS   S00944
REFERENCE    S00944
#authors     Honee, G.; van der Salm, T.; Visser, B.
#journal     Nucleic Acids Res. (1988) 16:6240
#title       Nucleotide sequence of crystal protein gene isolated from B.
            thuringiensis subspecies entomocidus 60.5 coding for a
            toxin highly active against Spodoptera species.
#cross-references MUID:88289380
#accession     S00944
##molecule_type DNA
##residues     1-1189 ##label HON
##cross-references EMBL:X07518
#note          translation of nucleotide sequence not given
CLASSIFICATION #superfamily parasporal crystal protein
SUMMARY         #length 1189 #molecular-weight 134836 #checksum 5153
```

```
Query Match      73.3%; Score 44; DB 6; Length 1189;
Best Local Similarity 44.4%; Pred. No. 1.45e+01;
Matches          4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
```

```
Db      344 reangeppr 352
      |:~:~:~|
Qy      1 QQSNEDPPR 9
```

```
RESULT      9
ENTRY       C38601 #type fragment
TITLE       Ig kappa chain V region (2B5) - mouse (fragment)
ORGANISM     #formal_name Mus musculus #common_name house mouse
DATE         30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change
            23-Mar-1993
ACCESSIONS   C38601
REFERENCE    A38601
#authors     Goshorn, S.C.; Retzel, E.; Jemmerson, R.
#journal     J. Biol. Chem. (1991) 266:2134-2142
#title       Common structural features among monoclonal antibodies
            binding the same antigenic region of cytochrome c.
```

Mar 18 10:16

US-08-612-929-28.rpr

7

```
##cross-references MUID:91115823
#accession C38601
##status preliminary
##molecule_type mRNA
##residues 1-65 ##label GOS
##cross-references GB:M57980
SUMMARY #length 65 #checksum 8125

Query Match 71.7%; Score 43; DB 12; Length 65;
Best Local Similarity 100.0%; Pred. No. 2.24e+01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 46 qgsndp 52
|||||
Qy 1 QQSNEP 7

RESULT 10
ENTRY #type fragment
TITLE Ig kappa chain V region - mouse (fragment)
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 07-Oct-1994 #sequence_revision 26-May-1995 #text_change
26-May-1995
ACCESSIONS S42193
REFERENCE S42176
#authors Mo, J.A.; Bona, C.A.; Holmdahl, R.
#journal Eur. J. Immunol. (1993) 23:2503-2510
#title Variable region gene selection of immunoglobulin G-expressing
B cells with specificity for a defined epitope on type II
collagen.
#accession S42193
##status preliminary
##molecule_type DNA
##residues 1-81 ##label MOJ
##cross-references EMBL:Z25456
##note the authors translated the codon GTT for residue 36 as
Ala
SUMMARY #length 81 #checksum 9746

Query Match 71.7%; Score 43; DB 12; Length 81;
Best Local Similarity 100.0%; Pred. No. 2.24e+01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 75 qgsndp 81
|||||
Qy 1 QQSNEP 7

RESULT 11
ENTRY #type fragment
TITLE Ig kappa chain V region - mouse (fragment)
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 28-Sep-1994 #sequence_revision 21-Jul-1995 #text_change
21-Jul-1995
ACCESSIONS S42189
REFERENCE S42176
#authors Mo, J.A.; Bona, C.A.; Holmdahl, R.
#journal Eur. J. Immunol. (1993) 23:2503-2510
#title Variable region gene selection of immunoglobulin G-expressing
B cells with specificity for a defined epitope on type II
collagen.
#accession S42189
##status preliminary
##molecule_type DNA
```

Mar 18 10:16

US-08-612-929-28.rpr

8

```
##residues 1-85 ##label MOJ
##cross-references EMBL:Z25448
SUMMARY #length 85 #checksum 7866

Query Match 71.7%; Score 43; DB 12; Length 85;
Best Local Similarity 100.0%; Pred. No. 2.24e+01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 79 qgsndp 85
|||||
Qy 1 QQSNEP 7

RESULT 12
ENTRY #type fragment
TITLE Ig kappa chain V region - mouse (fragment)
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
13-Jan-1995
ACCESSIONS S42190
REFERENCE S42176
#authors Mo, J.A.; Bona, C.A.; Holmdahl, R.
#journal Eur. J. Immunol. (1993) 23:2503-2510
#title Variable region gene selection of immunoglobulin G-expressing
B cells with specificity for a defined epitope on type II
collagen.
#accession S42190
##status preliminary
##molecule_type DNA
##residues 1-87 ##label MOJ
##cross-references EMBL:Z25450
SUMMARY #length 87 #checksum 2354

Query Match 71.7%; Score 43; DB 12; Length 87;
Best Local Similarity 100.0%; Pred. No. 2.24e+01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 81 qgsndp 87
|||||
Qy 1 QQSNEP 7

RESULT 13
ENTRY #type fragment
TITLE Ig kappa chain V region - mouse (fragment)
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 28-Sep-1994 #sequence_revision 21-Jul-1995 #text_change
21-Jul-1995
ACCESSIONS S42194
REFERENCE S42176
#authors Mo, J.A.; Bona, C.A.; Holmdahl, R.
#journal Eur. J. Immunol. (1993) 23:2503-2510
#title Variable region gene selection of immunoglobulin G-expressing
B cells with specificity for a defined epitope on type II
collagen.
#accession S42194
##status preliminary
##molecule_type DNA
##residues 1-88 ##label MOJ
##cross-references EMBL:Z25458
SUMMARY #length 88 #checksum 4364

Query Match 71.7%; Score 43; DB 12; Length 88;
Best Local Similarity 100.0%; Pred. No. 2.24e+01;
```



Mar 13 10:16

US-08-612-929-28 tpr

9

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 82 qgsnedp 88  
|||||||  
Qy 1 QQSNEDP 7

RESULT 14

ENTRY S42187 #type fragment  
TITLE Ig kappa chain V region - mouse (fragment)  
ORGANISM #formal\_name Mus musculus #common\_name house mouse  
DATE 28-Sep-1994 #sequence\_revision 21-Jul-1995 #text\_change  
21-Jul-1995  
ACCESSIONS S42187  
REFERENCE S42176  
#authors Mo, J.A.; Bona, C.A.; Holmdahl, R.  
#journal Eur. J. Immunol. (1993) 23:2503-2510  
#title Variable region gene selection of immunoglobulin G-expressing  
B cells with specificity for a defined epitope on type II  
collagen.  
#accession S42187  
##status preliminary  
##molecule\_type DNA  
##residues 1-90 #label MOJ  
##cross-references EMBL:225444  
SUMMARY #length 90 #checksum 9303

Query Match 71.7%; Score 43; DB 12; Length 90;  
Best Local Similarity 100.0%; Pred. No. 2.24e+01;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 84 qgsnedp 90  
|||||||  
Qy 1 QQSNEDP 7

RESULT 15

ENTRY B49442 #type fragment  
TITLE Ig light chain V region (50.1) - mouse (fragment)  
ORGANISM #formal\_name Mus musculus #common\_name house mouse  
DATE 21-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change  
21-Jul-1995  
ACCESSIONS B49442  
REFERENCE A49442  
#authors Stura, E.A.; Stanfield, R.L.; Fieser, G.G.; Silver, S.;  
Roguska, M.; Hincapie, L.M.; Simmerman, H.K.B.; Profy,  
A.T.; Wilson, I.A.  
#journal Proteins (1992) 14:499-508  
#title Crystallization, sequence, and preliminary crystallographic  
data for an antipeptide Fab 50.1 and peptide complexes with  
the principal neutralizing determinant of HIV-1 gp120.  
#accession B49442  
##status preliminary; not compared with conceptual translation  
##molecule\_type DNA  
##residues 1-96 #label STU  
SUMMARY #length 96 #checksum 7322

Query Match 71.7%; Score 43; DB 12; Length 96;  
Best Local Similarity 100.0%; Pred. No. 2.24e+01;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 85 qgsnedp 91  
|||||||  
Qy 1 QQSNEDP 7

Mar 18 10:16

US-08-612-929-28 tpr

10

Search completed: Tue Mar 18 10:18:13 1997  
Job time : 19 secs.

\*\*\*\*\*

WATERMAN

(TM)

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MPorch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Mar 18 10:18:30 1997; MasPar time 2.12 Seconds  
43.783 Million cell updates/sec

Tabular output not generated.

Title: >US-08-612-929-28

Description: (1-9) from US08612929.pep

Perfect Score: 60

Sequence: 1 QQSNEPPR 9

Scoring table: PAM 150

Gap 15

Searched: 88003 seqs, 10295656 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: a-geneseq25

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13  
14:part14 15:part15 16:part16 17:part17 18:part18

Statistics: Mean 14.223; Variance 40.970; scale 0.347

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	60	100.0	9	13 R70201	Humanized antibody 3B	6.85e-01
2	60	100.0	131	13 R75355	Humanized antibody 3B	6.85e-01
3	51	85.0	9	13 R70197	MAB 3B9 light chain C	8.52e+00
4	51	85.0	131	13 R70202	Humanized antibody 3B	8.52e+00
5	51	85.0	131	6 R29008	p64-k4 protein produc	8.52e+00
6	51	85.0	132	13 R70189	Mouse MAB 3B9 light c	8.52e+00
7	49	81.7	209	2 R12300	ORF-2 of Herpes Virus	1.47e+01
8	47	78.3	131	6 R32123	Anti-CD4 antibody MT	2.53e+01
9	45	75.0	132	7 R37716	Mouse 4C10 anti-idiot	4.32e+01
10	44	73.3	17	12 R66145	CD-4 antibody variabl	5.63e+01
11	44	73.3	103	9 R47933	Light chain region of	5.63e+01
12	44	73.3	111	9 R47935	Humanised light chain	5.63e+01

13	44	73.3	115	1	R04134	Anti-leu 3a light cha	5.63e+01
14	44	73.3	131	1	R04132	Anti-leu 3a light cha	5.63e+01
15	44	73.3	823	1	P81502	delta-endotoxin again	5.63e+01
16	44	73.3	823	1	P80972	Sequence encoded by 3	5.63e+01
17	44	73.3	1163	14	R85147	CryIC/CryIA(B) chim	5.63e+01
18	44	73.3	1189	8	R39757	Delta endotoxin.	5.63e+01
19	44	73.3	1189	3	R10193	Insecticidal crystal	5.63e+01
20	44	73.3	1189	13	R71463	Crystall protein encod	5.63e+01
21	44	73.3	1189	2	R10130	Lepidopteran-active t	5.63e+01
22	44	73.3	1190	14	R85150	CryIC/CryIA(B) altern	5.63e+01
23	44	73.3	9	14	R75477	Mouse antibody light	7.32e+01
24	43	71.7	9	14	R75478	Mouse antibody light	7.32e+01
25	43	71.7	106	6	R33309	MaE15 light chain.	7.32e+01
26	43	71.7	111	11	R60306	Chimeric anti HIV ant	7.32e+01
27	43	71.7	111	9	R47494	Murine anti-CD18 Ab 6	7.32e+01
28	43	71.7	111	11	R60302	Anti HIV antibody lig	7.32e+01
29	43	71.7	111	10	R55127	Mouse-human chimeric	7.32e+01
30	43	71.7	111	10	R55123	Mouse anti-HIV mu5.5	7.32e+01
31	43	71.7	111	9	R47492	Humanised anti-CD18 A	7.32e+01
32	43	71.7	111	1	P90541	Immunoglobulin L chai	7.32e+01
33	43	71.7	112	3	R13089	Murine 1B4 light chai	7.32e+01
34	43	71.7	112	5	R24575	Human x mouse modifie	7.32e+01
35	43	71.7	131	1	P90543	Amino acids sequence	7.32e+01
36	42	70.0	175	1	P91482	Translation product o	9.51e+01
37	42	70.0	1434	17	R94380	Mouse patched protein	9.51e+01
38	42	70.0	1447	17	R75375	Human patched protein	9.51e+01
39	41	68.3	132	3	R10920	kappa light chain var	1.23e+02
40	41	68.3	146	11	R58877	Rat-413 cadherin part	1.23e+02
41	41	68.3	146	17	R87119	Protocadherin clone R	1.23e+02
42	40	66.7	110	10	R60810	Light chain variable	1.60e+02
43	40	66.7	111	9	R48622	Sequence of the human	1.60e+02
44	40	66.7	112	14	R79158	Human IgE receptor-bi	1.60e+02
45	40	66.7	715	15	R80482	Recombinant bovine ad	1.60e+02

## ALIGNMENTS

RESULT 1

ID R70201; standard; Protein; 9 AA.

AC R70201;

DT 20-SEP-1995 (first entry)

DE Humanized antibody 3B9 light chain CDR.

KW Humanized antibody; antibody engineering; monoclonal antibody;

KW MAB; interleukin-4; IL-4; allergy; CDR;

KW complementarity determining region.

OS Homo sapiens.

PN W09507301-A.

PD 16-MAR-1995.

PF 07-SEP-1994; U10308.

PR 07-SEP-1993; US-117366.

PR 14-OCT-1993; US-136783.

PA (SMIK ) SMITHKLINE BEECHAM CORP.

PA (SMIK ) SMITHKLINE BEECHAM PLC.

PI Gross MS, Holmes SD, Sylvester DR;

DR WPI; 95-123387/16.

PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived from high affinity mAbs - useful in treatment of IL-4-mediated PT and IgE-mediated allergic conditions

PS Disclosure; Page 28; 97pp; English.

CC A humanized antibody light chain variable region and signal CC sequence is given in R75355. The signal sequence is also CC provided in R70194. The sequences of the first 2 CDRs CC are identical to mouse anti-human IL-4 MAb 3B9 light chain CC CDRs (given in R70195-96), but the third (R70201) differs

Mar 18 10:16

US-08-612-929-28.rag

3

CC by a single amino acid from the native mouse CDR (R70197).  
SQ Sequence 9 AA;

Query Match 100.0%; Score 60; DB 13; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6.85e-01;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 qgsnedppr 9  
|||||

Qy 1 QQSNEPPR 9

RESULT 2

ID R75355 standard; Protein; 131 AA.  
AC R75355;  
DT 20-SEP-1995 (first entry)  
DE Humanized antibody 3B9 light chain.  
KW Humanized antibody; antibody engineering; monoclonal antibody;  
KW Mab; interleukin-4; IL-4; allergy.  
OS Homo sapiens.

FH Key Location/Qualifiers

FT Peptide 1..20

FT /label= Sig\_peptide

FT Region 43..57

FT /label= CDR

FT /note= "complementarity determining region"

FT Region 73..79

FT /label= CDR

FT /note= "complementarity determining region"

FT Region 112..120

FT /label= CDR

FT /note= "complementarity determining region"

PN W09507301-A.

PD 16-MAR-1995.

PF 07-SEP-1994; U10308.

PR 07-SEP-1993; US-117366.

PR 14-OCT-1993; US-136783.

PA (SMIK ) SMITHKLINE BEECHAM CORP.

PA (SMIK ) SMITHKLINE BEECHAM PLC.

PI Gross MS, Holmes SD, Sylvester DR;

DR WPI; 95-123387/16.

DR N-PSDB; Q73986.

PT Chimeric and humanised IL-4 monoclonal antibodies (mabs), derived  
PT from high affinity mabs - useful in treatment of IL-4-mediated  
PT and IgE-mediated allergic conditions

PS Disclosure; Fig.5; 97pp; English.

CC A humanized antibody light chain variable region and signal  
CC sequence is given in R75355. The signal sequence is also  
CC provided in R70194. The sequences of the first 2 CDRs

CC are identical to mouse anti-human IL-4 Mab 3B9 light chain

CC CDRs (given in R70195-96), but the third (R70201) differs

CC by a single amino acid from the native mouse CDR (R70197).

SQ Sequence 131 AA;

Query Match 100.0%; Score 60; DB 13; Length 131;  
Best Local Similarity 100.0%; Pred. No. 6.85e-01;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 112 qgsnedppr 120

|||||

Qy 1 QQSNEPPR 9

RESULT 3

Mar 18 10:16

US-08-612-929-28.rag

4

ID R70197 standard; Protein; 9 AA.

AC R70197;

DT 20-SEP-1995 (first entry)

DE Mab 3B9 light chain CDR.

KW Chimeric antibody; humanized antibody; antibody engineering;

KW monoclonal antibody; Mab; interleukin-4; IL-4; allergy; CDR;

KW complementarity determining region.

OS Mus sp.

PN W09507301-A.

PD 16-MAR-1995.

PF 07-SEP-1994; U10308.

PR 07-SEP-1993; US-117366.

PR 14-OCT-1993; US-136783.

PA (SMIK ) SMITHKLINE BEECHAM CORP.

PA (SMIK ) SMITHKLINE BEECHAM PLC.

PI Gross MS, Holmes SD, Sylvester DR;

DR WPI; 95-123387/16.

PT Chimeric and humanised IL-4 monoclonal antibodies (mabs), derived  
PT from high affinity mabs - useful in treatment of IL-4-mediated  
PT and IgE-mediated allergic conditions

PS Disclosure; Page 56; 97pp; English.

CC Spleen cells from mice immunized with human IL-4 were used to prepare  
CC hybridomas, which were screened for anti-IL-4 Mab secretion. Only  
CC clone 3B9 was positive. cDNA clones of the 3B9 light and heavy

CC chains were cloned into pCEV7f+ and transformed into E. coli

CC DH5-alpha. A light chain cDNA clone was sequenced (083490) that

CC encoded the protein given in R70189. 3 CDRs (R70195-97) were

CC identified.

SQ Sequence 9 AA;

Query Match 85.0%; Score 51; DB 13; Length 9;

Best Local Similarity 100.0%; Pred. No. 8.52e+00;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 qgsnedpp 8

|||||

Qy 1 QQSNEPP 8

RESULT 4

ID R70202 standard; Protein; 131 AA.

AC R70202;

DT 20-SEP-1995 (first entry)

DE Humanized antibody 3B9 light chain.

KW Humanized antibody; antibody engineering; monoclonal antibody;

KW Mab; interleukin-4; IL-4; allergy.

OS Homo sapiens.

PN W09507301-A.

PD 16-MAR-1995.

PF 07-SEP-1994; U10308.

PR 07-SEP-1993; US-117366.

PR 14-OCT-1993; US-136783.

PA (SMIK ) SMITHKLINE BEECHAM CORP.

PA (SMIK ) SMITHKLINE BEECHAM PLC.

PI Gross MS, Holmes SD, Sylvester DR;

DR WPI; 95-123387/16.

DR N-PSDB; Q83520.

PT Chimeric and humanised IL-4 monoclonal antibodies (mabs), derived  
PT from high affinity mabs - useful in treatment of IL-4-mediated  
PT and IgE-mediated allergic conditions

PS Disclosure; Page 71-72; 97pp; English.

CC A humanized antibody light chain variable region and signal

CC sequence is given in R75355. The signal sequence is also

CC provided in R70194. The sequences of the 3 CDRs

Mar 18 10:16

US-08-612-929-28.rag

5

CC are identical to mouse anti-human IL-4 Mab 3B9 light chain  
CC CDRs (given in R70195-97).  
SQ Sequence 131 AA;

Query Match 85.0%; Score 51; DB 13; Length 131;  
Best Local Similarity 100.0%; Pred. No. 8.52e+00;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 112 qgsnedpp 119  
|||||||  
QY 1 QQSNEDEPP 8

RESULT 5  
ID R29008 standard; Protein; 131 AA.

AC R29008;  
DT 30-MAR-1993 (first entry)  
DE p64-k4 protein product.  
KW Human; antibody; interleukin-6; receptor; IL-6R; light chain; L; H;  
KW heavy chain; variable region; mouse; monoclonal; hybridoma; AUK64-7;  
KW plasmid; p64-k4; p64-h2.  
OS Synthetic.

FH Key Location/Qualifiers  
FT Peptide 1..20  
FT /note= "Signal peptide"  
FT Protein 21..131  
FT /note= "Mature peptide"  
PN W09219759-A.  
PD 12-NOV-1992.  
PE 24-APR-1992; J00544.  
PR 25-APR-1991; JP-095476.  
PR 19-FEB-1992; JP-032084.  
PA (CHUGAI SEIYAKU KK.  
PI Bendig MW, Jones ST, Saldanha JW, Sato K, Tsuchiya M;  
DR WPI; 92-398882/48.

DR N-PSDB; Q30757.  
PT Reconstituted human antibody to human interleukin-6 receptor -  
PT has low antigenicity and contains mouse V-region complementarity  
PT determining regions  
PS Disclosure; Page 124-125; 207pp; Japanese.

CC The sequences given in R29008-09 were encoded by plasmids which were  
CC used in example to illustrate the production of a human antibody which  
CC recognises human interleukin-6 receptor (IL-6R). The antibody  
CC comprises light (L) chain and heavy (H) chain variable regions which  
CC were derived from a mouse monoclonal antibody produced from the  
CC hybridoma AUK64-7 which contained the plasmids p64-k4 and p64-h2.  
SQ Sequence 131 AA;

Query Match 85.0%; Score 51; DB 6; Length 131;  
Best Local Similarity 100.0%; Pred. No. 8.52e+00;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 113 qgsnedpp 120  
|||||||  
QY 1 QQSNEDEPP 8

RESULT 6  
ID R70189 standard; Protein; 132 AA.

AC R70189;  
DT 20-SEP-1995 (first entry)  
DE Mouse Mab 3B9 light chain.  
KW Chimeric antibody; humanized antibody; antibody engineering;  
KW monoclonal antibody; Mab; interleukin-4; IL-4; allergy.

Mar 18 10:16

US-08-612-929-28.rag

6

OS Mus sp. Location/Qualifiers  
FH Key 1..20  
FT Peptide /label= Sig\_peptide  
FT Region 44..58  
FT /label= CDR  
FT /note= "complementarity determining region"  
FT Region 74..80  
FT /label= CDR  
FT /note= "complementarity determining region"  
FT Region 113..121  
FT /label= CDR  
FT /note= "complementarity determining region"  
PN W09507301-A.  
PD 16-MAR-1995.  
PF 07-SEP-1994; U10308.  
PR 07-SEP-1993; US-117366.  
PR 14-OCT-1993; US-136783.  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
PA (SMIK ) SMITHKLINE BEECHAM PLC.  
PI Gross MS, Holmes SD, Sylvester DR;  
DR WPI; 95-123387/16.  
DR N-PSDB; Q83490.  
PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived  
PT from high affinity mAbs - useful in treatment of IL-4-mediated  
PT and IgE-mediated allergic conditions  
PS Disclosure; Fig.1; 97pp; English.  
CC Spleen cells from mice immunized with human IL-4 were used to prepare  
CC hybridomas, which were screened for anti-IL-4 Mab secretion. Only  
CC clone 3B9 was positive. cDNA clones of the 3B9 light and heavy  
CC chains were cloned into pCEM7f+ and transformed into E. coli  
CC DH5-alpha. The clones were sequenced (Q83490-91), and used for  
CC antibody engineering.  
SQ Sequence 132 AA;

Query Match 85.0%; Score 51; DB 13; Length 132;  
Best Local Similarity 100.0%; Pred. No. 8.52e+00;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 113 qgsnedpp 120  
|||||||  
QY 1 QQSNEDEPP 8

RESULT 7  
ID R12300 standard; Protein; 209 AA.  
AC R12300;  
DT 13-AUG-1991 (first entry)  
DE ORF-2 of Herpes Virus of turkeys genome insertion region.  
KW HVT; vaccine.  
OS Synthetic.  
PN EP-431668-A.  
PD 12-JUN-1991.  
PF 21-NOV-1990; 203076.  
PR 04-DEC-1989; EP-203071.  
PR 21-NOV-1990; EP-203076.  
PA (ALKU ) AKZO NV.

PI Sondermeijer PJA, Claessens JAJ, Mockett APA;  
DR WPI; 91-172965/24.  
PT Recombinant HVT contg. heterologous gene - the gene is situated  
PT in defined insert region in genome, recombinant HVT can be used  
PT to produce vector vaccine.  
PS Claim 1; Page 14; 30pp; English.  
CC The sequence (SEQ ID NO:2) is encoded by ORF-2 of the HVT genome.

CC The DNA contains a BgIII site into which DNA encoding an epitope  
 CC can be inserted for the prodn. of a viral vaccine. Sequences en-  
 CC coding, for example, Newcastle Disease Virus or Marek's disease  
 CC antigens can be inserted for vaccines for poultry.  
 CC See also R12301-R12303.  
 SQ Sequence 209 AA;

Query Match 81.7%; Score 49; DB 2; Length 209;  
 Best Local Similarity 75.0%; Pred. No. 1.47e+01;  
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 112 qnneppr 119  
 |:|:|:|  
 Qy 2 QSNEDPPR 9

RESULT 8  
 ID R32123 standard; Protein; 131 AA.  
 AC R32123;  
 DT 02-JUN-1993 (first entry)  
 DE Anti-CD4 antibody MT 3.10 light chain variable region.  
 KW immunosuppression; tissue transplantation; graft; L chain; V region;  
 KW T-helper cell inhibition; transplant rejection; MAb;  
 KW interleukin-2 receptor.

FT Key Location/Qualifiers  
 FT Peptide 1..20  
 FT /label= signal  
 FT Region 21..120  
 FT /label= Variable  
 FT Region 121..131  
 FT /label= J1  
 PN DE4143214-A.  
 PD 28-JAN-1993.  
 PF 30-DEC-1991; 143214.  
 PR 25-JUL-1991; DE-124759.  
 PR 30-DEC-1991; DE-143214.  
 PA (BOE ) BOEHRINGER MANNHEIM GMBH.  
 PI Kaluza B, Riethmuller G, Scheuer W, Weidle U;  
 DR WPI; 93-037582/05.  
 DR N-PSDB; Q36609.

PT Synergistic antibody compen. for use as immunosuppressant -  
 PT comprises monoclonal anti-CD4 antibodies and monoclonal anti-IL2R  
 PT alpha- or anti-IL2R beta antibodies  
 PS Claim 5; Page 11; 18pp; German.  
 CC This sequence is the light chain variable region of a preferred  
 CC anti-CD4 monoclonal antibody for use in the claimed synergistic  
 CC composition. MAb MT 3.10 is deposited as clone 3.101/8B10 (ECACC  
 CC 90090702). The anti-CD4 antibody is used with at least one anti-IL2R  
 CC alpha or beta antibody. Individually the antibodies are strongly  
 CC inhibiting and when used together their immunosuppressive properties  
 CC are improved; they synergistically inhibit T-helper cell  
 CC proliferation to effectively inhibit transplant rejection at low  
 CC doses without significantly reducing the general immune response.  
 CC See also Q36608-Q36616.  
 SQ Sequence 131 AA;

Query Match 78.3%; Score 47; DB 6; Length 131;  
 Best Local Similarity 87.5%; Pred. No. 2.53e+01;  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 113 qgsedpp 120  
 |:|:|:|  
 Qy 1 QQSNEDPP 8

RESULT 9  
 ID R37716 standard; Protein; 132 AA.  
 AC R37716;  
 DT 30-SEP-1993 (first entry)  
 DE Mouse 4C10 anti-idiotypic Ab light chain V region.  
 KW MAIA; monoclonal antibody; hybridoma; organ transplant rejection;  
 KW immuno-modulator; cancer; treatment; diagnosis; melanoma;  
 KW anti-cancer immunity; enhancement; suppression.  
 OS Mus musculus.  
 FH Key Location/Qualifiers  
 FT Misc difference 31  
 FT /note= "Thr -> Ser, from PCR substituted gene"  
 PN W09310221-A.  
 PD 27-MAY-1993.  
 PF 12-NOV-1992; U10166.  
 PR 13-NOV-1991; US-791934.  
 PA (REGC ) UNIV CALIFORNIA.  
 PI Hastings A, Irie RF, Morrison SL.  
 DR WPI; 93-182538/22.  
 PT Chimeric murine-human anti-idiotypic monoclonal antibodies -  
 PT useful as immuno-modulators for treating and diagnosing cancers,  
 PT and for suppressing organ transplant rejection and auto-immune  
 PT diseases  
 PS Disclosure; Page 30-31; 46pp; English.  
 CC The sequence is that of the 4C10 anti-idiotypic Ab light chain V region  
 CC which was used in the construction of a murine/human monoclonal  
 CC anti-idiotypic antibody (MAIA). The MAIA elicits an anti-ganglioside  
 CC response and produces antibodies which induce cytotoxic destruction  
 CC of cancer cells bearing the gangliosides. It can be used for treating  
 CC cancers partic. melanomas. It can also be used as an immunomodulator to  
 CC enhance anti-cancer immunity, suppress organ transplant rejection and  
 CC suppress autoimmune disease. The MAIA can also be used in the diagnosis  
 CC of cancers.  
 SQ Sequence 132 AA;

Query Match 75.0%; Score 45; DB 7; Length 132;  
 Best Local Similarity 77.8%; Pred. No. 4.32e+01;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 113 qgsedptw 121  
 |:|:|:|:|  
 Qy 1 QQSNEDPPR 9

RESULT 10  
 ID R66145 standard; peptide; 17 AA.  
 AC R66145;  
 DT 12-JUL-1995 (first entry)  
 DE CD-4 antibody variable region complementary peptide.  
 KW CD-4 antibody variable region; complementary peptide;  
 KW extra-corporeal blood circulation; cell filter material.  
 OS Synthetic.  
 PN J06296663-A.  
 PD 27-SEP-1994.  
 PF 17-MAR-1993; JP-057206.  
 PR (TOYM ) TOYOBO KK.  
 DR WPI; 94-346316/43.  
 PT Material for collecting cells positive for CD-4 antibody -  
 PT comprises nonwoven fabric having keto-alkyl halide functional gp  
 PS Example 3; Page 8; 9pp; Japanese.  
 CC R66140-R66146 are peptides complementary to the variable region  
 CC of the CD-4 antibody, these peptides are fixed onto a claimed

CC nonwoven fabric (average fibre dia. of 1-30 microns) coated with  
 CC keto-alkyl halide functional groups. This material can be used  
 CC as a filter for CD-4 positive cells in a medical treatment  
 CC involving the extra-corporeal circulation of blood.  
 SQ Sequence 17 AA;

Query Match 73.3%; Score 44; DB 12; Length 17;  
 Best Local Similarity 87.5%; Pred. No. 5.63e+01;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 9 gqsvdpp 16  
 :| | | | |  
 QY 1 QQSNEDPP 8

## RESULT 11

ID R47933 standard; Protein; 103 AA.  
 AC R47933;  
 DT 24-JUL-1994 (first entry)  
 DE Light chain region of 23F2G.  
 KW Amplification; 23F2G; humanised antibody; heavy chain; light chain;  
 KW hybridoma; inflammation; CD18; human leukocyte integrins; mAb 60.3;  
 KW monoclonal antibody; LFA-1; adhesion; migration; multiple  
 KW sclerosis; MS.  
 PN W09402175-A.  
 PD 03-FEB-1994.  
 PF 16-JUL-1993; U06734.  
 PR 16-JUL-1992; US-915068.  
 PR 10-MAY-1993; US-060699.  
 PA (ICOS-) ICOS CORP.  
 PA (UNIW ) UNIV WASHINGTON.  
 PI Rose LM;  
 DR WPI; 94-048551/06.  
 DR N-PSDB; Q55915.  
 PT Antibodies immunologically reactive with the CD18 of human  
 PT leukocyte integrins and/or competing with mAb 60.3 for binding to  
 PT human LFA-1 - for alleviating symptoms associated with  
 PT inflammatory disease states  
 PS Example 6; Page 43; 58pp; English.  
 CC Total RNA was isolated from the hybridoma cell line 23F2G and first  
 CC strand cDNA was synthesised using the total RNA as a template. The  
 CC first strand cDNA was used as a template for PCR to obtain double  
 CC stranded DNA fragments encoding the variable regions of both the  
 CC heavy and light chains of monoclonal antibody 23F2G. The sequence  
 CC shown is that of the light chain variable region of MAb 23F2G  
 CC The humanised form of MAb 23F2G may be administered to  
 CC alleviate symptoms associated with inflammatory disease states, esp.  
 CC for the inhibition of inflammatory processes associated with  
 CC multiple sclerosis. The MAb blocks leukocyte adhesion and  
 CC migration to inflammatory sites. The MAb is an anti-CD18 integrin  
 CC antibody which competes with MAb 60.3 for binding to LFA-1.  
 CC See also R47931-6.  
 SQ Sequence 103 AA;

Query Match 73.3%; Score 44; DB 9; Length 103;  
 Best Local Similarity 75.0%; Pred. No. 5.63e+01;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 85 hqndedpp 92  
 :| | | | |  
 QY 1 QQSNEDPP 8

## RESULT 12

ID R47935 standard; Protein; 111 AA.  
 AC R47935;  
 DT 24-JUL-1994 (first entry)  
 DE Humanised light chain region of 23F2G.  
 KW Amplification; 23F2G; humanised antibody; heavy chain; light chain;  
 KW hybridoma; inflammation; CD18; human leukocyte integrins; mAb 60.3;  
 KW monoclonal antibody; LFA-1; adhesion; migration; multiple  
 KW sclerosis; MS.  
 PN W09402175-A.  
 PD 03-FEB-1994.  
 PF 16-JUL-1993; U06734.  
 PR 16-JUL-1992; US-915068.  
 PR 10-MAY-1993; US-060699.  
 PA (ICOS-) ICOS CORP.  
 PA (UNIW ) UNIV WASHINGTON.  
 PI Rose LM;  
 DR WPI; 94-048551/06.  
 DR N-PSDB; Q55917.  
 PT Antibodies immunologically reactive with the CD18 of human  
 PT leukocyte integrins and/or competing with mAb 60.3 for binding to  
 PT human LFA-1 - for alleviating symptoms associated with  
 PT inflammatory disease states  
 PS Example 6; Page 45; 58pp; English.  
 CC Total RNA was isolated from the hybridoma cell line 23F2G and first  
 CC strand cDNA was synthesised using the total RNA as a template. The  
 CC first strand cDNA was used as a template for PCR to obtain double  
 CC stranded DNA fragments encoding the variable regions of both the  
 CC heavy and light chains of monoclonal antibody 23F2G. The sequence  
 CC shown is a humanised form of the light chain variable region of MAb  
 CC 23F2G. The humanised form of MAb 23F2G may be administered to  
 CC alleviate symptoms associated with inflammatory disease states, esp.  
 CC for the inhibition of inflammatory processes associated with  
 CC multiple sclerosis. The MAb blocks leukocyte adhesion and  
 CC migration to inflammatory sites. The MAb is an anti-CD18 integrin  
 CC antibody which competes with MAb 60.3 for binding to LFA-1.  
 CC See also R47931-6.  
 SQ Sequence 111 AA;

Query Match 73.3%; Score 44; DB 9; Length 111;  
 Best Local Similarity 75.0%; Pred. No. 5.63e+01;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 93 hqndedpp 100  
 :| | | | |  
 QY 1 QQSNEDPP 8

## RESULT 13

ID R04134 standard; protein; 115 AA.  
 AC R04134;  
 DT 06-SEP-1990 (first entry)  
 DE Anti-Leu 3a light chain variable region gene product, KOL/206 VL.  
 KW HIV; AIDS; anti-Leu3a; vaccine; ds.  
 OS Mus musculus.  
 PN EP-365209-A.  
 PD 25-APR-1990.  
 PF 11-OCT-1989; 010415.  
 PR 17-OCT-1988; US-260558.  
 PA (BECT) Becton Dickinson Co.  
 PI Hinton R, Oi VT;  
 DR WPI; 90-126329/17.  
 DR N-PSDB; Q04041.  
 PT New chimeric variants of murine antibody anti-leucine -  
 PT contg. human antibody regions, and DNA encoding sequences.

PS Claim 4; Fig 4; 12pp; English.

CC Variants of murine monoclonal anti-CD4 antibody, anti-leu3A can be

CC used to form chimeric mouse-variable, human-constant region Abs

CC suggested as being useful as a vaccine to HIV.

SQ Sequence 115 AA;

Query Match 73.3%; Score 44; DB 1; Length 115;

Best Local Similarity 87.5%; Pred. No. 5.63e+01;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 96 qgsyedpp 103

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Qy 1 QQSNEPPP 8

#### RESULT 14

ID R04132 standard; protein; 131 AA.

AC R04132;

DT 06-SEP-1990 (first entry)

DE Anti-Leu 3a light chain variable region gene product, 206 Vx.

KW HIV; AIDS; anti-Leu3A; vaccine; ds.

OS Mus musculus.

PN EP-365209-A.

PD 25-APR-1990.

PF 11-OCT-1989; 010415.

PR 17-OCT-1988; US-260558.

PA (BECT) Becton Dickinson Co.

PI Hinton R. Oi VT;

DR WPI; 90-126329/17.

DR N-PSDB; Q04039.

PT New chimeric variants of murine antibody anti-leucine -

PT contg. human antibody regions, and DNA encoding sequences.

PS Claim 1; Fig 2; 12pp; English.

CC Variants of murine monoclonal anti-CD4 antibody, anti-leu3A can be

CC used to form chimeric mouse-variable, human-constant region Abs

CC suggested as being useful as a vaccine to HIV.

SQ Sequence 131 AA;

Query Match 73.3%; Score 44; DB 1; Length 131;

Best Local Similarity 87.5%; Pred. No. 5.63e+01;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 113 qgsyedpp 120

|||||

Qy 1 QQSNEPPP 8

#### RESULT 15

ID P81502 standard; protein; 823 AA.

AC P81502;

DT 23-OCT-1990 (first entry)

DE delta-endotoxin against Lepidoptera larvae

KW Lepidoptera larvae; insecticide; Bacillus thuringiensis;

KW Spodoptera littoralis; delta endotoxin; ss.

OS synthetic.

FH Key Location/Qualifiers

FT Region 1..620

FT /label=N-terminal half

FT /note="responsible for toxicity"

PN W08809812-A.

PD 15-DEC-1988.

PF 09-JUN-1988; F00292.

PR 12-JUN-1987; DK-002990.

PA (NOVO) Novo Industri A/S.

PI Sanchis V, Lereclus D, Menou G;

DR WPI; 88-368626/51.

DR N-PSDB; N91949.

PT New nucleotide sequences encoding new polypeptide -

PT with selective action against lepidopteran larvae esp Spodoptera

PT littoralis

PS Claim 14; Page 52; 65pp; French.

CC Polypeptide is encoded by a 3kb HindIII-PstI fragment of

CC Bacillus thuringiensis. Recombinant sequences can also be

CC constructed from 2 diff strains of B.thuringiensis. The sequence

CC between bases 50 to 985 is claimed separately as this encodes "at

CC least a part of the N-terminal region of an insecticidal

CC polypeptide". There is a variable amino acid at posn 124 which is

CC Ala in the sequence given here but which is Glu in the shorter

CC sequence.

SQ Sequence 823 AA;

Query Match 73.3%; Score 44; DB 1; Length 823;

Best Local Similarity 44.4%; Pred. No. 5.63e+01;

Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 344 reangeppr 352

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Qy 1 QQSNEPPP 9

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Run on: Tue Mar 18 10:09:20 1997; MasPar time 2.23 Seconds  
124.694 Million cell updates/sec  
Tabular output not generated.

Title: >US-08-612-929-16  
Description: (1-15) from US08612929.pep  
Perfect Score: 102  
Sequence: 1 KASQSDVDYDGDGYM 15

Scoring table: PAM 150  
Gap 15

Searched: 52205 seqs, 18531385 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: swiss-prot33  
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10

Statistics: Mean 26.187; Variance 34.386; scale 0.762

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	102	100.0	111	5	KV30_MOUSE IG KAPPA CHAIN V-III	7.90e-11
2	102	100.0	111	5	KV3N_MOUSE IG KAPPA CHAIN V-III	7.90e-11
3	102	100.0	111	5	KV3M_MOUSE IG KAPPA CHAIN V-III	7.90e-11
4	102	100.0	111	5	KV3Q_MOUSE IG KAPPA CHAIN V-III	7.90e-11
5	96	94.1	110	5	KV3P_MOUSE IG KAPPA CHAIN V-III	2.46e-09
6	94	92.2	111	5	KV3L_MOUSE IG KAPPA CHAIN V-III	7.64e-09
7	60	58.8	111	5	KV3C_MOUSE IG KAPPA CHAIN V-III	3.36e-01
8	60	58.8	112	5	KV3C_MOUSE IG KAPPA CHAIN V-III	3.36e-01
9	58	56.9	679	6	PB2_STRN PENICILLIN-BINDING PR	8.29e-01
10	57	55.9	113	5	KV2B_HUMAN IG KAPPA CHAIN V-II R	1.29e+00
11	56	54.9	108	5	KV3V_MOUSE IG KAPPA CHAIN V-III	2.00e+00
12	56	54.9	111	5	KV3H_MOUSE IG KAPPA CHAIN V-III	2.00e+00
13	56	54.9	111	5	KV3J_MOUSE IG KAPPA CHAIN V-III	2.00e+00

14	56	54.9	111	5	KV3K_MOUSE IG KAPPA CHAIN V-III	2.00e+00
15	56	54.9	131	5	KV3I_MOUSE IG KAPPA CHAIN V-III	2.00e+00
16	56	54.9	459	2	CCMH_HAEN CYTOCHROME C-TYPE BIO	2.00e+00
17	56	54.9	512	9	VC02_VACCC PROTEIN C2.	2.00e+00
18	56	54.9	512	9	VC02_VACCC PROTEIN C2.	2.00e+00
19	55	53.9	272	9	TYPH_MYCHO THYMIDINE PHOSPHORYLA	3.09e+00
20	54	52.9	57	6	NG4_DROME NEW-GLUE PROTEIN 4 PR	4.74e+00
21	54	52.9	111	5	KV3A_MOUSE IG KAPPA CHAIN V-III	4.74e+00
22	54	52.9	112	5	KV3B_MOUSE IG KAPPA CHAIN V-III	4.74e+00
23	54	52.9	133	5	KV2F_HUMAN IG KAPPA CHAIN V-III	4.74e+00
24	54	52.9	452	9	VE2_HPV17 E2 PROTEIN.	4.74e+00
25	54	52.9	501	9	VGLC_HSVMD SECRETORY GLYCOPROTEI	4.74e+00
26	54	52.9	501	9	VGLC_HSVMB SECRETORY GLYCOPROTEI	4.74e+00
27	54	52.9	501	9	VGLC_HSVMB SECRETORY GLYCOPROTEI	4.74e+00
28	54	52.9	505	9	VGLC_HSVMB SECRETORY GLYCOPROTEI	4.74e+00
29	54	52.9	716	5	KIF2_MOUSE KINESIN-LIKE PROTEIN	4.74e+00
30	54	52.9	1955	1	AGRI_CHICK AGRIN PRECURSOR.	4.74e+00
31	54	52.9	3951	9	VGF1_IBVB F1 PROTEIN.	4.74e+00
32	53	52.0	83	4	IBB3_SOYBN BOWMAN-BIRK TYPE PROT	7.22e+00
33	53	52.0	416	10	YRM6_CAEEL HYPOTHETICAL 46.4 KD	7.22e+00
34	53	52.0	591	9	VR2_SALCH 65 KD VIRULENCE PROTE	7.22e+00
35	53	52.0	593	9	VR2_SALDU 65 KD VIRULENCE PROTE	7.22e+00
36	52	51.0	269	9	TRUA_HAEN PSEUDOURIDYLATE SYNTH	1.09e+01
37	52	51.0	270	9	TRUA_ECOLI PSEUDOURIDYLATE SYNTH	1.09e+01
38	52	51.0	319	10	YK5_CAEEL PROBABLE G PROTEIN-CO	1.09e+01
39	52	51.0	334	9	VE2_BPVA E2 PROTEIN.	1.09e+01
40	52	51.0	396	8	SH11_CHICK SOX-11 PROTEIN.	1.09e+01
41	52	51.0	638	3	ER72_MOUSE PROTEIN DISULFIDE ISO	1.09e+01
42	52	51.0	643	3	ER72_RAT PROTEIN DISULFIDE ISO	1.09e+01
43	52	51.0	855	9	VGLH_HSV4 GLYCOPROTEIN H PRECUR	1.09e+01
44	52	51.0	2291	8	RREP_BEV RNA-DIRECTED RNA POLY	1.09e+01
45	51	50.0	323	10	YAMB_THETU HYPOTHETICAL 35.6 KD	1.65e+01

## ALIGNMENTS

RESULT	1	STANDARD;	PRT;	111 AA.
ID	KV30_MOUSE			
AC	P01667;			
DT	21-JUL-1986 (REL. 01, CREATED)			
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)			
DE	01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)			
DE	IG KAPPA CHAIN V-III REGION (PC 6308).			
OS	MUS MUSCULUS (MOUSE).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
OC	EUTHERIA; RODENTIA.			
RN	[1]			
RP	SEQUENCE.			
RX	MEDLINE; 79073152.			
RA	WEIGERT M., GATHAITAN L., LOH E., SCHILLING J., HOOD L.E.;			
RL	NATURE 276:785-790(1978).			
DR	PIR; C01937; KVM508.			
DR	HSSP; P01679; IGG8.			
KW	IMMUNOGLOBULIN V REGION.			
FT	DOMAIN 1 23			
FT	DOMAIN 24 38			
FT	DOMAIN 39 53			
FT	DOMAIN 54 60			
FT	DOMAIN 61 92			
FT	DOMAIN 93 101			
FT	DOMAIN 102 111			
FT	DISULFID 23 92			
FT	NON_TER 111 111			
SQ	SEQUENCE 111 AA; 12071 MW; F7865271 CRC32;			



Mar 18 10:07

US-08-612-929-16.rsp

3

Query Match 100.0%; Score 102; DB 5; Length 111;  
Best Local Similarity 100.0%; Pred. No. 7.90e-11;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 24 kasqsvdydgsym 38  
|||||  
Qy 1 KASQSVDDYDGSYMN 15

RESULT 2

ID KV3N MOUSE STANDARD; PRT; 111 AA.  
AC P01666;  
DT 21-JUL-1986 (REL. 01, CREATED)  
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)  
DE IG KAPPA CHAIN V-III REGION (PC 7183).  
OS MUS MUSCULUS (MOUSE).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; RODENTIA.  
RN [1]  
RP SEQUENCE.  
RX MEDLINE; 79073152.  
RA WEIGERT M., GATMAITAN L., LOH E., SCHILLING J., HOOD L.E.;  
RL NATURE 276:785-790 (1978).  
DR PIR; B01937; KVM583.  
DR HSP; P01679; IGGB.  
KW IMMUNOGLOBULIN V REGION.  
FT DOMAIN 1 23  
FT DOMAIN 24 38  
FT DOMAIN 39 53  
FT DOMAIN 54 60  
FT DOMAIN 61 92  
FT DOMAIN 93 101  
FT DOMAIN 102 111  
FT DISULFID 23 92  
FT NON TER 111 111  
SQ SEQUENCE 111 AA; 11952 MW; 041902B8 CRC32;

Query Match 100.0%; Score 102; DB 5; Length 111;  
Best Local Similarity 100.0%; Pred. No. 7.90e-11;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 24 kasqsvdydgsym 38  
|||||  
Qy 1 KASQSVDDYDGSYMN 15

RESULT 3

ID KV3M MOUSE STANDARD; PRT; 111 AA.  
AC P01665;  
DT 21-JUL-1986 (REL. 01, CREATED)  
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)  
DE IG KAPPA CHAIN V-III REGION (PC 7043).  
OS MUS MUSCULUS (MOUSE).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; RODENTIA.  
RN [1]  
RP SEQUENCE.  
RX MEDLINE; 79073152.  
RA WEIGERT M., GATMAITAN L., LOH E., SCHILLING J., HOOD L.E.;  
RL NATURE 276:785-790 (1978).  
DR PIR; A01937; KVM543.

Mar 18 10:07

US-08-612-929-16.rsp

4

DR HSP; P01679; IGGB.  
KW IMMUNOGLOBULIN V REGION.  
FT DOMAIN 1 23  
FT DOMAIN 24 38  
FT DOMAIN 39 53  
FT DOMAIN 54 60  
FT DOMAIN 61 92  
FT DOMAIN 93 101  
FT DOMAIN 102 111  
FT DISULFID 23 92  
FT NON TER 111 111  
SQ SEQUENCE 111 AA; 12002 MW; ADC728CA CRC32;

Query Match 100.0%; Score 102; DB 5; Length 111;  
Best Local Similarity 100.0%; Pred. No. 7.90e-11;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 24 kasqsvdydgsym 38  
|||||  
Qy 1 KASQSVDDYDGSYMN 15

RESULT 4

ID KV3Q MOUSE STANDARD; PRT; 111 AA.  
AC P01669;  
DT 21-JUL-1986 (REL. 01, CREATED)  
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)  
DE IG KAPPA CHAIN V-III REGION (PC 7769).  
OS MUS MUSCULUS (MOUSE).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; RODENTIA.  
RN [1]  
RP SEQUENCE.  
RX MEDLINE; 79073152.  
RA WEIGERT M., GATMAITAN L., LOH E., SCHILLING J., HOOD L.E.;  
RL NATURE 276:785-790 (1978).  
DR PIR; E01937; KVM569.  
DR HSP; P01679; IACV.  
KW IMMUNOGLOBULIN V REGION.  
FT DOMAIN 1 23  
FT DOMAIN 24 38  
FT DOMAIN 39 53  
FT DOMAIN 54 60  
FT DOMAIN 61 92  
FT DOMAIN 93 101  
FT DOMAIN 102 111  
FT DISULFID 23 92  
FT NON TER 111 111  
SQ SEQUENCE 111 AA; 12011 MW; 9CB705B9 CRC32;

Query Match 100.0%; Score 102; DB 5; Length 111;  
Best Local Similarity 100.0%; Pred. No. 7.90e-11;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 24 kasqsvdydgsym 38  
|||||  
Qy 1 KASQSVDDYDGSYMN 15

RESULT 5

ID KV3P MOUSE STANDARD; PRT; 110 AA.  
AC P01668;  
DT 21-JUL-1986 (REL. 01, CREATED)

Mar 18 10:07

US-08-612-929-16.rsp

5

DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)  
DE IG KAPPA CHAIN V-III REGION (PC 7210).  
OS MUS MUSCULUS (MOUSE).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; RODENTIA.  
RN [1]  
RP SEQUENCE.  
RX MEDLINE; 79073152.  
RA WEIGERT M., GATMAITAN L., LOH E., SCHILLING J., HOOD L.E.;  
RL NATURE 276:785-790(1978).  
DR PIR; D01937; KVM510.  
DR HSP; P01679; IGGB.  
KW IMMUNOGLOBULIN V REGION.  
FT DOMAIN 1 23  
FT DOMAIN 24 38  
FT DOMAIN 39 53  
FT DOMAIN 54 60  
FT DOMAIN 61 92  
FT DOMAIN 93 100  
FT DOMAIN 101 110  
FT DISULFID 23 92  
FT NON TER 110 110  
SQ SEQUENCE 110 AA; 11950 MW; BF45B542 CRC32;

Query Match 94.1%; Score 96; DB 5; Length 110;  
Best Local Similarity 93.3%; Pred. No. 2.46e-09;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 24 kasqvdydgsym 38  
|||||:|||||  
QY 1 KASQVDYDGSYMN 15

RESULT 6  
ID KV3L MOUSE STANDARD; PRT; 111 AA.  
AC P01664;  
DT 21-JUL-1986 (REL. 01, CREATED)  
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)  
DE IG KAPPA CHAIN V-III REGION (CBPC 101).  
OS MUS MUSCULUS (MOUSE).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; RODENTIA.  
RN [1]  
RP SEQUENCE.  
RX MEDLINE; 79012520.  
RA MCKEAN D.J., BELL M., POTTER M.;  
RL PROC. NATL. ACAD. SCI. U.S.A. 75:3913-3917(1978).  
CC -1- THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.  
DR PIR; A01936; KVM5C1.  
DR HSP; P01679; IGGB.  
KW IMMUNOGLOBULIN V REGION.  
FT DOMAIN 1 23  
FT DOMAIN 24 38  
FT DOMAIN 39 53  
FT DOMAIN 54 60  
FT DOMAIN 61 92  
FT DOMAIN 93 101  
FT DOMAIN 102 111  
FT DISULFID 23 92  
FT NON TER 111 111  
SQ SEQUENCE 111 AA; 11964 MW; A2AC84C7 CRC32;

Mar 18 10:07

US-08-612-929-16.rsp

6

Query Match 92.2%; Score 94; DB 5; Length 111;  
Best Local Similarity 86.7%; Pred. No. 7.64e-09;  
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
Db 24 kasqvdydgsym 38  
|||||:|||||  
QY 1 KASQVDYDGSYMN 15

RESULT 7  
ID KV3C MOUSE STANDARD; PRT; 111 AA.  
AC P01656;  
DT 21-JUL-1986 (REL. 01, CREATED)  
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)  
DE IG KAPPA CHAIN V-III REGION (MOPC 70).  
OS MUS MUSCULUS (MOUSE).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; RODENTIA.  
RN [1]  
RP SEQUENCE.  
RX MEDLINE; 67056897.  
RA GRAY W.R., DREYER W.J., HOOD L.E.;  
RL SCIENCE 155:465-467(1967).  
CC -1- THIS IS A BENCE-JONES PROTEIN.  
DR PIR; A01930; KVM580.  
DR HSP; P01679; IGGB.  
KW IMMUNOGLOBULIN V REGION; BENCE-JONES PROTEIN.  
FT DOMAIN 1 23  
FT DOMAIN 24 38  
FT DOMAIN 39 53  
FT DOMAIN 54 60  
FT DOMAIN 61 92  
FT DOMAIN 93 101  
FT DOMAIN 102 111  
FT DISULFID 23 92  
FT NON TER 111 111  
SQ SEQUENCE 111 AA; 11904 MW; 76BA04CC CRC32;

Query Match 58.8%; Score 60; DB 5; Length 111;  
Best Local Similarity 60.0%; Pred. No. 3.36e-01;  
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 24 rasesvdngisfmm 38  
:|||||:|||||  
QY 1 KASQVDYDGSYMN 15

RESULT 8  
ID KV3G MOUSE STANDARD; PRT; 112 AA.  
AC P01659;  
DT 21-JUL-1986 (REL. 01, CREATED)  
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)  
DE IG KAPPA CHAIN V-III REGION (TEPC 124).  
OS MUS MUSCULUS (MOUSE).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; RODENTIA.  
RN [1]  
RP SEQUENCE.  
RX MEDLINE; 73140225.  
RA MCKEAN D.J., POTTER M., HOOD L.E.;  
RL BIOCHEMISTRY 12:760-771(1973).  
DR PIR; A01933; KVM532.

Mar 18 10:07

US-08-612-929-16.rsp

7

DR HSP; P01679; ICGB.  
 KW IMMUNOGLOBULIN V REGION.  
 FT DOMAIN 1 23  
 FT DOMAIN 24 38  
 FT DOMAIN 29 53  
 FT DOMAIN 54 60  
 FT DOMAIN 61 92  
 FT DOMAIN 93 101  
 FT DOMAIN 102 111  
 FT DISULFID 23 92  
 FT NON TER 112 112  
 SQ SEQUENCE 112 AA; 12339 MW; 4504DDOE CRC32;

Query Match 58.8%; Score 60; DB 5; Length 112;  
 Best Local Similarity 46.7%; Pred. No. 3.36e-01;  
 Matches 7; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Db 24 raszsvnwygnsfmz 38  
 QY 1 KASQSDYDGDSTYN 15

RESULT 9  
 ID PBP2 STRPN STANDARD; PRT; 679 AA.  
 AC P10524;  
 DT 01-JUL-1989 (REL. 11, CREATED)  
 DT 01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)  
 DT 01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)  
 DE PENICILLIN-BINDING PROTEIN 2B.  
 GN PENA.  
 OS STREPTOCOCCUS PNEUMONIAE.  
 OC PROKARYOTA; FIRMICUTES; COCCI; STREPTOCOCCACEAE.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=R6;  
 RX MEDLINE; 90016914.  
 RA DOWSON C.G., HUTCHISON A., SPRATT B.G.;  
 RL NUCLEIC ACIDS RES. 17:7518-7518(1989).

[2]  
 RN SEQUENCE OF 194-679 FROM N.A.  
 RP STRAIN=64147, AND R6;  
 RX MEDLINE; 89237905.  
 RA DOWSON C.G., HUTCHISON A., SPRATT B.G.;  
 RL MOL. MICROBIOL. 3:95-102(1989).  
 CC -1- SIMILARITY: ONLY SMALL REGIONS OF SIMILARITY (AROUND THE ACTIVE SITE SERINE) TO OTHER PENICILLIN-RECOGNIZING ENZYMES.  
 DR EMBL; X13137; G47400; -.  
 DR EMBL; X16022; G984233; -.  
 DR EMBL; X13136; G47398; -.  
 DR PIR; S06000; S06000.  
 KW CELL WALL; PEPTIDOGLYCAN SYNTHESIS; ANTIBIOTIC RESISTANCE.  
 FT VARIANT 332 332  
 FT VARIANT 425 431  
 FT VARIANT 445 445  
 FT VARIANT 475 475  
 FT VARIANT 488 488  
 FT VARIANT 511 511  
 FT VARIANT 537 537  
 FT VARIANT 596 596  
 FT VARIANT 673 675  
 SQ SEQUENCE 679 AA; 73722 MW; 85F09C45 CRC32;

Query Match 56.9%; Score 58; DB 6; Length 679;  
 Best Local Similarity 38.5%; Pred. No. 8.29e-01;

Mar 18 10:07

US-08-612-929-16.rsp

8

Matches 5; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Db 435 avqaleysentym 447  
 QY 2 ASQSDYDGDSTYN 14

RESULT 10  
 ID KV2B HUMAN STANDARD; PRT; 113 AA.  
 AC P01615;  
 DT 21-JUL-1986 (REL. 01, CREATED)  
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DT 01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)  
 DE IG KAPPA CHAIN V-II REGION (FR).  
 OS HOMO SAPIENS (HUMAN).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; PRIMATES.  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE; 76253627.  
 RA RIESEN W.F., JATON J.-C.;  
 RL BIOCHEMISTRY 15:3829-3833(1976).  
 CC -1- THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S MACROGLOBULIN THAT BINDS PHOSPHORYLCHOLINE.  
 DR PIR; A01886; K2HUFR.  
 DR HSP; P01607; IJEL.  
 KW IMMUNOGLOBULIN V REGION.  
 FT DOMAIN 1 23  
 FT DOMAIN 24 39  
 FT DOMAIN 40 54  
 FT DOMAIN 55 61  
 FT DOMAIN 62 93  
 FT DOMAIN 94 102  
 FT DOMAIN 103 112  
 FT DISULFID 23 93  
 FT NON TER 113 113  
 SQ SEQUENCE 113 AA; 12660 MW; 53CADDDE CRC32;

Query Match 55.9%; Score 57; DB 5; Length 113;  
 Best Local Similarity 37.5%; Pred. No. 1.29e+00;  
 Matches 6; Conservative 8; Mismatches 1; Indels 1; Gaps 1;

Db 24 rasqslvrbqbtlyb 39  
 QY 1 KASQSDYDGDSTYN 15

RESULT 11  
 ID KV3V MOUSE STANDARD; PRT; 108 AA.  
 AC P01674;  
 DT 21-JUL-1986 (REL. 01, CREATED)  
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)  
 DE IG KAPPA CHAIN V-III REGION (PC 2154).  
 OS MUS MUSCULUS (MOUSE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; RODENTIA.  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE; 79073152.  
 RA WEIGERT M., GATMAITAN L., LOH E., SCHILLING J., HOOD L.E.;  
 RL NATURE 276:785-790(1978).  
 DR PIR; A01940; KMS54.  
 DR HSP; P01679; IACY.

Mar 18 10:07

US-08-612-929-16.rsp

9

KW IMMUNOGLOBULIN V REGION.

FT DOMAIN 1 23  
 FT DOMAIN 24 38  
 FT DOMAIN 39 53  
 FT DOMAIN 54 60  
 FT DOMAIN 61 92  
 FT DOMAIN 93 101  
 FT DOMAIN 102 108  
 FT DISULFID 23 92  
 FT NON\_TER 108 108  
 SQ SEQUENCE 108 AA; 11699 MW; E28989CC CRC32;

Query Match 54.9%; Score 56; DB 5; Length 108;

Best Local Similarity 60.0%; Pred. No. 2.00e+00;

Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Db 24 raesvdsygnsfmh 38

:||||| i:|:

Qy 1 KASQSDVDGDSYMN 15

RESULT 12

ID KV3H MOUSE STANDARD; PRT; 111 AA.  
 AC P01660;  
 DT 21-JUL-1986 (REL. 01, CREATED)  
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)  
 DE IG KAPPA CHAIN V-III REGION (PC 3741 AND TEPC 111).  
 OS MUS MUSCULUS (MOUSE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; RODENTIA.  
 RN [1]  
 RP SEQUENCE (PC 3741).  
 RX MEDLINE; 79073152.  
 RA WEIGERT M., GATMAITAN L., LOH E., SCHILLING J., HOOD L.E.;  
 RL NATURE 276:785-790(1978).  
 RN [2]  
 RP SEQUENCE (TEPC 111).  
 RX MEDLINE; 79012520.  
 RA MCKEAN D.J., BELL M., POTTER M.;  
 RL PROC. NATL. ACAD. SCI. U.S.A. 75:3913-3917(1978).  
 CC -!- THE PC 3741 AND TEPC 111 SEQUENCES ARE IDENTICAL.  
 DR PIR; A01934; KVMG37.  
 DR HSSP; P01679; IGGB.  
 KW IMMUNOGLOBULIN V REGION.  
 FT DOMAIN 1 23  
 FT DOMAIN 24 38  
 FT DOMAIN 39 53  
 FT DOMAIN 54 60  
 FT DOMAIN 61 92  
 FT DOMAIN 93 101  
 FT DOMAIN 102 111  
 FT DISULFID 23 92  
 FT NON\_TER 111 111  
 SQ SEQUENCE 111 AA; 12099 MW; 76502E89 CRC32;

Query Match 54.9%; Score 56; DB 5; Length 111;

Best Local Similarity 53.3%; Pred. No. 2.00e+00;

Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Db 24 raesvdsygnsfmh 38

:||||| i:|:

Qy 1 KASQSDVDGDSYMN 15

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10

RESULT 13  
 ID KV3J MOUSE STANDARD; PRT; 111 AA.  
 AC P01662;  
 DT 21-JUL-1986 (REL. 01, CREATED)  
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)  
 DE IG KAPPA CHAIN V-III REGION (ABPC 22 AND PC 9245).  
 OS MUS MUSCULUS (MOUSE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; RODENTIA.  
 RN [1]  
 RP SEQUENCE (ABPC 22).  
 RX MEDLINE; 79012520.  
 RA MCKEAN D.J., BELL M., POTTER M.;  
 RL PROC. NATL. ACAD. SCI. U.S.A. 75:3913-3917(1978).  
 RN [2]  
 RP SEQUENCE (PC 9245).  
 RX MEDLINE; 79073152.  
 RA WEIGERT M., GATMAITAN L., LOH E., SCHILLING J., HOOD L.E.;  
 RL NATURE 276:785-790(1978).  
 CC -!- THE ABPC22 AND PC9241 SEQUENCES ARE IDENTICAL.  
 DR PIR; A01935; KVMG36.  
 DR HSSP; P01679; IACY.  
 KW IMMUNOGLOBULIN V REGION.  
 FT DOMAIN 1 23  
 FT DOMAIN 24 38  
 FT DOMAIN 39 53  
 FT DOMAIN 54 60  
 FT DOMAIN 61 92  
 FT DOMAIN 93 101  
 FT DOMAIN 102 111  
 FT DISULFID 23 92  
 FT NON\_TER 111 111  
 SQ SEQUENCE 111 AA; 12041 MW; 711C554A CRC32;

Query Match 54.9%; Score 56; DB 5; Length 111;

Best Local Similarity 53.3%; Pred. No. 2.00e+00;

Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Db 24 raesvdsygnsfmh 38

:||||| i:|:

Qy 1 KASQSDVDGDSYMN 15

RESULT 14

ID KV3K MOUSE STANDARD; PRT; 111 AA.  
 AC P01663;  
 DT 21-JUL-1986 (REL. 01, CREATED)  
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)  
 DE IG KAPPA CHAIN V-III REGION (PC 4050).  
 OS MUS MUSCULUS (MOUSE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; RODENTIA.  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE; 79073152.  
 RA WEIGERT M., GATMAITAN L., LOH E., SCHILLING J., HOOD L.E.;  
 RL NATURE 276:785-790(1978).  
 DR PIR; A01935; KVMG36.  
 DR HSSP; P01679; IACY.  
 KW IMMUNOGLOBULIN V REGION.  
 FT DOMAIN 1 23  
 FT DOMAIN 24 38  
 FT DOMAIN 39 53  
 FT DOMAIN 54 60  
 FT DOMAIN 61 92  
 FT DOMAIN 93 101  
 FT DOMAIN 102 111  
 FT DISULFID 23 92  
 FT NON\_TER 111 111  
 SQ SEQUENCE 111 AA; 12041 MW; 711C554A CRC32;

Query Match 54.9%; Score 56; DB 5; Length 111;

Best Local Similarity 53.3%; Pred. No. 2.00e+00;

Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Db 24 raesvdsygnsfmh 38

:||||| i:|:

Qy 1 KASQSDVDGDSYMN 15

FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING 1.  
 FT DOMAIN 39 53 FRAMEWORK 2.  
 FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING 2.  
 FT DOMAIN 61 92 FRAMEWORK 3.  
 FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING 3.  
 FT DOMAIN 102 111 FRAMEWORK 4.  
 FT DISULFID 23 92 BY SIMILARITY.  
 FT NON TER 111 111  
 SQ SEQUENCE 111 AA; 12005 MW; 5EBF3264 CRC32;

Query Match 54.9%; Score 56; DB 5; Length 111;  
 Best Local Similarity 53.3%; Pred. No. 2.00e+00;  
 Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Db 24 rasesvdsygnsfmh 38  
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 QY 1 KASQSDYDGD SYMN 15

RESULT 15  
 ID KV3I MOUSE STANDARD; PRT; 131 AA.  
 AC P01661;  
 DT 21-JUL-1986 (REL. 01, CREATED)  
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)  
 DE IG KAPPA CHAIN PRECURSOR V-III REGION (MOPC 63).  
 OS MUS MUSCULUS (MOUSE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUATHERIA; RODENTIA.  
 RN [1]  
 RP SEQUENCE OF 1-35.  
 RX MEDLINE; 78235887.  
 RA BURSTEIN Y., SCHECHTER I.;  
 RL BIOCHEMISTRY 17:2392-2400(1978).  
 RN [2]  
 RP SEQUENCE OF 21-131.  
 RX MEDLINE; 73140225.  
 RA MCKEAN D.J., POTTER M., HOOD L.E.;  
 RL BIOCHEMISTRY 12:760-771(1973).  
 RN [3]  
 RP REVISIONS.  
 RX MEDLINE; 79012520.  
 RA MCKEAN D.J., BELL M., POTTER M.;  
 RL PROC. NATL. ACAD. SCI. U.S.A. 75:3913-3917(1978).  
 DR PIR; A01935; KVM5M6.  
 DR HSP; P01679; IACY.  
 KW IMMUNOGLOBULIN V REGION; SIGNAL.  
 FT SIGNAL 1 20  
 FT CHAIN 21 131 IG KAPPA CHAIN V-III REGION (MOPC 63).  
 FT DOMAIN 21 43 FRAMEWORK 1.  
 FT DOMAIN 44 58 COMPLEMENTARITY-DETERMINING 1.  
 FT DOMAIN 59 73 FRAMEWORK 2.  
 FT DOMAIN 74 80 COMPLEMENTARITY-DETERMINING 2.  
 FT DOMAIN 81 112 FRAMEWORK 3.  
 FT DOMAIN 113 121 COMPLEMENTARITY-DETERMINING 3.  
 FT DOMAIN 122 131 FRAMEWORK 4.  
 FT DISULFID 43 112 BY SIMILARITY.  
 FT NON TER 131 131  
 SQ SEQUENCE 131 AA; 14291 MW; 9D55A06B CRC32;

Query Match 54.9%; Score 56; DB 5; Length 131;  
 Best Local Similarity 53.3%; Pred. No. 2.00e+00;  
 Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Db 44 rasesvdsygnsfmh 38  
 :||:|||| |:|:|:  
 QY 1 KASQSDYDGD SYMN 15

Search completed: Tue Mar 18 10:09:29 1997  
 Job time : 9 secs.

(T)

Result No.	Score	Query		DB	ID	Description	Pred. No.
		Match	Length				
1	102	100.0	81	12	S42193	Ig kappa chain V reg	2.14e-08
2	102	100.0	85	12	S42189	Ig kappa chain V reg	2.14e-08
3	102	100.0	87	12	S42190	Ig kappa chain V reg	2.14e-08
4	102	100.0	88	12	S42194	Ig kappa chain V reg	2.14e-08
5	102	100.0	90	12	S42187	Ig kappa chain V reg	2.14e-08
6	102	100.0	93	12	A38601	Ig kappa chain V reg	2.14e-08
7	102	100.0	111	2	KVMS43	Ig kappa chain V reg	2.14e-08
8	102	100.0	111	2	KVMS93	Ig kappa chain V reg	2.14e-08
9	102	100.0	111	2	KVMS08	Ig kappa chain V reg	2.14e-08
10	102	100.0	111	2	KVMS69	Ig kappa chain V reg	2.14e-08
11	96	94.1	110	2	KVMS10	Ig kappa chain V reg	3.65e-07
12	96	94.1	112	5	S19971	Ig kappa chain V reg	3.65e-07

## ALIGNMENTS

RESULT	1
ENTRY	S42193
TITLE	Ig kappa chain V region - mouse (fragment)
ORGANISM	#formal_name Mus musculus #common name house mouse
DATE	07-Oct-1994 #sequence_revision 26-May-1995 #text_change 26-May-1995
ACCESSIONS	S42193
REFERENCE	S42176
#authors	Mo, J.A.; Bona, C.A.; Holmdahl, R.
#journal	Eur. J. Immunol. (1993) 23:2503-2510
#title	Variable region gene selection of immunoglobulin G-expressing B cells with specificity for a defined epitope on type II collagen.

SUMMARY #length 81 #checksum 9746

Query Match 100.0%; Score 102; DB 12; Length 81;  
Best Local Similarity 100.0%; Pred. No. 2.14e-08;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Mar 18 10:08

US-08-612-929-16.mpr

3

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QY 1 KASQSVYDGD SYM 15

RESULT 2

ENTRY S42189 #type fragment

TITLE Ig kappa chain V region - mouse (fragment)

ORGANISM #formal name Mus musculus #common name house mouse

DATE 28-Sep-1994 #sequence\_revision 21-Jul-1995 #text\_change

21-Jul-1995

ACCESSIONS S42189

REFERENCE S42176

#authors Mo, J.A.; Bona, C.A.; Holmdahl, R.

#journal Eur. J. Immunol. (1993) 23:2503-2510

#title Variable region gene selection of immunoglobulin G-expressing

B cells with specificity for a defined epitope on type II

#accession S42189

#status preliminary

#molecule type DNA

#residues 1-85 #label MOJ

#cross-references EMBL:225448

SUMMARY #length 85 #checksum 7866

Query Match

Best Local Similarity 100.0%; Score 102; DB 12; Length 85;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 10 kasqsvdydgsym 24

|||||

QY 1 KASQSVYDGD SYM 15

RESULT 3

ENTRY S42190 #type fragment

TITLE Ig kappa chain V region - mouse (fragment)

ORGANISM #formal name Mus musculus #common name house mouse

DATE 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change

13-Jan-1995

ACCESSIONS S42190

REFERENCE S42176

#authors Mo, J.A.; Bona, C.A.; Holmdahl, R.

#journal Eur. J. Immunol. (1993) 23:2503-2510

#title Variable region gene selection of immunoglobulin G-expressing

B cells with specificity for a defined epitope on type II

#accession S42190

#status preliminary

#molecule type DNA

#residues 1-87 #label MOJ

#cross-references EMBL:225450

SUMMARY #length 87 #checksum 2354

Query Match

Best Local Similarity 100.0%; Score 102; DB 12; Length 87;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 12 kasqsvdydgsym 26

|||||

QY 1 KASQSVYDGD SYM 15

RESULT 4

ENTRY S42194 #type fragment

TITLE

ORGANISM #formal name Mus musculus #common name house mouse

DATE 28-Sep-1994 #sequence\_revision 21-Jul-1995 #text\_change

21-Jul-1995

ACCESSIONS S42194

REFERENCE S42176

#authors Mo, J.A.; Bona, C.A.; Holmdahl, R.

#journal Eur. J. Immunol. (1993) 23:2503-2510

#title Variable region gene selection of immunoglobulin G-expressing

B cells with specificity for a defined epitope on type II

#accession S42194

#status preliminary

#molecule type DNA

#residues 1-88 #label MOJ

#cross-references EMBL:225458

SUMMARY #length 88 #checksum 4364

Query Match

Best Local Similarity 100.0%; Score 102; DB 12; Length 88;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 13 kasqsvdydgsym 27

|||||

QY 1 KASQSVYDGD SYM 15

RESULT 5

ENTRY S42187 #type fragment

TITLE Ig kappa chain V region - mouse (fragment)

ORGANISM #formal name Mus musculus #common name house mouse

DATE 28-Sep-1994 #sequence\_revision 21-Jul-1995 #text\_change

21-Jul-1995

ACCESSIONS S42187

REFERENCE S42176

#authors Mo, J.A.; Bona, C.A.; Holmdahl, R.

#journal Eur. J. Immunol. (1993) 23:2503-2510

#title Variable region gene selection of immunoglobulin G-expressing

B cells with specificity for a defined epitope on type II

#accession S42187

#status preliminary

#molecule type DNA

#residues 1-90 #label MOJ

#cross-references EMBL:225444

SUMMARY #length 90 #checksum 9303

Query Match

Best Local Similarity 100.0%; Score 102; DB 12; Length 90;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 15 kasqsvdydgsym 29

|||||

QY 1 KASQSVYDGD SYM 15

RESULT 6

ENTRY A38601 #type fragment

TITLE Ig kappa chain V region (IG3) - mouse (fragment)

ORGANISM #formal name Mus musculus #common name house mouse

DATE 30-Aug-1991 #sequence\_revision 30-Aug-1991 #text\_change

23-Mar-1993

ACCESSIONS A38601

REFERENCE A38601

Mar 18 10:08

US-08-612-929-16.rpr

5

```
#authors      Goshorn, S.C.; Retzel, E.; Jermerson, R.
#journal      J. Biol. Chem. (1991) 266:2134-2142
#title        Common structural features among monoclonal antibodies
               binding the same antigenic region of cytochrome c.
#cross-references MUID:91115823
#accession    A38601
               preliminary
#status       #molecule_type mRNA
#residues     1-93 ##label GOS
#cross-references GB:M57978
SUMMARY       #length 93 #checksum 6635

Query Match   100.0%; Score 102; DB 12; Length 93;
Best Local Similarity 100.0%; Pred. No. 2.14e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 5 kasqsvdydgsym 19
   |||||
Qy 1 KASQSVDYDGSYMN 15

RESULT 7
ENTRY   KWMS43      #type complete
TITLE   Ig kappa chain V region (PC7043) - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE     01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change
         05-Apr-1995
ACCESSIONS A01937
REFERENCE   A93204
#authors   Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
#journal   Nature (1978) 276:785-790
#title     Rearrangement of genetic information may produce
           immunoglobulin diversity.
#cross-references MUID:79073152
#accession A01937
#molecule_type protein
#residues  1-111 ##label WEI

CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
FEATURE
23-92      #disulfide_bonds #status predicted
SUMMARY    #length 111 #molecular_weight 12002 #checksum 438

Query Match   100.0%; Score 102; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 2.14e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 24 kasqsvdydgsym 38
   |||||
Qy 1 KASQSVDYDGSYMN 15

RESULT 8
ENTRY   KWMS83      #type complete
TITLE   Ig kappa chain V region (PC7183) - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE     30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change
         30-Sep-1993
ACCESSIONS B01937; A01937
REFERENCE   A93204
#authors   Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
#journal   Nature (1978) 276:785-790
#title     Rearrangement of genetic information may produce
           immunoglobulin diversity.
#cross-references MUID:79073152
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Mar 18 10:08

US-08-612-929-16.rpr

6

```
#accession    B01937
#molecule_type protein
#residues     1-111 ##label WEI
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS      immunoglobulin
FEATURE        #disulfide_bonds #status predicted
23-92          #length 111 #molecular_weight 11952 #checksum 9
SUMMARY

Query Match   100.0%; Score 102; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 2.14e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 24 kasqsvdydgsym 38
   |||||
Qy 1 KASQSVDYDGSYMN 15

RESULT 9
ENTRY   KWMS08      #type complete
TITLE   Ig kappa chain V region (PC6308) - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE     30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change
         30-Sep-1993
ACCESSIONS C01937; A01937
REFERENCE   A93204
#authors   Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
#journal   Nature (1978) 276:785-790
#title     Rearrangement of genetic information may produce
           immunoglobulin diversity.
#cross-references MUID:79073152
#accession C01937
#molecule_type protein
#residues     1-111 ##label WEI

CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS      immunoglobulin
FEATURE        #disulfide_bonds #status predicted
23-92          #length 111 #molecular_weight 12071 #checksum 2195
SUMMARY

Query Match   100.0%; Score 102; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 2.14e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 24 kasqsvdydgsym 38
   |||||
Qy 1 KASQSVDYDGSYMN 15

RESULT 10
ENTRY   KWMS69      #type complete
TITLE   Ig kappa chain V region (PC7769) - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE     30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change
         30-Sep-1993
ACCESSIONS E01937; A01937
REFERENCE   A93204
#authors   Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
#journal   Nature (1978) 276:785-790
#title     Rearrangement of genetic information may produce
           immunoglobulin diversity.
#cross-references MUID:79073152
#accession   E01937
#molecule_type protein
```



Mar 18 10:08

US-08-612-929-16 rpr

7

##residues 1-111 ##label WEI  
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology  
KEYWORDS immunoglobulin  
FEATURE  
23-92 #disulfide bonds #status predicted  
SUMMARY #length 111 #molecular-weight 12011 #checksum 562

Query Match 100.0%; Score 102; DB 2; Length 111;  
Best Local Similarity 100.0%; Pred. No. 2.14e-08;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 24 kasqldydgdsym 38  
|||||:|||||  
Qy 1 KASQSDYDGD SYM 15

RESULT 11  
ENTRY KWMS10 #type complete  
TITLE Ig kappa chain V region (PC7210) - mouse  
ORGANISM #formal name Mus musculus #common name house mouse  
DATE 30-Jun-1993 #sequence\_revision 30-Jun-1993 #text\_change 30-Sep-1993  
ACCESSIONS D01937; A01937  
REFERENCE A93204  
#authors Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.  
#journal Nature (1978) 276:785-790  
#title Rearrangement of genetic information may produce immunoglobulin diversity.  
#cross-references M01D:79073152  
#accession D01937  
##molecule\_type protein  
##residues 1-110 ##label WEI  
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology  
KEYWORDS immunoglobulin  
FEATURE  
23-92 #disulfide bonds #status predicted  
SUMMARY #length 110 #molecular-weight 11950 #checksum 6378

Query Match 94.1%; Score 96; DB 2; Length 110;  
Best Local Similarity 93.3%; Pred. No. 3.65e-07;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 24 kasqldydgdsym 38  
|||||:|||||  
Qy 1 KASQSDYDGD SYM 15

RESULT 12  
ENTRY S19971 #type fragment  
TITLE Ig kappa chain V region (CD4 mAb clone M-T310 and others) - mouse (fragment)  
ORGANISM #formal name Mus musculus #common name house mouse  
DATE 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 01-Dec-1995  
ACCESSIONS S19971; S19973  
REFERENCE S19963  
#authors Weissenhorn, W.; Riethmuller, G.; Weiss, E.M.; Rieber, E.P.  
#submission submitted to the EMBL Data Library, March 1992  
#description Structural characterization of CD4 mAb.  
#accession S19971  
##molecule\_type mRNA  
##residues 1-112 ##label WEI  
#cross-references EMBL:X65091  
#experimental\_source clone M-T310

Mar 18 10:08

US-08-612-929-16 rpr

8

##accession S19973  
##molecule\_type mRNA  
##residues 1-112 ##label WEI  
#cross-references EMBL:X65092  
#experimental\_source M-T404  
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology  
SUMMARY #length 112 #checksum 4782

Query Match 94.1%; Score 96; DB 5; Length 112;  
Best Local Similarity 93.3%; Pred. No. 3.65e-07;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 24 kasqldydgdsym 38  
|||||:|||||  
Qy 1 KASQSDYDGD SYM 15

RESULT 13  
ENTRY PHI226 #type fragment  
TITLE Ig kappa chain precursor V region (M-T310) - human (fragment)  
ORGANISM #formal name Homo sapiens #common name man  
DATE 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 30-Apr-1995  
ACCESSIONS PHI226  
REFERENCE PHI224  
#authors Weissenhorn, W.; Scheuer, W.; Kaluza, B.; Schwirzke, M.; Reiter, C.; Fliieger, D.; Lenz, H.; Weiss, E.H.; Rieber, E.P.; Riethmuller, G.; Weidle, U.H.  
#journal Gene (1992) 121:271-278  
#title Combinatorial functions of two chimeric antibodies directed to human CD4 and one directed to the alpha-chain of the human interleukin-2 receptor.  
#accession PHI226  
##molecule\_type mRNA  
##residues 1-131 ##label WEI  
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology  
KEYWORDS immunoglobulin  
FEATURE  
1-20 #domain signal sequence #status predicted #label SIG\  
21-131 #product Ig light chain V region #status predicted #label MAT  
SUMMARY #length 131 #checksum 4648

Query Match 94.1%; Score 96; DB 5; Length 131;  
Best Local Similarity 93.3%; Pred. No. 3.65e-07;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 44 kasqldydgdsym 58  
|||||:|||||  
Qy 1 KASQSDYDGD SYM 15

RESULT 14  
ENTRY S09966 #type fragment  
TITLE Ig kappa chain V-J region (IE10) - mouse (fragment)  
ORGANISM #formal name Mus musculus #common name house mouse  
DATE 12-Feb-1993 #sequence\_revision 12-Feb-1993 #text\_change 30-Sep-1993  
ACCESSIONS S09966  
REFERENCE S09955  
#authors Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jatón, J.C.; Izui, S.  
#journal Eur. J. Immunol. (1990) 20:771-777  
#title Variable region sequences of pathogenic anti-mouse red blood

Mar 18 10:08

US-08-612-929-16.rpt

9

cell autoantibodies from autoimmune NZB mice.

#cross-references MUID:90269328  
#accession S09966  
##molecule type mRNA  
##residues 1-111 ##label REI  
##cross-references EMBL:X51854  
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology  
SUMMARY #length 111 #checksum 3572

Query Match 93.1%; Score 95; DB 5; Length 111;  
Best Local Similarity 93.3%; Pred. No. 5.82e-07;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 24 kasxsvdydgdgysyn 38  
|||||  
QY 1 KASQSVDYDGDGYSYN 15

RESULT 15

ENTRY KVMSC1 #type complete  
TITLE Ig kappa chain V region (CBPC 101) - mouse  
ORGANISM #formal name Mus musculus #common name house mouse  
DATE 30-Nov-1980 #sequence\_revision 30-Nov-1980 #text\_change 05-Apr-1995

ACCESSIONS A01936  
REFERENCE A93822  
#authors McKean, D.J.; Bell, M.; Potter, M.  
#journal Proc. Natl. Acad. Sci. U.S.A. (1978) 75:3913-3917  
#title Mechanisms of antibody diversity: multiple genes encode structurally related mouse kappa variable regions.

#cross-references MUID:79012520  
#accession A01936

##molecule type protein  
##residues 1-111 ##label MCK  
COMMENT This chain was isolated from a myeloma protein.  
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology

FEATURE 23-92  
SUMMARY #disulfide\_bonds #status predicted  
#length 111 #molecular\_weight 11964 #checksum 1507

Query Match 92.2%; Score 94; DB 2; Length 111;  
Best Local Similarity 86.7%; Pred. No. 9.27e-07;  
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 24 kasqsvdytgesyn 38  
|||||  
QY 1 KASQSVDYDGDGYSYN 15

Search completed: Tue Mar 18 10:09:56 1997  
Job time : 11 secs.



CC encoded the protein given in R70189. 3 CDRs (R70195-97) were  
 CC identified.  
 SQ Sequence 15 AA;

Query Match 100.0%; Score 102; DB 13; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2.86e-04;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 kasqsvdydgdsgym 15  
 |||||||  
 Qy 1 KASQSVDYDGDGYM 15

## RESULT 2

ID R66143 standard; peptide; 19 AA.  
 AC R66143;  
 DT 12-JUL-1995 (first entry)  
 DE CD-4 antibody variable region complementary peptide.  
 KW CD-4 antibody variable region; complementary peptide;  
 KW extra-corporeal blood circulation; cell filter material.  
 OS Synthetic.  
 PN J06269663-A.  
 PD 27-SEP-1994.  
 PF 17-MAR-1993; 057206.  
 PR 17-MAR-1993; JP-057206.  
 PA (TOYM) TOY080 KK.  
 DR WPI; 94-346316/43.  
 PT Material for collecting cells positive for CD-4 antibody -  
 PT comprises nonwoven fabric having keto-alkyl halide functional gp  
 PS Example 1; Page 6; 9pp; Japanese.  
 CC R66140-R66146 are peptides complementary to the variable region  
 CC of the CD-4 antibody, these peptides are fixed onto a claimed  
 CC nonwoven fabric (average fibre dia. of 1-30 microns) coated with  
 CC keto-alkyl halide functional groups. This material can be used  
 CC as a filter for CD-4 positive cells in a medical treatment  
 CC involving the extra-corporeal circulation of blood.  
 SQ Sequence 19 AA;

Query Match 100.0%; Score 102; DB 12; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 2.86e-04;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 5 kasqsvdydgdsgym 19  
 |||||||  
 Qy 1 KASQSVDYDGDGYM 15

## RESULT 3

ID R33309 standard; Protein; 106 AA.  
 AC R33309;  
 DT 05-JUL-1993 (first entry)  
 DE MAE15 light chain.  
 KW Antibody; high affinity; FCEH; low affinity; FCEH;  
 KW IgE receptor; histamine; mast cell; basophil; Kabat;  
 KW CDR; murine; MAE11; MAE13; MAE15; MAE17.  
 OS Synthetic.  
 PN W09304173-A.  
 PD 04-MAR-1993.  
 PF 14-AUG-1992; U06860.  
 PR 14-AUG-1991; US-744768.  
 PR 07-MAY-1992; US-879495.  
 PA (GETH) GENENTECH INC.  
 PI Jardieu PM, Presta LG;  
 DR WPI; 93-094004/11.

PT Polypeptide(s) binding to specific Fc epsilon receptors - act as  
 PT IgE antagonists; useful for treating and preventing IgE-mediated  
 PT disorders e.g. allergies  
 PS Disclosure; Fig 2; 113pp; English.  
 CC Antibodies capable of binding FCEH-bound IgE but which are  
 CC substantially incapable of binding FCEH-bound IgE or inducing  
 CC histamine release from mast cells or basophils, comprise a human  
 CC Kabat CDR domain into which has been substituted a positionally  
 CC analogous residue from a Kabat CDR domain of the murine anti-huIgE  
 CC antibodies MAE11, MAE13, MAE15 or MAE17.  
 SQ Sequence 106 AA;

Query Match 100.0%; Score 102; DB 6; Length 106;  
 Best Local Similarity 100.0%; Pred. No. 2.86e-04;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 24 kasqsvdydgdsgym 38  
 |||||||  
 Qy 1 KASQSVDYDGDGYM 15

## RESULT 4

ID R60302 standard; Protein; 111 AA.  
 AC R60302;  
 DT 09-MAR-1995 (first entry)  
 DE Anti HIV antibody light chain variable region.  
 KW Antibody; heavy chain; light chain; human immunodeficiency virus;  
 KW HIV; acquired immune deficiency syndrome; AIDS: treatment;  
 KW prophylaxis; Mus musculus; Homo sapiens.  
 OS Mus musculus.  
 FH Key Location/Qualifiers  
 FT Region 1..23  
 FT /label= Framework region 1.  
 FT Region 24..38  
 FT /label= CDR1.  
 FT Region 39..53  
 FT /label= Framework region 2.  
 FT Region 54..60  
 FT /label= CDR2.  
 FT Region 61..92  
 FT /label= Framework region 3.  
 FT Region 93..101  
 FT /label= CDR3.  
 FT Region 102..111  
 FT /label= Framework region 4.  
 PN W09415969-A.  
 PD 21-JUL-1994.  
 PF 14-JAN-1993; J00039.  
 PR 14-JAN-1993; AD-032671.  
 PR 14-JAN-1993; WO-J00039.  
 PA (KAGA) CEMO SERO THERAPEUTIC RES INST.  
 PI Eda Y, Kimachi K, Maeda H, Osatomi K, Shiosaki K;  
 PI Tokiyoshi S;  
 DR WPI; 94-249145/30.  
 DR N-PSDB; Q70372.  
 PT Recombinant chimeric anti HIV antibody - useful for the treatment  
 PT and prevention of HIV  
 PS Claim 15; Figure 4; 51pp; Japanese.  
 CC The recombinant antibody light chain has neutralising activity  
 CC against HIV. Chimeric antibodies comprising both mouse and human  
 CC sequences are useful in the treatment/prevention of AIDS caused by  
 CC HIV.  
 SQ Sequence 111 AA;

Query Match 100.0%; Score 102; DB 11; Length 111;  
Best Local Similarity 100.0%; Pred. No. 2.86e-04;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 24 kasqsvdydgsym 38  
|||||  
Qy 1 KASQSVDYDGSYNN 15

## RESULT 5

ID R33305 standard; protein; 111 AA.  
AC R33305;  
DT 05-JUL-1993 (first entry)  
DE MaEl1 light chain.  
KW Antibody; high affinity; FCEH; low affinity; FCEL;  
KW IgE receptor; histamine; mast cell; basophil; Kabat;  
KW CDR; murine; MAE11; MAE13; MAE15; MAE17.  
OS Synthetic.  
PN W09304173-A.  
PD 04-MAR-1993.  
PF 14-AUG-1992; 006860.  
PR 14-AUG-1991; US-744768.  
PR 07-MAY-1992; US-879495.  
PA (GETH ) GENENTECH INC.  
PI Jardiou PM, Presta LG;  
DR WPI; 93-094004/11.  
PT Polypeptide(s) binding to specific Fc epsilon receptors - act as  
PT IgE antagonists; useful for treating and preventing IgE-mediated  
PT disorders e.g. allergies  
PS Disclosure; Fig 2; 113pp; English.  
CC Antibodies capable of binding FCEL-bound IgE but which are  
CC substantially incapable of binding FCEH-bound IgE or inducing  
CC histamine release from mast cells or basophils, comprise a human  
CC Kabat CDR domain into which has been substituted a positionally  
CC analogous residue from a Kabat CDR domain of the murine anti-huIgE  
CC antibodies MAE11, MAE13, MAE15 or MAE17.  
SQ Sequence 111 AA;

Query Match 100.0%; Score 102; DB 6; Length 111;  
Best Local Similarity 100.0%; Pred. No. 2.86e-04;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 24 kasqsvdydgsym 38  
|||||  
Qy 1 KASQSVDYDGSYNN 15

## RESULT 6

ID R60306 standard; Protein; 111 AA.  
AC R60306;  
DT 13-MAR-1995 (first entry)  
DE Chimeric anti HIV antibody light chain variable region.  
KW Antibody; heavy chain; light chain; human immunodeficiency virus;  
KW HIV; acquired immune deficiency syndrome; AIDS: treatment;  
KW prophylaxis; Mus musculus; Homo sapiens.  
OS Chimeric Homo sapiens  
OS Chimeric Mus musculus.  
FH Key Location/Qualifiers  
FT Region 1..23  
FT /label= Framework region 1.  
FT Region 24..38  
FT /label= CDR1.  
FT /note= "Mouse derived amino acid sequence."  
FT Region 39..53

FT /label= Framework region 2.  
FT Region 54..60  
FT /label= CDR2.  
FT /note= "Mouse derived amino acid sequence."  
FT Region 61..92  
FT /label= Framework region 3.  
FT Region 93..101  
FT /label= CDR3.  
FT /note= "Mouse derived amino acid sequence."  
FT Region 102..111  
FT /label= Framework region 4.  
PN W09415969-A.  
PD 21-JUL-1994.  
PF 14-JAN-1993; J00039.  
PR 14-JAN-1993; AU-032671.  
PR 14-JAN-1993; W0-J00039.  
PA (KAGA ) CEMO SERO THERAPEUTIC RES INST.  
PI Eda Y, Kimachi K, Maeda H, Osatomi K, Shioasaki K;  
PI Tokiyoshi S;  
DR WPI; 94-249145/30.  
DR N-PSDB; R60306.  
PT Recombinant chimeric anti HIV antibody - useful for the treatment  
PT and prevention of HIV  
PS Claim 14; Figure 12; 51pp; Japanese.  
CC The recombinant antibody light chain has neutralising activity  
CC against HIV. Chimeric antibodies comprising both mouse and human  
CC sequences are useful in the treatment/prevention of AIDS caused by  
CC HIV.  
SQ Sequence 111 AA;

Query Match 100.0%; Score 102; DB 11; Length 111;  
Best Local Similarity 100.0%; Pred. No. 2.86e-04;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 24 kasqsvdydgsym 38  
|||||  
Qy 1 KASQSVDYDGSYNN 15

## RESULT 7

ID R55127 standard; Protein; 111 AA.  
AC R55127;  
DT 30-JUN-1995 (first entry)  
DE Mouse-human chimeric anti-HIV mu5.5-derived light chain V region.  
KW Immunoglobulin; heavy chain; anti-HIV antibody; neutralisation;  
KW human immunodeficiency virus; variable region; VL chain; murine;  
KW chimeric; humanised.  
OS Chimeric Mus musculus.  
OS Chimeric Homo sapiens.  
FH Key Location/Qualifiers  
FT Region 1..23  
FT /label= FR1  
FT /note= "human"  
FT Region 24..38  
FT /label= CDR1  
FT /note= "murine"  
FT Region 39..53  
FT /label= FR2  
FT Region 54..60  
FT /label= CDR2  
FT /note= "murine"  
FT Region 61..92  
FT /label= FR3  
FT /note= "human"

FT Region 93..101  
 FT /label= CDR3  
 FT /note= "murine"  
 FT Region 102..111  
 FT /label= FR4  
 FT /note= "human"  
 PN J06125783-A.  
 PD 10-MAY-1994.  
 PE 28-DEC-1991; 359808.  
 PR 28-DEC-1991; JP-359808.  
 PA (KAGA-) 2H KAGAKU KESSEI-RYOHO KENKYUSHO.  
 DR WPI; 94-187942/23.  
 DR N-PSDB; Q65558.  
 PT Mouse-human chimeric anti-HIV antibody heavy and light chains -  
 PT and recombinant antibody consisting of the H- and L-chains,  
 PT useful in AIDS therapy  
 PS Claim 5; Fig 12; 22pp; Japanese.  
 CC Murine monoclonal antibodies mu 39.1 and mu 5.5 both neutralise HIV.  
 CC The heavy and light chain variable regions from these antibodies  
 CC were sequenced (R55120-R55123). The murine anti-HIV CDRs were  
 CC introduced into human framework regions to construct chimeric  
 CC antibodies (R55124-R55127).  
 SQ Sequence 111 AA;

Query Match 100.0%; Score 102; DB 10; Length 111;  
 Best Local Similarity 100.0%; Pred. No. 2.86e-04;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 24 kasqsvdydgsym 38  
 |||||  
 QY 1 KASQSVDYDGSYMN 15

## RESULT 8

ID R55123 standard; Protein; 111 AA.  
 AC R55123;  
 DT 27-JAN-1995 (first entry)  
 DE Mouse anti-HIV mu5.5 light chain variable region.  
 KW Immunoglobulin; heavy chain; anti-HIV antibody; neutralisation;  
 KW human immunodeficiency virus; variable region; VH chain; murine.  
 OS Mus musculus.  
 FH Key Location/Qualifiers  
 FT Region 1..23  
 FT /label= FR1  
 FT Region 24..38  
 FT /label= CDR1  
 FT Region 39..53  
 FT /label= FR2  
 FT Region 54..60  
 FT /label= CDR2  
 FT Region 61..92  
 FT /label= FR3  
 FT Region 93..101  
 FT /label= CDR3  
 FT Region 102..111  
 FT /label= FR4  
 PN J06125783-A.  
 PD 10-MAY-1994.  
 PE 28-DEC-1991; 359808.  
 PR 28-DEC-1991; JP-359808.  
 PA (KAGA-) 2H KAGAKU KESSEI-RYOHO KENKYUSHO.  
 DR WPI; 94-187942/23.  
 DR N-PSDB; Q65554.  
 PT Mouse-human chimeric anti-HIV antibody heavy and light chains -

PT and recombinant antibody consisting of the H- and L-chains,  
 PT useful in AIDS therapy  
 PS Example 3; Fig 4; 22pp; Japanese.  
 CC Murine monoclonal antibodies mu 39.1 and mu 5.5 both neutralise HIV.  
 CC The heavy and light chain variable regions from these antibodies  
 CC were sequenced (R55120-R55123). The murine anti-HIV CDRs were  
 CC introduced into human framework regions to construct chimeric  
 CC antibodies (R55124-R55127).  
 SQ Sequence 111 AA;

Query Match 100.0%; Score 102; DB 10; Length 111;  
 Best Local Similarity 100.0%; Pred. No. 2.86e-04;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 24 kasqsvdydgsym 38  
 |||||  
 QY 1 KASQSVDYDGSYMN 15

## RESULT 9

ID P90541 standard; protein; 111 AA.  
 AC P90541;  
 DT 20-OCT-1989 (first entry)  
 DE Immunoglobulin L chain variable region.  
 KW Immunoglobulin; L chain variable region; HIV.  
 OS Mus musculus  
 PN EP-327000-A.  
 PD 09-AUG-1989.  
 PF 30-JAN-1989; 101583.  
 PR 30-JAN-1988; JP-20255.  
 PR 08-JUL-1988; JP-171385.  
 PA (\*\*\*\*) The Chemo-Sero-Therapeutic Research Institute.  
 PI Maeda H, Eda Y, Kimachi K, Tokiyoshi S, Matsushita S, Hattori T,  
 PI Takatsuki K;  
 DR WPI; 89-229050/32.  
 DR N-PSDB; N90491, N90492, N90493.  
 PT Chimeric anti-human immune virus antibodies - contg. mouse variable  
 PT regions and human constant regions for diagnosis, treatment and  
 PT prevention of AIDS  
 PS Claim 5; page 15; 33pp; English.  
 CC The sequence is an L chain variable region from an immunoglobulin with  
 CC anti-HIV neutralising activity. See N90491-3, and N90495.  
 SQ Sequence 111 AA;

Query Match 100.0%; Score 102; DB 1; Length 111;  
 Best Local Similarity 100.0%; Pred. No. 2.86e-04;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 24 kasqsvdydgsym 38  
 |||||  
 QY 1 KASQSVDYDGSYMN 15

## RESULT 10

ID R24575 standard; Protein; 112 AA.  
 AC R24575;  
 DT 08-DEC-1992 (first entry)  
 DE Human x mouse modified anti-HIV antibody Light chain RL0.5beta.  
 KW Heavy; light; CDR; HIV; AIDS; REI; 0.5beta.  
 OS Synthetic.  
 FH Key Location/Qualifiers  
 FT Region 1..23  
 FT /label= FR1  
 FT Region 24..38

FT /label= CDR1 39..53  
FT Region  
FT /label= FR2 54..60  
FT Region  
FT /label= CDR2 61..92  
FT Region  
FT /label= FR3 93..101  
FT Region  
FT /label= CDR3 102..112  
FT Region  
FT /label= FR4  
PN J04141095-A.  
PD 14-MAY-1992.  
PF 02-OCT-1990; 266091.  
PR 02-OCT-1990; JP-266091.  
PA (KAGA ) KAGAKU OYOBI KESSEI RYOHO.  
DR WPI; 92-212765/26.  
PT New recombinant modified anti-HIV antibodies - comprise human x  
PT mouse modified antibody H and L chains  
PS Disclosure; Fig 2; 15pp; Japanese.  
CC The framework regions (FR) are derived from the human antibody  
CC REI. The CDRs are mouse monoclonal antibody 0.5beta derived  
CC sequences. The anti-HIV modified antibody can be used for the  
CC prophylaxis and treatment of AIDS.  
CC Specific examples of the H chain are given in R24556-58 and  
CC R24560-62. A specific example of the L chain is given in R24575.  
SQ Sequence 112 AA;

Query Match 100.0%; Score 102; DB 5; Length 112;  
Best Local Similarity 100.0%; Pred. No. 2.86e-04;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 24 kasqsvdydgsym 38  
|||||  
QY 1 KASQSVDYDGD SYM 15

RESULT 11  
ID R04134 standard; protein; 115 AA.  
AC R04134;  
DT 06-SEP-1990 (first entry)  
DE Anti-leu 3a light chain variable region gene product, KOL/206 V1.  
KW HIV; AIDS; anti-Leu3A; vaccine; ds.  
OS Mus musculus.  
PN EP-365209-A.  
PD 25-APR-1990.  
PF 11-OCT-1989; 010415.  
PR 17-OCT-1988; US-260558.  
PA (BECT) Becton Dickinson Co.  
PI Hinton R, Oi VT;  
DR WPI; 90-126329/17.  
DR N-PSDB; Q04041.  
PT New chimeric variants of murine antibody anti-leucine -  
PT contg. human antibody regions, and DNA encoding sequences.  
PS Claim 4; Fig 4; 12pp; English.  
CC Variants of murine monoclonal anti-CD4 antibody, anti-leu3A can be  
CC used to form chimeric mouse-variable, human-constant region Abs  
CC suggested as being useful as a vaccine to HIV.  
SQ Sequence 115 AA;

Query Match 100.0%; Score 102; DB 1; Length 115;  
Best Local Similarity 100.0%; Pred. No. 2.86e-04;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 27 kasqsvdydgsym 41  
|||||  
QY 1 KASQSVDYDGD SYM 15

RESULT 12  
ID R48618 standard; Protein; 120 AA.  
AC R48618;  
DT 03-SEP-1994 (first entry)  
DE Sequence of the monoclonal antibody BAT123 light chain  
DE variable region.  
KW Epitope; monoclonal antibody; BAT123; variable light.  
OS Synthetic.  
PN W09404574-A.  
PD 03-MAR-1994.  
PF 24-AUG-1993; U07967.  
PR 24-AUG-1992; WO-007111.  
PR 22-APR-1993; US-039457.  
PA (NISP ) NISSIN SHOKUHIN KAISHA LTD.  
PI Onno T;  
DR WPI; 94-083117/10.  
PT New humanised antibody specific for epitope on HIV-1 gp 120 -  
PT able to neutralise infection of HG cells, also nucleic acid  
PT encoding it, useful for passive immunisation to treat or prevent  
PT HIV-1 infection  
PS Example; Page 47; 91pp; English.  
CC GPGR is a portion of HIV-1 gp120 or gp160 protein. Monoclonal  
CC antibodies (MAbs) that react with this and which have the capacity  
CC to neutralise the infection of H9 cells in culture by live HIV-1  
CC strains MN and 11IB are claimed. Specifically illustrating the  
CC invention are the murine MAb (designated NM-01) produced by  
CC hybridoma cell line HB 10726 which is deposited under ATCC No. HB  
CC 10726. The DNA sequences of the variable regions of the heavy and  
CC light chains of MAB NM-01 were cloned by PCR using cDNA generated  
CC from hybridoma HB 10726 cytoplasmic RNA as template. The DNA was  
CC then sequenced. The DNA and deduced AA sequences are given in  
CC Q56685/R48613; Q56686/R48615. Resequencing the variable regions  
CC of MAB NM-01 resulted in the sequences set out in Q56687/R48614  
CC and Q56688/R48616. The heavy chain variable region of NM-01  
CC differs from that of the MAB BA123, as reported in Liou et al.,  
CC by 46 AAs out of a total of 120. The light chain variable regions  
CC of these two Abs differ by 23 AAs. Significantly, the three CDRs  
CC in the heavy chain (V-H) of the NM-01 molecule are about 41 to 90%  
CC different in sequence from those of BAT123, while the sequences of  
CC the three CDRs in the light chain (V-L) vary by about 29-47%  
CC compared to NM-01.  
SQ Sequence 120 AA;

Query Match 100.0%; Score 102; DB 9; Length 120;  
Best Local Similarity 100.0%; Pred. No. 2.86e-04;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 24 kasqsvdydgsym 38  
|||||  
QY 1 KASQSVDYDGD SYM 15

RESULT 13  
ID R75355 standard; Protein; 131 AA.  
AC R75355;  
DT 20-SEP-1995 (first entry)  
DE Humanized antibody 3B9 light chain.  
KW Humanized antibody; antibody engineering; monoclonal antibody;  
KW MAb; interleukin-4; IL-4; allergy.

OS Homo sapiens.  
FH Key Location/Qualifiers  
FT Peptide 1..20  
FT /label= Sig\_peptide  
FT Region 43..57  
FT /label= CDR  
FT /note= "complementarity determining region"  
FT Region 73..79  
FT /label= CDR  
FT /note= "complementarity determining region"  
FT Region 112..120  
FT /label= CDR  
FT /note= "complementarity determining region"  
PN WO9507301-A.  
PD 16-MAR-1995.  
PF 07-SEP-1994; U10308.  
PR 07-SEP-1993; US-117366.  
PR 14-OCT-1993; US-136783.  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
PA (SMIK ) SMITHKLINE BEECHAM PLC.  
PI Gross MS, Holmes SD, Sylvester DR;  
DR WPI; 95-123387/16.  
DR N-PSDB; Q73986.  
PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived from high affinity mAbs - useful in treatment of IL-4-mediated  
PT and IgE-mediated allergic conditions  
PS Disclosure; Fig.5; 97pp; English.  
CC A humanized antibody light chain variable region and signal sequence is given in R75355. The signal sequence is also provided in R70194. The sequences of the first 2 CDRs are identical to mouse anti-human IL-4 MAb 3B9 light chain CDRs (given in R70195-96), but the third (R70201) differs by a single amino acid from the native mouse CDR (R70197).  
SQ Sequence 131 AA;  
Query Match 100.0%; Score 102; DB 13; Length 131;  
Best Local Similarity 100.0%; Pred. No. 2.86e-04;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 43 kasqsvdydgsym 57  
Qy 1 KASQSVDYDGD SYM 15  
RESULT 14  
ID P90543 standard; protein; 131 AA.  
AC P90543;  
DT 20-OCT-1989 (first entry)  
DE Amino acids sequence of a V chi region gene.  
KW V cji region; immunoglobulin; L chain variable region; HIV.  
OS Mus musculus  
PN EP-327000-A.  
PD 09-AUG-1989.  
PF 30-JAN-1989; 101583.  
PR 30-JAN-1988; JP-20255.  
PR 08-JUL-1988; JP-171385.  
PA The Chemo-Sero-Therapeutic Research Institute.  
PI Maeda H, Eda Y, Kimachi K, Tokiyoshi S, Matsushita S, Hattori T, Takatsuki K;  
DR WPI; 89-229050/32.  
DR N-PSDB; N90495.  
PT Chimeric anti-human immune virus antibodies - contg. mouse variable regions and human constant regions for diagnosis, treatment and prevention of AIDS

PS Disclosure; Fig 8; 33pp; English.  
CC The sequence is encoded by a V chi region gene (see N90495).  
CC The sequence from Asp 21 encodes the L chain variable region.  
SQ Sequence 131 AA;  
Query Match 100.0%; Score 102; DB 1; Length 131;  
Best Local Similarity 100.0%; Pred. No. 2.86e-04;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 44 kasqsvdydgsym 58  
Qy 1 KASQSVDYDGD SYM 15  
RESULT 15  
ID R04132 standard; protein; 131 AA.  
AC R04132;  
DT 06-SEP-1990 (first entry)  
DE Anti-Leu 3a light chain variable region gene product, 206 Vx.  
KW HIV; AIDS; anti-Leu3A; vaccine; ds.  
OS Mus musculus.  
PN EP-365209-A.  
PD 23-APR-1990.  
PR 11-OCT-1989; 010415.  
PR 17-OCT-1988; US-260558.  
PA (BECT) Becton Dickinson Co.  
PI Hinton R, Oi VT;  
DR WPI; 90-126329/17.  
DR N-PSDB; Q04039.  
PT New chimeric variants of murine antibody anti-leucine -  
PT contg. human antibody regions, and DNA encoding sequences.  
PS Claim 1; Fig 2; 12pp; English.  
CC Variants of murine monoclonal anti-CD4 antibody, anti-leu3A can be used to form chimeric mouse-variable, human-constant region Abs suggested as being useful as a vaccine to HIV.  
SQ Sequence 131 AA;  
Query Match 100.0%; Score 102; DB 1; Length 131;  
Best Local Similarity 100.0%; Pred. No. 2.86e-04;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 44 kasqsvdydgsym 58  
Qy 1 KASQSVDYDGD SYM 15  
RESULT 16  
ID R70202 standard; Protein; 131 AA.  
AC R70202;  
DT 20-SEP-1995 (first entry)  
DE Humanized antibody 3B9 light chain.  
KW Humanized antibody; antibody engineering; monoclonal antibody; MAb; interleukin-4; IL-4; allergy.  
OS Homo sapiens.  
PN WO9507301-A.  
PD 16-MAR-1995.  
PF 07-SEP-1994; U10308.  
PR 07-SEP-1993; US-117366.  
PR 14-OCT-1993; US-136783.  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
PA (SMIK ) SMITHKLINE BEECHAM PLC.  
PI Gross MS, Holmes SD, Sylvester DR;  
DR WPI; 95-123387/16.  
DR N-PSDB; Q83520.



PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived  
PT from high affinity mAbs - useful in treatment of IL-4-mediated  
PT and IgE-mediated allergic conditions  
PS Disclosure; Page 71-72; 97pp; English.  
CC A humanized antibody light chain variable region and signal  
CC sequence is given in R75355. The signal sequence is also  
CC provided in R70194. The sequences of the 3 CDRs  
CC are identical to mouse anti-human IL-4 Mab 3B9 light chain  
CC CDRs (given in R70195-97).  
SQ Sequence 131 AA;

Query Match 100.0%; Score 102; DB 13; Length 131;  
Best Local Similarity 100.0%; Pred. No. 2.86e-04;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 43 kasqsvdydgsymn 57  
|||||  
Qy 1 KASQSVDYDGD SYMN 15

RESULT 17  
ID R70189 standard; Protein; 132 AA.  
AC R70189;  
DT 20-SEP-1995 (first entry)  
DE Mouse Mab 3B9 light chain.  
KW Chimeric antibody; humanized antibody; antibody engineering;  
KW monoclonal antibody; Mab; interleukin-4; IL-4; allergy.  
OS Mus sp.  
FH Key Location/Qualifiers  
FT Peptide 1..20  
FT /label= Sig\_peptide  
FT Region 44..58  
FT /label= CDR  
FT /note= "complementarity determining region"  
FT Region 74..80  
FT /label= CDR  
FT /note= "complementarity determining region"  
FT Region 113..121  
FT /label= CDR  
FT /note= "complementarity determining region"  
PN W09507301-A.  
PD 16-MAR-1995.  
PF 07-SEP-1994; U10308.  
PR 07-SEP-1993; US-117366.  
PR 14-OCT-1993; US-136783.  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
PA (SMIK ) SMITHKLINE BEECHAM PLC.  
PI Gross MS, Holmes SD, Sylvester DR;  
PI WPI; 95-123387/16.  
DR N-PDB; Q83490.  
PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived  
PT from high affinity mAbs - useful in treatment of IL-4-mediated  
PT and IgE-mediated allergic conditions  
PS Disclosure; Fig.1; 97pp; English.  
CC Spleen cells from mice immunized with human IL-4 were used to prepare  
CC hybridomas, which were screened for anti-IL-4 Mab secretion. Only  
CC clone 3B9 was positive. cDNA clones of the 3B9 light and heavy  
CC chains were cloned into pGEM7f+ and transformed into E. coli  
CC DH5-alpha. The clones were sequenced (Q83490-91), and used for  
CC antibody engineering.  
SQ Sequence 132 AA;

Query Match 100.0%; Score 102; DB 13; Length 132;  
Best Local Similarity 100.0%; Pred. No. 2.86e-04;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 44 kasqsvdydgsymn 58  
|||||  
Qy 1 KASQSVDYDGD SYMN 15

Search completed: Wed Mar 19 15:53:35 1997  
Job time : 15 secs.



Mar 18 10:08

US-08-612-929-18.rsp

3

Query Match 100.0%; Score 35; DB 5; Length 110;  
Best Local Similarity 100.0%; Pred. No. 1.92e+00;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 54 aasles 60  
Qy 1 AASNLES 7

RESULT 2

ID KV3Q MOUSE STANDARD; PRT; 111 AA.  
AC P01669;  
DT 21-JUL-1986 (REL. 01, CREATED)  
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)  
DE IG KAPPA CHAIN V-III REGION (PC 7769).  
OS MUS MUSCULUS (MOUSE).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; RODENTIA.  
RN [1]  
RP SEQUENCE.  
RX MEDLINE; 79073152.  
RA WEIGERT M., GATWALTAN L., LOH E., SCHILLING J., HOOD L.E.;  
RL NATURE 276:785-790(1978).  
DR PIR; E01937; KWS69.  
DR HSP; P01679; IACY.  
KW IMMUNOGLOBULIN V REGION.  
FT DOMAIN 1 23  
FT DOMAIN 24 38  
FT DOMAIN 39 53  
FT DOMAIN 54 60  
FT DOMAIN 61 92  
FT DOMAIN 93 101  
FT DOMAIN 102 111  
FT DISULFID 23 92  
FT NON TER 111 111  
SQ SEQUENCE 111 AA; 12011 MW; 9CB705B9 CRC32;

Query Match 100.0%; Score 35; DB 5; Length 111;  
Best Local Similarity 100.0%; Pred. No. 1.92e+00;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 54 aasles 60  
Qy 1 AASNLES 7

RESULT 3

ID KV3N MOUSE STANDARD; PRT; 111 AA.  
AC P01666;  
DT 21-JUL-1986 (REL. 01, CREATED)  
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)  
DE IG KAPPA CHAIN V-III REGION (PC 7183).  
OS MUS MUSCULUS (MOUSE).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; RODENTIA.  
RN [1]  
RP SEQUENCE.  
RX MEDLINE; 79073152.  
RA WEIGERT M., GATWALTAN L., LOH E., SCHILLING J., HOOD L.E.;  
RL NATURE 276:785-790(1978).  
DR PIR; B01937; KWS83.

Mar 18 10:08

US-08-612-929-18.rsp

4

DR HSP; P01679; IGGB.  
KW IMMUNOGLOBULIN V REGION.  
FT DOMAIN 1 23  
FT DOMAIN 24 38  
FT DOMAIN 39 53  
FT DOMAIN 54 60  
FT DOMAIN 61 92  
FT DOMAIN 93 101  
FT DOMAIN 102 111  
FT DISULFID 23 92  
FT NON TER 111 111  
SQ SEQUENCE 111 AA; 11952 MW; 041902B8 CRC32;

Query Match 100.0%; Score 35; DB 5; Length 111;  
Best Local Similarity 100.0%; Pred. No. 1.92e+00;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 54 aasles 60  
Qy 1 AASNLES 7

RESULT 4

ID KV3M MOUSE STANDARD; PRT; 111 AA.  
AC P01655;  
DT 21-JUL-1986 (REL. 01, CREATED)  
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)  
DE IG KAPPA CHAIN V-III REGION (PC 7043).  
OS MUS MUSCULUS (MOUSE).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; RODENTIA.  
RN [1]  
RP SEQUENCE.  
RX MEDLINE; 79073152.  
RA WEIGERT M., GATWALTAN L., LOH E., SCHILLING J., HOOD L.E.;  
RL NATURE 276:785-790(1978).  
DR PIR; A01937; KWS43.  
DR HSP; P01679; IGGB.  
KW IMMUNOGLOBULIN V REGION.  
FT DOMAIN 1 23  
FT DOMAIN 24 38  
FT DOMAIN 39 53  
FT DOMAIN 54 60  
FT DOMAIN 61 92  
FT DOMAIN 93 101  
FT DOMAIN 102 111  
FT DISULFID 23 92  
FT NON TER 111 111  
SQ SEQUENCE 111 AA; 12002 MW; ADC728CA CRC32;

Query Match 100.0%; Score 35; DB 5; Length 111;  
Best Local Similarity 100.0%; Pred. No. 1.92e+00;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 54 aasles 60  
Qy 1 AASNLES 7

RESULT 5

ID KV3L MOUSE STANDARD; PRT; 111 AA.  
AC P01664;  
DT 21-JUL-1986 (REL. 01, CREATED)

DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)  
 DE IC KAPPA CHAIN V-III REGION (CBPC 101).  
 OS MUS MUSCULUS (MOUSE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; RODENTIA.  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE; 79012520.  
 RA MCKEAN D.J., BELL M., POTTER M.;  
 RL PROC. NATL. ACAD. SCI. U.S.A. 75:3913-3917(1978).  
 CC -!- THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.  
 DR PIR; A01936; KWSCL.  
 DR HSP; P01679; IGBB.  
 KW IMMUNOGLOBULIN V REGION.  
 FT DOMAIN 1 23 FRAMEWORK 1.  
 FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING 1.  
 FT DOMAIN 39 53 FRAMEWORK 2.  
 FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING 2.  
 FT DOMAIN 61 92 FRAMEWORK 3.  
 FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING 3.  
 FT DOMAIN 102 111 FRAMEWORK 4.  
 FT DISULFID 23 92 BY SIMILARITY.  
 FT NON TER 111 111  
 SQ SEQUENCE 111 AA; 11964 MW; A2AC84C7 CRC32;

Query Match 100.0%; Score 35; DB 5; Length 111;  
 Best Local Similarity 100.0%; Pred. No. 1.92e+00;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 54 aasnles 60  
 |||||  
 Qy 1 AASNLES 7

RESULT 6  
 ID YIEO HAEIN STANDARD; PRT; 463 AA.  
 AC P44903;  
 DT 01-NOV-1995 (REL. 32, CREATED)  
 DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)  
 DE HYPOTHETICAL PROTEIN H10852.  
 GN H10852.  
 OS HAEMOPHILUS INFLUENZAE.  
 OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;  
 OC PASTEURILLACEAE.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=RD / RW20;  
 RX MEDLINE; 95350630.  
 RA FLEISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F.,  
 RA KERIYAVAGE A.R., BULT C.J., TOMB J.-F., DOUGHERTY B.A., MERRICK J.M.,  
 RA MCKENNEY K., SUTTON G., FITZHUGH W., FIELDS C.A., COCAYNE J.D.,  
 RA SCOTT J.D., SHIRLEY R., LIU L.-I., GLODEK A., KELLEY J.M.,  
 RA WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLUM E., COTTON M.D.,  
 RA UTTERBACK T.R., HANNA M.C., NGUYEN D.T., SAUDEK D.M., BRANDON R.C.,  
 RA FINE L.D., FRITCHMAN J.L., FUHRMANN J.L., GEORHAGEN N.S.M.,  
 RA GUEHM C.L., McDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O.,  
 RA VENTER J.C.;  
 RL SCIENCE 269:496-512(1995).  
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE  
 (PROBABILE).  
 CC -!- SIMILARITY: STRONG, TO E.COLI YIEO.  
 CC -!- SIMILARITY: BELONGS TO THE MAJOR FACILITATOR FAMILY (ALSO KNOWN

CC AS THE DRUG RESISTANCE TRANSLOCASE FAMILY).  
 DR EMBL; L45490; G1005907; -.  
 DR EMBL; U32766; G925898; -.  
 KW HYPOTHETICAL PROTEIN; TRANSPORT; TRANSMEMBRANE; INNER MEMBRANE.  
 FT TRANSMEM 10 30 POTENTIAL.  
 FT TRANSMEM 49 69 POTENTIAL.  
 FT TRANSMEM 82 102 POTENTIAL.  
 FT TRANSMEM 107 127 POTENTIAL.  
 FT TRANSMEM 139 159 POTENTIAL.  
 FT TRANSMEM 165 185 POTENTIAL.  
 FT TRANSMEM 197 217 POTENTIAL.  
 FT TRANSMEM 225 245 POTENTIAL.  
 FT TRANSMEM 267 287 POTENTIAL.  
 FT TRANSMEM 298 318 POTENTIAL.  
 FT TRANSMEM 328 348 POTENTIAL.  
 FT TRANSMEM 354 374 POTENTIAL.  
 FT TRANSMEM 393 413 POTENTIAL.  
 FT TRANSMEM 429 449 POTENTIAL.  
 SQ SEQUENCE 463 AA; 50002 MW; 5CAE40A0 CRC32;

Query Match 100.0%; Score 35; DB 10; Length 463;  
 Best Local Similarity 100.0%; Pred. No. 1.92e+00;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 94 aasnles 100  
 |||||  
 Qy 1 AASNLES 7

RESULT 7  
 ID VP9 WTVNU STANDARD; PRT; 313 AA.  
 AC P31611;  
 DT 01-JUL-1993 (REL. 26, CREATED)  
 DT 01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)  
 DT 01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)  
 DE STRUCTURAL PROTEIN P9 (CAPSOMERE PROTEIN P9) (PROTEIN P9S11).  
 OS WOUND TUMOR VIRUS (STRAIN NJ) (WTV).  
 OC VIRIDAE; DS-RNA NONENVELOPED VIRUSES; REOVIRIDAE; PHYTOREOVIRUSES.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 92074261.  
 RA HILLMAN B.I., ANZOILA J.V., HALPERN B.T., CAVILEER T.D., NUSS D.L.;  
 RL VIROLOGY 185:896-900(1991).  
 CC -!- SIMILARITY: TO RICE DWARF VIRUS S9 AND RICE GALL DWARF VIRUS S10.  
 DR EMBL; M77020; G336173; -.  
 DR PIR; C41705; QMXRW.  
 KW NONSTRUCTURAL PROTEIN.  
 SQ SEQUENCE 313 AA; 35551 MW; D42189CE CRC32;

Query Match 97.1%; Score 34; DB 9; Length 313;  
 Best Local Similarity 85.7%; Pred. No. 4.16e+00;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 294 aasnles 300  
 |||||  
 Qy 1 AASNLES 7

RESULT 8  
 ID VP9 WTV STANDARD; PRT; 313 AA.  
 AC P12326;  
 DT 01-OCT-1989 (REL. 12, CREATED)  
 DT 01-OCT-1989 (REL. 12, LAST SEQUENCE UPDATE)  
 DT 01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)

DE STRUCTURAL PROTEIN P9 (CAPSOMERE PROTEIN P9) (PROTEIN P9S11).

GN S11.

OS ROUND TUMOR VIRUS (HTV).

OC VIRIDAE; DS-RNA NONENVELOPED VIRUSES; REOVIRIDAE; PHYTOREOVIRUSES.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE; 89263810.

RA DALL D.J., ANZOLA J.V., XU Z., NUSS D.L.;

RL NUCLEIC ACIDS RES. 17:3599-3599(1989).

CC -!- SIMILARITY: TO RICE DWARF VIRUS S9 AND RICE GALL DWARF VIRUS S10.

DR EMBL; X14219; G62265; -.

DR PIR; S04139; OMXWHT.

SQ SEQUENCE 313 AA; 35606 MW; 85FB39FC CRC32;

Query Match 97.1%; Score 34; DB 9; Length 313;

Best Local Similarity 85.7%; Pred. No. 4.16e+00;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 294 aasnlde 300  
|||||

Qy 1 AASNLES 7

RESULT 9

ID KL68 DROME STANDARD; PRT; 784 AA.

AC P46867;

DT 01-NOV-1995 (REL. 32, CREATED)

DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)

DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)

DE KINESIN-LIKE PROTEIN KLP68D.

GN KLP68D OR KLP5.

OS DROSOPHILA MELANOGASTER (FRUIT FLY).

OC EUKARYOTA; METAZOA; ARTHROPODA; INSECTA; DIPTERA.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE; 95050960.

RA PESAVENTO P.A., STEWART R.J., GOLDSTEIN L.S.B.;

RL J. CELL BIOL. 127:1041-1048(1994).

RN [2]

RP SEQUENCE OF 220-342 FROM N.A.

RX MEDLINE; 92020874.

RA STEWART R.J., PESAVENTO P.A., MOERPEL D.N., GOLDSTEIN L.S.B.;

RL PROC. NATL. ACAD. SCI. U.S.A. 88:8470-8474(1991).

CC -!- FUNCTION: PLUS-END DIRECTED MICROTUBULE MOTOR THAT MAY BE USED FOR

CC ANTEROGRADE AXONAL TRANSPORT AND COULD CONCEIVABLY MOVE CARGOES IN

CC FLY NEURONS DIFFERENT THAN THOSE MOVED BY KINESIN HEAVY CHAIN OR

CC OTHER PLUS-END DIRECTED MOTORS.

CC -!- TISSUE SPECIFICITY: EXPRESSED PRIMARILY IN THE CENTRAL NERVOUS

CC SYSTEM AND IN A SUBSET OF THE PERIPHERAL NERVOUS SYSTEM DURING

CC EMBRYOGENESIS.

CC -!- SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. KINESIN

CC II SUBFAMILY.

DR EMBL; U15974; G565090; -.

DR EMBL; M74431; G157792; -.

DR FLYBASE; FBGN0004381; KLP68D.

DR PROSITE; PS00411; KINESIN MOTOR DOMAIN.

KW MOTOR PROTEIN; MICROTUBULES; ATP-BINDING; COILED COIL.

FT NP BIND 106 113 ATP (POTENTIAL).

FT CONFLICT 220 221 SS -> TC (IN REF. 2).

FT CONFLICT 338 342 GSPAK -> VRQV (IN REF. 2).

SQ SEQUENCE 784 AA; 88193 MW; D705B2F2 CRC32;

Query Match 97.1%; Score 34; DB 5; Length 784;

Best Local Similarity 85.7%; Pred. No. 4.16e+00;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 751 aasnlde 757  
|||||

Qy 1 AASNLES 7

RESULT 10

ID KV30 MOUSE STANDARD; PRT; 111 AA.

AC P01667;

DT 21-JUL-1986 (REL. 01, CREATED)

DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)

DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)

DE IC KAPPA CHAIN V-III REGION (PC 6308).

OS MUS MUSCULUS (MOUSE).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

OC EUTHERIA; RODENTIA.

RN [1]

RP SEQUENCE.

RX MEDLINE; 79073152.

RA WEIGERT M., GATWALTAN L., LOH E., SCHILLING J., HOOD L.E.;

RL NATURE 276:785-790(1978).

DR PIR; C01937; KVM508.

DR HSP; P01679; 1GGB.

KW IMMUNOGLOBULIN V REGION.

FT DOMAIN 1 23 FRAMEWORK 1.

FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING 1.

FT DOMAIN 39 53 FRAMEWORK 2.

FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING 2.

FT DOMAIN 61 92 FRAMEWORK 3.

FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING 3.

FT DOMAIN 102 111 FRAMEWORK 4.

FT DISULFID 23 92 BY SIMILARITY.

FT NON TER 111 111

SQ SEQUENCE 111 AA; 12071 MW; F7865271 CRC32;

Query Match 94.3%; Score 33; DB 5; Length 111;

Best Local Similarity 85.7%; Pred. No. 8.83e+00;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 54 tasnlde 60  
|||||

Qy 1 AASNLES 7

RESULT 11

ID KICH HUMAN STANDARD; PRT; 456 AA.

AC P35790;

DT 01-JUN-1994 (REL. 29, CREATED)

DT 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)

DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)

DE CHOLINE KINASE (EC 2.7.1.32).

GN CHK OR CK1.

OS HOMO SAPIENS (HUMAN).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

OC EUTHERIA; PRIMATES.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE; 92316236.

RA HOSAKA K., TANAKA S., NIKAWA J.I., YAMASHITA S.;

RL FEBS LETT. 304:229-232(1992).

CC -!- FUNCTION: MAY HAVE A REGULATORY ROLE IN PHOSPHATIDYLCHOLINE

CC SYNTHESIS.

CC -!- CATALYTIC ACTIVITY: ATP + CHOLINE = ADP + O-PHOSPHOCHOLINE.

CC -!- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).  
CC -!- PATHWAY: INITIAL STEP OF THE CDP-CHOLINE AND CDP-ETHANOLAMINE  
CC PATHWAYS.  
CC -!- SIMILARITY: TO OTHER CHOLINE KINASES.  
DR EMBL; D10704; G219541; -.  
DR PIR; S23104; S23104.  
DR MIM; 118491; 11TH EDITION.  
KW TRANSFERASE; KINASE.  
FT ACT SITE 303 303 BY SIMILARITY.  
SQ SEQUENCE 456 AA; 52065 MW; BE4AB383 CRC32;

Query Match 94.3%; Score 33; DB 5; Length 456;

Best Local Similarity 85.7%; Pred. No. 8.83e+00;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 39 asadles 45  
|||||  
Qy 1 AASNLES 7

## RESULT 12

ID KV16 HUMAN STANDARD; PRT; 108 AA.  
AC P01599;  
DT 21-JUL-1986 (REL. 01, CREATED)  
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
DT 01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)  
DE IG KAPPA CHAIN V-I REGION (GAL).  
OS HOMO SAPIENS (HUMAN).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; PRIMATES.  
RN [1]  
RP SEQUENCE.  
RX MEDLINE; 75059122.  
RA LAURE C.J., WATANABE S., HILSCHMANN N.;  
RL HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 354:1503-1504 (1973).  
CC -!- THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
CC -!- THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S MACROGLOBULIN.  
DR PIR; A01867; KLHUGI.  
DR HSP; P01607; IDFB.  
KW IMMUNOGLOBULIN V REGION.  
FT DOMAIN 1 23 FRAMEWORK 1.  
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.  
FT DOMAIN 35 49 FRAMEWORK 2.  
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.  
FT DOMAIN 57 88 FRAMEWORK 3.  
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.  
FT DOMAIN 98 107 FRAMEWORK 4.  
FT DISULFID 23 88 BY SIMILARITY.  
FT NON TER 108 108  
SQ SEQUENCE 108 AA; 11814 MW; CCRAAD2 CRC32;

Query Match 91.4%; Score 32; DB 5; Length 108;

Best Local Similarity 85.7%; Pred. No. 1.84e+01;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 50 asadles 56  
|||||  
Qy 1 AASNLES 7

## RESULT 13

ID HMC3 MESAU STANDARD; PRT; 313 AA.  
AC Q04649;  
DT 01-JUN-1994 (REL. 29, CREATED)

DT 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)  
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)  
DE HOMEBOX PROTEIN CDX-3.  
GN CDX-3.  
OS MESOCRITETUS AURATUS (GOLDEN HAMSTER).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; RODENTIA.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 93051335.  
RA GERMAN M.S., WANG J., CHADWICK R.B., RUTTER W.J.;  
RL GENES DEV. 6:2165-2176 (1992).

CC -!- FUNCTION: ACTS AS A TRANSCRIPTIONAL ACTIVATOR BY BINDING TO THE  
CC FLAT ELEMENT WHICH IS A BETA-CELL-SPECIFIC TRANSCRIPTIONAL  
CC ENHANCER FOUND IN THE INSULIN GENE.  
CC -!- SUBCELLULAR LOCATION: NUCLEAR.  
CC -!- SIMILARITY: WITH OTHER "CAUDAL-TYPE" HOMEBOX DOMAINS.  
DR EMBL; X81404; G587458; -.  
DR PIR; A46233; A46233.  
DR HSP; P02833; ISAN.  
DR PROSITE; PS00027; HOMEBOX.

KW HOMEBOX; DNA-BINDING; DEVELOPMENTAL PROTEIN; NUCLEAR PROTEIN;  
KW TRANSCRIPTION REGULATION; ACTIVATOR.  
FT DOMAIN 46 53 POLY-ALA.  
FT DNA\_BIND 185 244 HOMEBOX (BY SIMILARITY).  
FT DOMAIN 113 124 HIS-RICH.  
FT DOMAIN 249 259 POLY-GLN.  
SQ SEQUENCE 313 AA; 33559 MW; 875299E1 CRC32;

Query Match 91.4%; Score 32; DB 4; Length 313;

Best Local Similarity 71.4%; Pred. No. 1.84e+01;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 51 asadles 57  
|||||  
Qy 1 AASNLES 7

## RESULT 14

ID KV16 HUMAN STANDARD; PRT; 108 AA.  
AC P01594;  
DT 21-JUL-1986 (REL. 01, CREATED)  
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
DT 01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)  
DE IG KAPPA CHAIN V-I REGION (AU).  
OS HOMO SAPIENS (HUMAN).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; PRIMATES.  
RN [1]  
RP SEQUENCE.  
RX MEDLINE; 72189444.  
RA SCHIEHL H., HILSCHMANN N.;  
RL HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 353:345-370 (1972).  
RN [2]  
RP X-RAY CRYSTALLOGRAPHY.  
RX MEDLINE; 77022433.  
RA FEHLHAMMER H., SCHIFFER M., EPP O., COLMAN P.M., LATTMAN E.E.,  
RA SCHWAGER P., STEIGEMANN W., SCHRAMM H.J.;  
RL BIOPHYS. STRUCT. MECH. 1:139-146 (1975).

CC -!- THE STRUCTURE OF THE V REGION WAS DETERMINED BY MOLECULAR  
CC REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V REGION OF  
CC THE KAPPA CHAIN REI.  
CC -!- THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
CC -!- THIS IS A BENCE-JONES PROTEIN.

Mar 18 10:08

US-08-612-929-18.rsp

11

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DR PIR; A01862; KIHDAU.
DR HSP; P01607; IICM.
KW IMMUNOGLOBULIN V REGION; BENCE-JONES PROTEIN.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 35 49 FRAMEWORK 2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 57 88 FRAMEWORK 3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 98 107 FRAMEWORK 4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11939 MW; B455AF00 CRC32;
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Query Match 88.6%; Score 31; DB 5; Length 108;
Best Local Similarity 100.0%; Pred. No. 3.73e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 51 asnles 56
|||||
Qy 2 ASNLES 7
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RESULT 15
ID KV3V MOUSE STANDARD; PRT; 108 AA.
AC P01674;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (PC 2154).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE.
RX MEDLINE; 79073152.
RA WEIGERT M., GATWAI TAN L., LOH E., SCHILLING J., HOOD L.E.;
RL NATURE 276:785-790(1978).
DR PIR; A01940; KWS54.
DR HSP; P01679; IACY.
KW IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 39 53 FRAMEWORK 2.
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 61 92 FRAMEWORK 3.
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 102 108 FRAMEWORK 4.
FT DISULFID 23 92 BY SIMILARITY.
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11699 MW; E28999CC CRC32;
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Query Match 88.6%; Score 31; DB 5; Length 108;
Best Local Similarity 100.0%; Pred. No. 3.73e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 55 asnles 60
|||||
Qy 2 ASNLES 7
```

Search completed: Tue Mar 18 10:10:50 1997  
Job time : 8 secs.

Result	No.	Score	Query		DB	ID	Description	Pred. No.
			Match	Length				
1	35	100.0	7	13	R70196	MAB 3B9 light chain C	1.22e+02	
2	35	100.0	15	12	R66144	CD-4 antibody variabl	1.22e+02	
3	35	100.0	106	6	R33309	MaE15 light chain.	1.22e+02	
4	35	100.0	111	11	R60302	Anti HIV antibody lig	1.22e+02	
5	35	100.0	111	10	R5127	Mouse-human chimeric	1.22e+02	
6	35	100.0	111	11	R60306	Chimeric anti HIV ant	1.22e+02	
7	35	100.0	111	10	R55123	Mouse anti-HIV mu5.5	1.22e+02	
8	35	100.0	111	1	P90541	Immunoglobulin L chai	1.22e+02	
9	35	100.0	112	5	R24575	Human x mouse modifie	1.22e+02	
10	35	100.0	115	1	R04134	Anti-Leu 3a light cha	1.22e+02	
11	35	100.0	131	13	R70202	Humanized antibody 3B	1.22e+02	
12	35	100.0	131	6	R32123	Anti-CD4 antibody MT	1.22e+02	



Mar 19 15:54

US-08-612-929-18.rag

3

CC encoded the protein given in R70189. 3 CDRs (R70195-97) were  
CC identified.  
SQ Sequence 7 AA;

Query Match 100.0%; Score 35; DB 13; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.22e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 aasles 7  
|||||||  
Qy 1 AASNLES 7

RESULT 2

ID R66144 standard; peptide; 15 AA.  
AC R66144;  
DT 12-JUL-1995 (first entry)  
DE CD-4 antibody variable region complementary peptide.  
KW CD-4 antibody variable region; complementary peptide;  
KW extra-corporeal blood circulation; cell filter material.  
OS Synthetic.  
PN J06269663-A.  
PD 27-SEP-1994.  
PF 17-MAR-1993; 057206.  
PR 17-MAR-1993; JP-057206.  
PA (TOYM) TOYOHOKK.  
DR WPI; 94-346316/43.  
PT Material for collecting cells positive for CD-4 antibody -  
PT comprises nonwoven fabric having keto-alkyl halide functional gp  
PS Example 2; Page 7; 9pp; Japanese.  
CC R66140-R66146 are peptides complementary to the variable region  
CC of the CD-4 antibody, these peptides are fixed onto a claimed  
CC nonwoven fabric (average fibre dia. of 1-30 microns) coated with  
CC keto-alkyl halide functional groups. This material can be used  
CC as a filter for CD-4 positive cells in a medical treatment  
CC involving the extra-corporeal circulation of blood.  
SQ Sequence 15 AA;

Query Match 100.0%; Score 35; DB 12; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.22e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 9 aasles 15  
|||||||  
Qy 1 AASNLES 7

RESULT 3

ID R33309 standard; Protein; 106 AA.  
AC R33309;  
DT 05-JUL-1993 (first entry)  
DE MAE15 light chain.  
KW Antibody; high affinity; FCEH; low affinity; FCEH;  
KW IgE receptor; histamine; mast cell; basophil; Kabat;  
KW CDR; murine; MAE11; MAE13; MAE15; MAE17.  
OS Synthetic.  
PN W09304173-A.  
PD 04-MAR-1993.  
PF 14-AUG-1992; U06860.  
PR 14-AUG-1991; US-744768.  
PR 07-MAY-1992; US-879495.  
PA (GETH) GENENTECH INC.  
PI Jardieu PM, Presta LG;  
DR WPI; 93-094004/11.

Mar 19 15:54

US-08-612-929-18.rag

4

PT Polypeptide(s) binding to specific Fc epsilon receptors - act as  
PT IgE antagonists; useful for treating and preventing IgE-mediated  
PT disorders e.g. allergies  
PS Disclosure; Fig 2; 113pp; English.  
CC Antibodies capable of binding FCEH-bound IgE but which are  
CC substantially incapable of binding FCEH-bound IgE or inducing  
CC histamine release from mast cells or basophils, comprise a human  
CC Kabat CDR domain into which has been substituted a positionally  
CC analogous residue from a Kabat CDR domain of the murine anti-huIgE  
CC antibodies MAE11, MAE13, MAE15 or MAE17.  
SQ Sequence 106 AA;

Query Match 100.0%; Score 35; DB 6; Length 106;  
Best Local Similarity 100.0%; Pred. No. 1.22e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 54 aasles 60  
|||||||  
Qy 1 AASNLES 7

RESULT 4

ID R60302 standard; Protein; 111 AA.  
AC R60302;  
DT 09-MAR-1995 (first entry)  
DE Anti HIV antibody light chain variable region.  
KW Antibody; heavy chain; light chain; human immunodeficiency virus;  
KW HIV; acquired immune deficiency syndrome; AIDS; treatment;  
KW prophylaxis; Mus musculus; Homo sapiens.  
OS Mus musculus.  
FH Key Location/Qualifiers  
FT Region 1..23  
FT /Label= Framework region 1.  
FT Region 24..38  
FT /Label= CDR1.  
FT Region 39..53  
FT /Label= Framework region 2.  
FT Region 54..60  
FT /Label= CDR2.  
FT Region 61..92  
FT /Label= Framework region 3.  
FT Region 93..101  
FT /Label= CDR3.  
FT Region 102..111  
FT /Label= Framework region 4.  
PN W09415969-A.  
PD 21-JUL-1994.  
PF 14-JAN-1993; J00039.  
PR 14-JAN-1993; AU-032671.  
PR 14-JAN-1993; WO-J00039.  
PA (KAGA) CEMO SERO THERAPEUTIC RES INST.  
PI Eda Y, Kimachi K, Maeda H, Osatomi K, Shiosaki K;  
PI Tokiyoshi S;  
DR WPI; 94-249145/30.  
DR N-PSDB; Q70372.  
PT Recombinant chimeric anti HIV antibody - useful for the treatment  
PT and prevention of HIV  
PS Claim 15; Figure 4; 51pp; Japanese.  
CC The recombinant antibody light chain has neutralising activity  
CC against HIV. Chimeric antibodies comprising both mouse and human  
CC sequences are useful in the treatment/prevention of AIDS caused by  
CC HIV.  
SQ Sequence 111 AA;

Query Match 100.0%; Score 35; DB 10; Length 111;  
Best Local Similarity 100.0%; Pred. No. 1.22e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 54 aasnles 60  
|||||||  
Qy 1 AASNLES 7

## RESULT 5

ID R55127 standard; Protein; 111 AA.  
AC R55127;  
DT 30-JAN-1995 (first entry)  
DE Mouse-human chimeric anti-HIV mu5.5-derived light chain V region.  
KW Immunoglobulin; heavy chain; anti-HIV antibody; neutralisation;  
KW human immunodeficiency virus; variable region; VL chain; murine;  
KW chimeric; humanised.  
OS Chimeric Mus musculus.  
OS Chimeric Homo sapiens.  
FH Key Location/Qualifiers  
FT Region 1..23  
FT /label= FR1  
FT /note= "human"  
FT /label= FR2  
FT /note= "murine"  
FT /label= CDR1  
FT /label= FR3  
FT /note= "human"  
FT /label= FR4  
FT /note= "human"  
PN J06125783-A.  
PD 10-MAY-1994.  
PF 28-DEC-1991; JP-359808.  
PR (KAGA-) ZH KAGAKU KESSEI-RYOHO KENKYUSHO.  
DR N-PSDB; Q65558.  
PT Mouse-human chimeric anti-HIV antibody heavy and light chains -  
PT and recombinant antibody consisting of the H- and L-chains,  
PT useful in AIDS therapy  
PS Claim 5; Fig 12; 22pp; Japanese.  
CC Murine monoclonal antibodies mu 39.1 and mu 5.5 both neutralise HIV.  
CC The heavy and light chain variable regions from these antibodies  
CC were sequenced (R55120-R55123). The murine anti-HIV CDRs were  
CC introduced into human framework regions to construct chimeric  
CC antibodies (R55124-R55127).  
SQ Sequence 111 AA;

Query Match 100.0%; Score 35; DB 10; Length 111;  
Best Local Similarity 100.0%; Pred. No. 1.22e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 54 aasnles 60  
|||||||

Qy 1 AASNLES 7

## RESULT 6

ID R60306 standard; Protein; 111 AA.  
AC R60306;  
DT 13-MAR-1995 (first entry)  
DE Chimeric anti HIV antibody light chain variable region.  
KW Antibody; heavy chain; light chain; human immunodeficiency virus;  
KW HIV; acquired immune deficiency syndrome; AIDS; treatment;  
KW prophylaxis; Mus musculus; Homo sapiens.  
OS Chimeric Homo sapiens  
OS Chimeric Mus musculus.  
FH Key Location/Qualifiers  
FT Region 1..23  
FT /label= Framework region 1.  
FT Region 24..38  
FT /label= CDR1.  
FT /note= "Mouse derived amino acid sequence."  
FT Region 39..53  
FT /label= Framework region 2.  
FT Region 54..60  
FT /label= CDR2.  
FT /note= "Mouse derived amino acid sequence."  
FT Region 61..92  
FT /label= Framework region 3.  
FT Region 93..101  
FT /label= CDR3.  
FT /note= "Mouse derived amino acid sequence."  
FT Region 102..111  
FT /label= Framework region 4.  
PN W09415969-A.  
PD 21-JUL-1994.  
PF 14-JAN-1993; J000039.  
PR 14-JAN-1993; AU-032671.  
PR 14-JAN-1993; WO-J00039.  
PA (KAGA ) CHEMA SERO THERAPEUTIC RES INST.  
PI Eda Y, Kimachi K, Maeda H, Osatomi K, Shiosaki K;  
PI Tokiyoshi S;  
DR WPI; 94-249145/30.  
DR N-PSDB; R60306.  
PT Recombinant chimeric anti HIV antibody - useful for the treatment  
PT and prevention of HIV  
PS Claim 14; Figure 12; 51pp; Japanese.  
CC The recombinant antibody light chain has neutralising activity  
CC against HIV. Chimeric antibodies comprising both mouse and human  
CC sequences are useful in the treatment/prevention of AIDS caused by  
CC HIV.  
SQ Sequence 111 AA;

Query Match 100.0%; Score 35; DB 11; Length 111;  
Best Local Similarity 100.0%; Pred. No. 1.22e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 54 aasnles 60  
|||||||  
Qy 1 AASNLES 7

## RESULT 7

ID R55123 standard; Protein; 111 AA.  
AC R55123;  
DT 27-JAN-1995 (first entry)  
DE Mouse anti-HIV mu5.5 light chain variable region.

Mar 19 15:54

US-08-612-929-18.rag

7

KW Immunoglobulin; heavy chain; anti-HIV antibody; neutralisation;  
KW human immunodeficiency virus; variable region; VH chain; murine.  
OS Mus musculus.  
FH Key Location/Qualifiers  
FT Region 1..23  
FT /label= FR1  
FT Region 24..38  
FT /label= CDR1  
FT Region 39..53  
FT /label= FR2  
FT Region 54..60  
FT /label= CDR2  
FT Region 61..92  
FT /label= FR3  
FT Region 93..101  
FT /label= CDR3  
FT Region 102..111  
FT /label= FR4  
FN J06125783-A.  
PD 10-MAY-1994.  
PF 28-DEC-1991; 359808.  
PA (KAGA-) ZH KAGAKU KESSEI-RYOHO KENKYUSHO.  
DR WPI; 94-187942/23.  
DR N-PSDB; Q65554.  
PT Mouse-human chimeric anti-HIV antibody heavy and light chains -  
PT and recombinant antibody consisting of the H- and L-chains,  
PT useful in AIDS therapy  
PS Example 3; Fig 4; 22pp; Japanese.  
CC Murine monoclonal antibodies mu 39.1 and mu 5.5 both neutralise HIV.  
CC The heavy and light chain variable regions from these antibodies  
CC were sequenced (R55120-R55123). The murine anti-HIV CDRs were  
CC introduced into human framework regions to construct chimeric  
CC antibodies (R55124-R55127).  
SQ Sequence 111 AA;

Query Match 100.0%; Score 35; DB 10; Length 111;  
Best Local Similarity 100.0%; Pred. No. 1.22e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 54 aasles 60  
|||||  
Qy 1 AASNLES 7

RESULT 8  
ID P90541 standard; protein; 111 AA.  
AC P90541;  
DT 20-OCT-1989 (first entry)  
DE Immunoglobulin L chain variable region.  
KW Immunoglobulin; L chain variable region; HIV.  
OS Mus musculus  
FN EP-327000-A.  
PD 09-AUG-1989.  
PF 30-JAN-1989; 101583.  
FR 30-JAN-1988; JP-20255.  
PR 08-JUL-1988; JP-171385.  
PA (\*\*\*\*) The Chemo-Sero-Therapeutic Research Institute.  
PI Maeda H, Eda Y, Kimachi K, Tokiyoshi S, Matsushita S, Hattori T,  
PI Takatsuki K;  
DR WPI; 89-229050/32.  
DR N-PSDB; N90491, N90492, N90493.  
PT Chimeric anti-human immune virus antibodies - contg. mouse variable  
PT regions and human constant regions for diagnosis, treatment and

Mar 19 15:54

US-08-612-929-18.rag

8

PT prevention of AIDS  
PS Claim 5; page 15; 33pp; English.  
CC The sequence is an L chain variable region from an immunoglobulin with  
CC anti-HIV neutralising activity. See N90491-3, and N90495.  
SQ Sequence 111 AA;

Query Match 100.0%; Score 35; DB 1; Length 111;  
Best Local Similarity 100.0%; Pred. No. 1.22e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 54 aasles 60  
|||||  
Qy 1 AASNLES 7

RESULT 9  
ID R24575 standard; Protein; 112 AA.  
AC R24575;  
DT 08-DEC-1992 (first entry)  
DE Human x mouse modified anti-HIV antibody Light chain RL0.5beta.  
KW Heavy; light; CDR; HIV; AIDS; REI; 0.5beta.  
OS Synthetic.  
FH Key Location/Qualifiers  
FT Region 1..23  
FT /label= FR1  
FT Region 24..38  
FT /label= CDR1  
FT Region 39..53  
FT /label= FR2  
FT Region 54..60  
FT /label= CDR2  
FT Region 61..92  
FT /label= FR3  
FT Region 93..101  
FT /label= CDR3  
FT Region 102..112  
FT /label= FR4  
FN J04141095-A.  
PD 14-MAY-1992. 266091.  
PF 02-OCT-1990; JP-266091.  
PR 02-OCT-1990; JP-266091.  
PA (KAGA) KAGAKU OYOBI KESSEI RYOHO.  
DR WPI; 92-212765/26.  
PT New recombinant modified anti-HIV antibodies - comprise human x  
PT mouse modified antibody H and L chains  
PS Disclosure; Fig 2; 15pp; Japanese.  
CC The framework regions (FR) are derived from the human antibody  
CC REI. The CDRs are mouse monoclonal antibody 0.5beta derived  
CC sequences. The anti-HIV modified antibody can be used for the  
CC prophylaxis and treatment of AIDS.  
CC Specific examples of the H chain are given in R24556-58 and  
CC R24560-62. A specific example of the L chain is given in R24575.  
SQ Sequence 112 AA;

Query Match 100.0%; Score 35; DB 5; Length 112;  
Best Local Similarity 100.0%; Pred. No. 1.22e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 54 aasles 60  
|||||  
Qy 1 AASNLES 7

RESULT 10

ID R04134 standard; protein; 115 AA.  
 AC R04134;  
 DT 06-SEP-1990 (first entry)  
 DE Anti-Leu 3a light chain variable region gene product, KOL/206 V1.  
 KW HIV; AIDS; anti-Leu3A; vaccine; ds.  
 OS Mus musculus.  
 PN EP-365209-A.  
 PD 25-APR-1990.  
 PF 11-OCT-1989; 010415.  
 PR 17-OCT-1988; US-260558.  
 PA (BECT) Becton Dickinson Co.  
 PI Hinton R, Oi VT;  
 DR WPI; 90-126329/17.  
 DR N-PSDB; Q04041.  
 PT New chimeric variants of murine antibody anti-leucine -  
 PT contg. human antibody regions, and DNA encoding sequences.  
 PS Claim 4; Fig 4; 12pp; English.  
 CC Variants of murine monoclonal anti-CD4 antibody, anti-leu3A can be  
 CC used to form chimeric mouse-variable, human-constant region Abs  
 CC suggested as being useful as a vaccine to HIV.  
 SQ Sequence 115 AA;

Query Match 100.0%; Score 35; DB 1; Length 115;  
 Best Local Similarity 100.0%; Pred. No. 1.22e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 57 aasles 63  
 QY 1 AASNLES 7

RESULT 11  
 ID R70202 standard; Protein; 131 AA.  
 AC R70202;  
 DT 20-SEP-1995 (first entry)  
 DE Humanized antibody 3B9 light chain.  
 KW Humanized antibody; antibody engineering; monoclonal antibody;  
 KW MAb; interleukin-4; IL-4; allergy.  
 OS Homo sapiens.  
 PN WO9507301-A.  
 PD 16-MAR-1995.  
 PF 07-SEP-1994; U10308.  
 PR 07-SEP-1993; US-117366.  
 PR 14-OCT-1993; US-136783.  
 PA (SMIK ) SMITHKLINE BEECHAM CORP.  
 PA (SMIK ) SMITHKLINE BEECHAM PLC.  
 PI Gross MS, Holmes SD, Sylvester DR;  
 DR WPI; 95-123387/16.  
 DR N-PSDB; Q83520.  
 PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived  
 PT from high affinity mAbs - useful in treatment of IL-4-mediated  
 PT and IgE-mediated allergic conditions  
 PS Disclosure; Page 71-72; 97pp; English.  
 CC A humanized antibody light chain variable region and signal  
 CC sequence is given in R75355. The signal sequence is also  
 CC provided in R70194. The sequences of the 3 CDRs  
 CC are identical to mouse anti-human IL-4 MAb 3B9 light chain  
 CC CDRs (given in R70195-97).  
 SQ Sequence 131 AA;

Query Match 100.0%; Score 35; DB 13; Length 131;  
 Best Local Similarity 100.0%; Pred. No. 1.22e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 73 aasles 79  
 QY 1 AASNLES 7

RESULT 12  
 ID R32123 standard; Protein; 131 AA.  
 AC R32123;  
 DT 02-JUN-1993 (first entry)  
 DE Anti-CD4 antibody MT 3.10 light chain variable region.  
 KW immunosuppression; tissue transplantation; graft; I chain; V region;  
 KW T-helper cell inhibition; transplant rejection; MAb;  
 KW interleukin-2 receptor.  
 FH Key Location/Qualifiers  
 FT Peptide 1..20  
 FT /label= signal 21..120  
 FT Region  
 FT /label= Variable  
 FT Region 121..131  
 FT /label= JI  
 PN DE4143214-A.  
 PD 28-JAN-1993.  
 PF 30-DEC-1991; 143214.  
 PR 25-JUL-1991; DE-124759.  
 PR 30-DEC-1991; DE-143214.  
 PA (BOEF ) BOEHRINGER MANNHEIM GMBH.  
 PI Kaluza B, Riethmueller G, Scheuer W, Weidle U;  
 DR WPI; 93-037582/05.  
 DR N-PSDB; Q36609.

PT Synergistic antibody compsn. for use as immunosuppressant -  
 PT comprises monoclonal anti-CD4 antibodies and monoclonal anti-IL2R  
 PT alpha- or anti-IL2R beta antibodies  
 PS Claim 5; Page 11; 18pp; German.  
 CC This sequence is the light chain variable region of a preferred  
 CC anti-CD4 monoclonal antibody for use in the claimed synergistic  
 CC composition. MAb MT 3.10 is deposited as clone 3.101/SB10 (ECACC  
 CC 90030702). The anti-CD4 antibody is used with at least one anti-IL2R  
 CC alpha or beta antibody. Individually the antibodies are strongly  
 CC inhibiting and when used together their immunosuppressive properties  
 CC are improved; they synergistically inhibit T-helper cell  
 CC proliferation to effectively inhibit transplant rejection at low  
 CC doses without significantly reducing the general immune response.  
 CC See also Q36608-Q36616.  
 SQ Sequence 131 AA;

Query Match 100.0%; Score 35; DB 6; Length 131;  
 Best Local Similarity 100.0%; Pred. No. 1.22e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 74 aasles 80  
 QY 1 AASNLES 7

RESULT 13  
 ID R75355 standard; Protein; 131 AA.  
 AC R75355;  
 DT 20-SEP-1995 (first entry)  
 DE Humanized antibody 3B9 light chain.  
 KW Humanized antibody; antibody engineering; monoclonal antibody;  
 KW MAb; interleukin-4; IL-4; allergy.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT Peptide 1..20

FT /label= sig\_peptide  
FT Region 43..57  
FT /label= CDR  
FT /note= "complementarity determining region"  
FT Region 73..79  
FT /label= CDR  
FT /note= "complementarity determining region"  
FT Region 112..120  
FT /label= CDR  
FT /note= "complementarity determining region"  
PN W09507301-A.  
PD 16-MAR-1995.  
PF 07-SEP-1994; U10308.  
PR 07-SEP-1993; US-117366.  
PR 14-OCT-1993; US-136783.  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
PA (SMIK ) SMITHKLINE BEECHAM PLC.  
PI Gross MS, Holmes SD, Sylvester DR;  
DR WPI; 95-123387/16.  
DR N-PSDB; Q73986.  
PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived  
PT from high affinity mAbs - useful in treatment of IL-4-mediated  
PT and IgE-mediated allergic conditions  
PS Disclosure; Fig.5; 97pp; English.  
CC A humanized antibody light chain variable region and signal  
CC sequence is given in R75355. The signal sequence is also  
CC provided in R70194. The sequences of the first 2 CDRs  
CC are identical to mouse anti-human IL-4 MAb 3B9 light chain  
CC CDRs (given in R70195-96), but the third (R70201) differs  
CC by a single amino acid from the native mouse CDR (R70197).  
SQ Sequence 131 AA;

Query Match 100.0%; Score 35; DB 13; Length 131;  
Best Local Similarity 100.0%; Pred. No. 1.22e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 73 aasles 79  
|||||||  
Qy 1 AASNLES 7

RESULT 14  
ID R04132 standard; protein; 131 AA.  
AC R04132;  
DT 06-SEP-1990 (first entry)  
DE Anti-Leu 3a light chain variable region gene product, 206 Vx.  
KW HIV; AIDS; anti-Leu3A; vaccine; ds.  
OS Mus musculus.  
PN EP-365209-A.  
PD 25-APR-1990.  
PF 11-OCT-1989; 010415.  
PR 17-OCT-1988; US-260558.  
PA (BECT) Becton Dickinson Co.  
PI Hinton R, Oi VT;  
DR WPI; 90-126329/17.  
DR N-PSDB; Q04039.  
PT New chimeric variants of murine antibody anti-leucine -  
PT contg. human antibody regions, and DNA encoding sequences.  
PS Claim 1; Fig 2; 12pp; English.  
CC Variants of murine monoclonal anti-CD4 antibody, anti-leu3A can be  
CC used to form chimeric mouse-variable, human-constant region Abs  
CC suggested as being useful as a vaccine to HIV.  
SQ Sequence 131 AA;

Query Match 100.0%; Score 35; DB 1; Length 131;  
Best Local Similarity 100.0%; Pred. No. 1.22e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 74 aasles 80  
|||||||  
Qy 1 AASNLES 7

RESULT 15  
ID P90543 standard; protein; 131 AA.  
AC P90543;  
DT 20-OCT-1989 (first entry)  
DE Amino acids sequence of a V chi region gene.  
KW V cji region; immunoglobulin; L chain variable region; HIV.  
OS Mus musculus  
PN EP-327000-A.  
PD 09-AUG-1989.  
PF 30-JAN-1989; 101583.  
PR 30-JAN-1988; JP-20255.  
PR 08-JUL-1988; JP-171385.  
PA The Chemo-Sero-Therapeutic Research Institute.  
PI Maeda H, Eda Y, Kimachi K, Tokiyoshi S, Matsushita S, Hattori T,  
PI Takatsuki K;  
DR WPI; 89-229050/32.  
DR N-PSDB; N90495.  
PT Chimeric anti-human immune virus antibodies - contg. mouse variable  
PT regions and human constant regions for diagnosis, treatment and  
PT prevention of AIDS  
PS Disclosure; Fig 8; 33pp; English.  
CC The sequence is encoded by a V chi region gene (see N90495).  
CC The sequence from Asp 21 encodes the L chain variable region.  
SQ Sequence 131 AA;

Query Match 100.0%; Score 35; DB 1; Length 131;  
Best Local Similarity 100.0%; Pred. No. 1.22e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 74 aasles 80  
|||||||  
Qy 1 AASNLES 7

RESULT 16  
ID R70189 standard; Protein; 132 AA.  
AC R70189;  
DT 20-SEP-1995 (first entry)  
DE Mouse MAb 3B9 light chain.  
KW Chimeric antibody; humanized antibody; antibody engineering;  
KW monoclonal antibody; MAb; interleukin-4; IL-4; allergy.  
OS Mus sp.  
PH Key Location/Qualifiers  
FT Peptide 1..20  
FT /label= sig\_peptide  
FT Region 44..58  
FT /label= CDR  
FT /note= "complementarity determining region"  
FT Region 74..80  
FT /label= CDR  
FT /note= "complementarity determining region"  
FT Region 113..121  
FT /label= CDR  
FT /note= "complementarity determining region"  
PN W09507301-A.

PD 16-MAR-1995.  
 PF 07-SEP-1994; U10308.  
 PR 07-SEP-1993; US-117366.  
 PR 14-OCT-1993; US-136783.  
 PA (SMIK ) SMITHKLINE BEECHAM CORP.  
 PA (SMIK ) SMITHKLINE BEECHAM PLC.  
 PI Gross MS, Holmes SD, Sylvester DR;  
 DR WPI; 95-123387/16.  
 DR N-PSDB; Q83490.  
 PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived  
 PT from high affinity mAbs - useful in treatment of IL-4-mediated  
 PT and IgE-mediated allergic conditions  
 PS Disclosure; Fig.1; 97pp; English.  
 CC Spleen cells from mice immunized with human IL-4 were used to prepare  
 CC hybridomas, which were screened for anti-IL-4 MAb secretion. Only  
 CC clone 3B9 was positive. cDNA clones of the 3B9 light and heavy  
 CC chains were cloned into pCEW7f+ and transformed into E. coli  
 CC DH5-alpha. The clones were sequenced (Q83490-91), and used for  
 CC antibody engineering.  
 SQ Sequence 132 AA;

Query Match 100.0%; Score 35; DB 13; Length 132;  
 Best Local Similarity 100.0%; Pred. No. 1.22e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 74 aasles 80  
 |||||  
 Qy 1 AASNLES 7

Search completed: Wed Mar 19 15:55:32 1997  
 Job time : 9 secs.



Mar 19 15:53

US-08-612-929-18.rpr

3

```
RESULT 2
ENTRY      C38601      #type fragment
TITLE      Ig kappa chain V region (2B5) - mouse (fragment)
ORGANISM   #formal_name Mus musculus #common_name house mouse
DATE       30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change
23-Mar-1993

ACCESSIONS C38601
REFERENCE   A38601
#authors   Goshorn, S.C.; Retzel, E.; Jermerson, R.
#journal   J. Biol. Chem. (1991) 266:2134-2142
#title     Common structural features among monoclonal antibodies
           binding the same antigenic region of cytochrome c.
#cross-references MIMD:91115823
#accession C38601
##status   preliminary
##molecule_type mRNA
##residues 1-65 #label GOS
##cross-references GB:M57980
SUMMARY    #length 65 #checksum 8125

Query Match 100.0%; Score 35; DB 12; Length 65;
Best Local Similarity 100.0%; Pred. No. 1.09e+01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 7 aasnles 13
|||||||
Qy 1 AASNLES 7

RESULT 3
ENTRY      S42189      #type fragment
TITLE      Ig kappa chain V region - mouse (fragment)
ORGANISM   #formal_name Mus musculus #common_name house mouse
DATE       28-Sep-1994 #sequence_revision 21-Jul-1995 #text_change
21-Jul-1995

ACCESSIONS S42189
REFERENCE   S42176
#authors   Mo, J.A.; Bona, C.A.; Holmdahl, R.
#journal   Eur. J. Immunol. (1993) 23:2503-2510
#title     Variable region gene selection of immunoglobulin G-expressing
           B cells with specificity for a defined epitope on type II
           collagen.
#accession S42189
##status   preliminary
##molecule_type DNA
##residues 1-85 #label MOJ
##cross-references EMBL:Z25448
SUMMARY    #length 85 #checksum 7866

Query Match 100.0%; Score 35; DB 12; Length 85;
Best Local Similarity 100.0%; Pred. No. 1.09e+01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 40 aasnles 46
|||||||
Qy 1 AASNLES 7

RESULT 4
ENTRY      S42190      #type fragment
TITLE      Ig kappa chain V region - mouse (fragment)
ORGANISM   #formal_name Mus musculus #common_name house mouse
```

Mar 19 15:53

US-08-612-929-18.rpr

4

```
DATE       13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
13-Jan-1995

ACCESSIONS S42190
REFERENCE   S42176
#authors   Mo, J.A.; Bona, C.A.; Holmdahl, R.
#journal   Eur. J. Immunol. (1993) 23:2503-2510
#title     Variable region gene selection of immunoglobulin G-expressing
           B cells with specificity for a defined epitope on type II
           collagen.
#accession S42190
##status   preliminary
##molecule_type DNA
##residues 1-87 #label MOJ
##cross-references EMBL:Z25450
SUMMARY    #length 87 #checksum 2354

Query Match 100.0%; Score 35; DB 12; Length 87;
Best Local Similarity 100.0%; Pred. No. 1.09e+01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 42 aasnles 48
|||||||
Qy 1 AASNLES 7

RESULT 5
ENTRY      S42194      #type fragment
TITLE      Ig kappa chain V region - mouse (fragment)
ORGANISM   #formal_name Mus musculus #common_name house mouse
DATE       28-Sep-1994 #sequence_revision 21-Jul-1995 #text_change
21-Jul-1995

ACCESSIONS S42194
REFERENCE   S42176
#authors   Mo, J.A.; Bona, C.A.; Holmdahl, R.
#journal   Eur. J. Immunol. (1993) 23:2503-2510
#title     Variable region gene selection of immunoglobulin G-expressing
           B cells with specificity for a defined epitope on type II
           collagen.
#accession S42194
##status   preliminary
##molecule_type DNA
##residues 1-88 #label MOJ
##cross-references EMBL:Z25458
SUMMARY    #length 88 #checksum 4364

Query Match 100.0%; Score 35; DB 12; Length 88;
Best Local Similarity 100.0%; Pred. No. 1.09e+01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 43 aasnles 49
|||||||
Qy 1 AASNLES 7

RESULT 6
ENTRY      S42187      #type fragment
TITLE      Ig kappa chain V region - mouse (fragment)
ORGANISM   #formal_name Mus musculus #common_name house mouse
DATE       28-Sep-1994 #sequence_revision 21-Jul-1995 #text_change
21-Jul-1995

ACCESSIONS S42187
REFERENCE   S42176
#authors   Mo, J.A.; Bona, C.A.; Holmdahl, R.
#journal   Eur. J. Immunol. (1993) 23:2503-2510
```



#title Variable region gene selection of immunoglobulin G-expressing  
B cells with specificity for a defined epitope on type II

collagen.

#accession S42187

##status preliminary

##molecule\_type DNA

##residues 1-90 ##label MOJ

##cross-references EMBL:Z25444

SUMMARY #length 90 #checksum 9303

Query Match 100.0%; Score 35; DB 12; Length 90;

Best Local Similarity 100.0%; Pred. No. 1.09e+01;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 45 aaslns 51

|||||||

Qy 1 AASNLES 7

RESULT 7

ENTRY A38601 #type fragment

TITLE Ig kappa chain V region (1G3) - mouse (fragment)

ORGANISM #formal name Mus musculus #common name house mouse

DATE 30-Aug-1991 #sequence\_revision 30-Aug-1991 #text\_change

23-Mar-1993

ACCESSIONS A38601

REFERENCE A38601

#authors Goshorn, S.C.; Retzel, E.; Jermerson, R.

#journal J. Biol. Chem. (1991) 266:2134-2142

#title Common structural features among monoclonal antibodies

binding the same antigenic region of cytochrome c.

#cross-references MUID:91115823

#accession A38601

##status preliminary

##molecule\_type mRNA

##residues 1-93 ##label GOS

##cross-references GB:M57978

SUMMARY #length 93 #checksum 6635

Query Match 100.0%; Score 35; DB 12; Length 93;

Best Local Similarity 100.0%; Pred. No. 1.09e+01;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 35 aaslns 41

|||||||

Qy 1 AASNLES 7

RESULT 8

ENTRY KWMS10 #type complete

TITLE Ig kappa chain V region (PC7210) - mouse

ORGANISM #formal name Mus musculus #common name house mouse

DATE 30-Jun-1993 #sequence\_revision 30-Jun-1993 #text\_change

30-Sep-1993

ACCESSIONS D01937; A01937

REFERENCE A93204

#authors Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.

#journal Nature (1978) 276:785-790

#title Rearrangement of genetic information may produce

immunoglobulin diversity.

#cross-references MUID:79073152

#accession D01937

##molecule\_type protein

##residues 1-110 ##label WEI

CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology  
KEYWORDS immunoglobulin

FEATURE

23-92 #disulfide bonds #status predicted

SUMMARY #length 110 #molecular-weight 11950 #checksum 6378

Query Match 100.0%; Score 35; DB 2; Length 110;

Best Local Similarity 100.0%; Pred. No. 1.09e+01;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 54 aaslns 60

|||||||

Qy 1 AASNLES 7

RESULT 9

ENTRY KWMS1 #type complete

TITLE Ig kappa chain V region (CBPC 101) - mouse

ORGANISM #formal name Mus musculus #common name house mouse

DATE 30-Nov-1980 #sequence\_revision 30-Nov-1980 #text\_change

05-Apr-1995

ACCESSIONS A01936

REFERENCE A93822

#authors McKean, D.J.; Bell, M.; Potter, M.

#journal Proc. Natl. Acad. Sci. U.S.A. (1978) 75:3913-3917

#title Mechanisms of antibody diversity: multiple genes encode

structurally related mouse kappa variable regions.

#cross-references MUID:79012520

#accession A01936

##molecule\_type protein

##residues 1-111 ##label MCK

COMMENT This chain was isolated from a myeloma protein.

CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology

FEATURE

23-92 #disulfide bonds #status predicted

SUMMARY #length 111 #molecular-weight 11964 #checksum 1507

Query Match 100.0%; Score 35; DB 2; Length 111;

Best Local Similarity 100.0%; Pred. No. 1.09e+01;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 54 aaslns 60

|||||||

Qy 1 AASNLES 7

RESULT 10

ENTRY KWMS69 #type complete

TITLE Ig kappa chain V region (PC7769) - mouse

ORGANISM #formal name Mus musculus #common name house mouse

DATE 30-Jun-1993 #sequence\_revision 30-Jun-1993 #text\_change

30-Sep-1993

ACCESSIONS E01937; A01937

REFERENCE A93204

#authors Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.

#journal Nature (1978) 276:785-790

#title Rearrangement of genetic information may produce

immunoglobulin diversity.

#cross-references MUID:79073152

#accession E01937

##molecule\_type protein

##residues 1-111 ##label WEI

CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology

KEYWORDS immunoglobulin

## FEATURE

23-92  
SUMMARY #disulfide\_bonds #status predicted  
#length 111 #molecular\_weight 12011 #checksum 662

Query Match 100.0%; Score 35; DB 2; Length 111;  
Best Local Similarity 100.0%; Pred. No. 1.09e+01;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 54 aasnlcs 60  
|||||||  
Qy 1 AASNLES 7

RESULT 11  
ENTRY KWMS83 #type complete  
TITLE Ig kappa chain V region (PC7183) - mouse  
ORGANISM #formal\_name Mus musculus #common\_name house mouse  
DATE 30-Jun-1993 #sequence\_revision 30-Jun-1993 #text\_change 30-Sep-1993

ACCESSIONS B01937; A01937  
REFERENCE A93204  
#authors Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.  
#journal Nature (1978) 276:785-790  
#title Rearrangement of genetic information may produce immunoglobulin diversity.

#cross-references M01D:79073152  
#accession B01937  
#molecule\_type protein  
##residues 1-111 ##label WEI

CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology

KEYWORDS immunoglobulin

FEATURE 23-92  
SUMMARY #disulfide\_bonds #status predicted  
#length 111 #molecular\_weight 11952 #checksum 9

Query Match 100.0%; Score 35; DB 2; Length 111;  
Best Local Similarity 100.0%; Pred. No. 1.09e+01;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 54 aasnlcs 60  
|||||||  
Qy 1 AASNLES 7

RESULT 12  
ENTRY KWMS43 #type complete  
TITLE Ig kappa chain V region (PC7043) - mouse  
ORGANISM #formal\_name Mus musculus #common\_name house mouse  
DATE 01-Sep-1981 #sequence\_revision 01-Sep-1981 #text\_change 05-Apr-1995

ACCESSIONS A01937  
REFERENCE A93204  
#authors Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.  
#journal Nature (1978) 276:785-790  
#title Rearrangement of genetic information may produce immunoglobulin diversity.

#cross-references M01D:79073152  
#accession A01937  
#molecule\_type protein  
##residues 1-111 ##label WEI

CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology

FEATURE 23-92  
SUMMARY #disulfide\_bonds #status predicted  
#length 111 #molecular\_weight 12002 #checksum 438

Query Match 100.0%; Score 35; DB 2; Length 111;  
Best Local Similarity 100.0%; Pred. No. 1.09e+01;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 54 aasnlcs 60  
|||||||  
Qy 1 AASNLES 7

RESULT 13  
ENTRY SI9971 #type fragment  
TITLE Ig kappa chain V region (CD4 mAb clone M-T310 and others) - mouse (fragment)

ORGANISM #formal\_name Mus musculus #common\_name house mouse  
DATE 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 01-Dec-1995

ACCESSIONS SI9971; SI9973  
REFERENCE SI9963  
#authors Weissenhorn, W.; Riethmueller, G.; Weiss, E.M.; Rieber, E.P.  
#submission submitted to the EMBL Data Library, March 1992  
#description Structural characterization of CD4 mAb.

#accession SI9971  
#molecule\_type mRNA  
##residues 1-112 ##label WEI  
##cross-references EMBL:X65091  
##experimental\_source clone M-T310

#accession SI9973  
#molecule\_type mRNA  
##residues 1-112 ##label WEW  
##cross-references EMBL:X65092  
##experimental\_source M-T404

CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology

SUMMARY #length 112 #checksum 4782

Query Match 100.0%; Score 35; DB 5; Length 112;  
Best Local Similarity 100.0%; Pred. No. 1.09e+01;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 54 aasnlcs 60  
|||||||  
Qy 1 AASNLES 7

RESULT 14  
ENTRY SI9976 #type fragment  
TITLE Ig kappa chain V region (M-T413) - mouse (fragment)

ORGANISM #formal\_name Mus musculus #common\_name house mouse  
DATE 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 12-Apr-1995

ACCESSIONS SI9976  
REFERENCE SI9963  
#authors Weissenhorn, W.; Riethmueller, G.; Weiss, E.M.; Rieber, E.P.  
#submission submitted to the EMBL Data Library, March 1992  
#description Structural characterization of CD4 mAb.

#accession SI9976  
##status preliminary  
#molecule\_type mRNA  
##residues 1-112 ##label WEI  
##cross-references EMBL:X65093

CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology

SUMMARY #length 112 #checksum 4816

Query Match 100.0%; Score 35; DB 5; Length 112;

Mar 19 15:53

US-08-612-929-18.rpr

9

Best Local Similarity 100.0%; Pred. No. 1.09e+01;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 54 aaslns 60  
|||||||  
Qy 1 AASNIES 7

RESULT 15

ENTRY PH1226 #type fragment  
TITLE Ig kappa chain precursor V region (M-T310) - human (fragment)  
ORGANISM #formal\_name Homo sapiens #common\_name man  
DATE 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 30-Apr-1995  
ACCESSIONS PH1226  
REFERENCE PH1224  
#authors Weissenhorn, W.; Scheuer, W.; Kaluza, B.; Schwirzke, M.; Reiter, C.; Flieger, D.; Lenz, H.; Weiss, E.H.; Rieber, E.P.; Riethmuller, G.; Weidle, U.H.  
#journal Gene (1992) 121:271-278  
#title Combinatorial functions of two chimeric antibodies directed to human CD4 and one directed to the alpha-chain of the human interleukin-2 receptor.

#accession PH1226  
#molecule\_type mRNA  
#residues 1-131 #label WEI  
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology  
KEYWORDS immunoglobulin  
FEATURE  
1-20 #domain signal sequence #status predicted #label SIG  
21-131 #product Ig light chain V region #status predicted  
#label WAI

SUMMARY #length 131 #checksum 4648

Query Match 100.0%; Score 35; DB 5; Length 131;  
Best Local Similarity 100.0%; Pred. No. 1.09e+01;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 74 aaslns 80  
|||||||  
Qy 1 AASNIES 7

RESULT 16

ENTRY B64160 #type complete  
TITLE hypothetical protein HI0852 - Haemophilus influenzae (strain Rd KW20)  
ORGANISM #formal\_name Haemophilus influenzae  
DATE 18-Aug-1995 #sequence\_revision 18-Aug-1995 #text\_change 18-Aug-1995

ACCESSIONS B64160  
REFERENCE A64000  
#authors Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kervage, A.R.; Bult, C.J.; Tomb, J.F.; Dougherty, B.A.; Merrick, J.M.; McKenney, K.; Sutton, G.; FitzHugh, W.; Fields, C.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.F.; Phillips, C.A.; Spriggs, T.; Hedblom, E.; Cotton, M.D.; Utterback, T.R.; Hanna, M.C.; Nguyen, D.T.; Saudek, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.; Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, J.C.

#journal Science (1995) 269:496-512  
#title Whole-genome random sequencing and assembly of Haemophilus

Mar 19 15:53

US-08-612-929-18.rpr

10

#accession B64160  
#status preliminary; sequence not shown; translation not shown  
#molecule\_type DNA  
#residues 1-463 #label TIGR  
#cross-references GB:I42023; TIGR:HI0852  
#note best homolog was a hypothetical protein from Escherichia coli

SUMMARY #length 463 #molecular-weight 50002 #checksum 8725

Query Match 100.0%; Score 35; DB 8; Length 463;  
Best Local Similarity 100.0%; Pred. No. 1.09e+01;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 94 aaslns 100  
|||||||  
Qy 1 AASNIES 7

Search completed: Wed Mar 19 15:55:06 1997  
Job time : 12 secs.

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WPPSRLH (TW)

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Mpsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Mar 18 10:13:17 1997; MaePar time 2.37 Seconds  
Tabular output not generated. 54.788 Million cell updates/sec

Title: >US-08-612-929-22  
Description: (1-7) from US08612929.pep  
Perfect Score: 45  
Sequence: 1 TSCMGVS 7

Scoring table: PAM 150  
Gap 15

Searched: 52205 seqs, 18531385 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: swiss-prot33  
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10

Statistics: Mean 19.683; Variance 19.771; scale 0.996

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description	Pred. No.
1	40	88.9	336	3	FLA1_BORBU	FLAGELLAR FILAMENT 41	7.43e+00
2	40	88.9	793	7	PPSA_ECOLI	PHOSPHOENOLPYRUVATE S	7.43e+00
3	40	88.9	857	5	MEDB_GIALA	MEDIAN BODY PROTEIN.	7.43e+00
4	40	88.9	1274	8	SRE3_BACSO	SURFACTIN SYNTHETASE	7.43e+00
5	39	86.7	58	2	CITB_SALTY	CITB PROTEIN (FRAGMEN	1.28e+01
6	39	86.7	417	4	GELS_XENLA	GELSOLIN (ACTIN-DEPOL	1.28e+01
7	39	86.7	841	6	MYFC_YEREN	OUTER MEMBRANE USHER	1.28e+01
8	38	84.4	130	3	FLHE_SALTY	FLAGELLAR PROTEIN FLH	2.18e+01
9	38	84.4	194	10	YF09_HAEIN	HYPOTHETICAL PROTEIN	2.18e+01
10	38	84.4	238	10	Y2AK_STRGR	HYPOTHETICAL 24.7 KD	2.18e+01
11	38	84.4	300	4	GLTC_BACSO	REGULATORY PROTEIN GL	2.18e+01
12	38	84.4	348	2	CTGF_MOUSE	CONNECTIVE TISSUE GRO	2.18e+01
13	38	84.4	349	2	CTGF_HUMAN	CONNECTIVE TISSUE GRO	2.18e+01

14	38	84.4	361	5	LIG_PHLRA	LIGNINASE III PRECURS	2.18e+01
15	38	84.4	719	6	PGCA_BOVIN	CARTILAGE-SPECIFIC PR	2.18e+01
16	37	82.2	384	7	POQ3_ACICA	COENZYME PQQ SYNTHESI	3.68e+01
17	37	82.2	505	3	FIXL_RHME	SENSOR PROTEIN FIXL (	3.68e+01
18	37	82.2	541	4	HXT2_YEAST	HIGH-AFFINITY GLUCOSE	3.68e+01
19	37	82.2	546	4	HXT0_YEAST	HEXOSE TRANSPORTER HX	3.68e+01
20	37	82.2	669	10	YH06_HAEIN	PROBABLE TRANSPORT PR	3.68e+01
21	36	80.0	205	7	PRCT_RAT	PROTEASOME THETA CHAI	6.13e+01
22	36	80.0	262	1	BACR_HALHA	BACTERIORHODOPSIN PRE	6.13e+01
23	36	80.0	317	2	CFXR_ALCED	RUBISCO OPERON TRANSC	6.13e+01
24	36	80.0	325	1	ARCB_HAEIN	AEROBIC RESPIRATION C	6.13e+01
25	36	80.0	376	10	YJ9M_YEAST	HYPOTHETICAL 41.6 KD	6.13e+01
26	36	80.0	449	6	NDOB_PSEPU	NAPHTHALENE 1,2-DIOXY	6.13e+01
27	36	80.0	457	4	HEMN_ECOLI	OXYGEN-INDEPENDENT CO	6.13e+01
28	36	80.0	462	7	PPB3_BACSO	ALKALINE PHOSPHATASE	6.13e+01
29	36	80.0	464	3	GALP_ECOLI	GALACTOSE-PROTON SYMP	6.13e+01
30	36	80.0	467	1	6PGD_SNP7	6-PHOSPHOGLUCONATE DE	6.13e+01
31	36	80.0	507	9	VGLG_VHSV0	SPIKE GLYCOPROTEIN PR	6.13e+01
32	36	80.0	524	7	PPBT_RAT	ALKALINE PHOSPHATASE	6.13e+01
33	36	80.0	524	7	PPBT_BOVIN	ALKALINE PHOSPHATASE	6.13e+01
34	36	80.0	530	7	PPB1_HUMAN	ALKALINE PHOSPHATASE	6.13e+01
35	36	80.0	535	7	PPB2_HUMAN	ALKALINE PHOSPHATASE	6.13e+01
36	36	80.0	538	8	TCMA_STRGA	TETRACENOMYCIN C RESI	6.13e+01
37	36	80.0	548	3	FUMB_ECOLI	FUMARATE HYDRATASE CL	6.13e+01
38	36	80.0	573	9	UREL_LACFE	ACID UREASE ALPHA SUB	6.13e+01
39	36	80.0	617	4	HEMA_MEASI	HEMAGGLUTININ-NEURAMI	6.13e+01
40	36	80.0	617	4	HEMA_MEASH	HEMAGGLUTININ-NEURAMI	6.13e+01
41	36	80.0	617	4	HEMA_MEASH	HEMAGGLUTININ-NEURAMI	6.13e+01
42	36	80.0	620	4	HEMA_MEASY	HEMAGGLUTININ-NEURAMI	6.13e+01
43	36	80.0	713	2	CDGU_BACCI	CYCLOMALTODEXTRIN GIU	6.13e+01
44	36	80.0	1161	7	POL_SFVI	POL POLYPROTEIN (CONT	6.13e+01
45	36	80.0	2149	8	RRPL_RVFEVZ	RNA-DIRECTED RNA POLY	6.13e+01

ALIGNMENTS

RESULT	1	FLA1_BORBU	STANDARD;	PRT;	336 AA.
AC	P11089; P15295;				
DT	01-JUL-1989 (REL. 11, CREATED)				
DT	01-JUL-1989 (REL. 11, LAST SEQUENCE UPDATE)				
DT	01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)				
DE	FLAGELLAR FILAMENT 41 KD CORE PROTEIN (FLAGELLIN) .				
GN	FLA.				
OS	BORRELIA BURGDORFERI (LYME DISEASE SPIROCHETE) .				
OC	PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; SPIROCHETES; SPIROCHAETALES;				
OC	SPIROCHAETACEAE.				
RN	[1]				
RP	SEQUENCE FROM N.A., AND SEQUENCE OF N-TERMINUS.				
RC	STRAIN=GEHO, AND ATCC 35210 / B31;				
RX	MEDLINE; 89263802.				
RA	GASSMANN G.S., KRAMER M.D., GOEBEL U.B., WALLICH R.;				
RL	NUCLEIC ACIDS RES. 17:3590-3590(1989).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=GEHO;				
RX	MEDLINE; 91139587.				
RA	GASSMANN G.S., JACOBS E., DEUTZMANN R., GOEBEL U.B.;				
RL	J. BACTERIOL. 173:1452-1459(1991).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=ATCC 35210 / B31;				
RX	MEDLINE; 90256248.				
RA	WALLICH R., MOTER S.E., SIMON M.M., EBNET K., HEIBERGER A.,				

RA KRAMER M.D.;  
 RL INFECT. IMMUN. 58:1711-1719(1990).  
 CC -!- FUNCTION: COMPONENT OF THE CORE OF THE FLAGELLA.  
 CC -!- SUBUNIT: OUTER LAYER COMPOSED OF REPEATING UNITS OF FLAA AND A  
 CC CORE THAT CONTAINS ONE OR ALL OF FIVE ANTIGENICALLY RELATED  
 CC POLYPEPTIDE.  
 CC -!- SUBCELLULAR LOCATION: PERIPLASMIC FLAGELLUM.  
 CC -!- SIMILARITY: TO OTHER BACTERIAL FLAGELLINS.  
 DR EMBL; X15660; G39359; -.  
 DR EMBL; X15661; G39361; -.  
 DR EMBL; X16833; G39357; -.  
 DR EMBL; X56334; G289000; -.  
 DR PIR; A41470; FLYYB3.  
 DR PIR; A60276; A60276.  
 DR PIR; A38450; A38450.  
 DR PIR; S04091; S04091.  
 DR PROSITE; PS00588; FLAGELLA\_BB\_ROD.  
 KW FLAGELLA; PERIPLASMIC.  
 FT VARIANT 180 180 N -> T (IN STRAIN B31).  
 FT VARIANT 279 279 D -> N (IN STRAIN B31).  
 SQ SEQUENCE 336 AA; 35765 MW; 77882759 CRC32;

Query Match 88.9%; Score 40; DB 3; Length 336;  
 Best Local Similarity 71.4%; Pred. No. 7.43e+00;  
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 43 aaamgvs 49  
 :::|||||  
 QY 1 TSGMGVS 7

RESULT 2  
 ID PPSA ECOLI STANDARD; PRT; 793 AA.  
 AC P23538;  
 DT 01-NOV-1991 (REL. 20, CREATED)  
 DT 01-DEC-1992 (REL. 24, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)  
 DE PHOSPHENOLPYRUVATE SYNTHASE (EC 2.7.9.2) (PYRUVATE.WATER DIKINASE)  
 DE (PEP SYNTHASE).  
 GN PPSA OR PPS.  
 OS ESCHERICHIA COLI.  
 OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;  
 OC ENTEROBACTERIACEAE.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA HOLZSCHU D.L., MCELVER J.A., LIAO C.C., BERRY A.J  
 RL SUBMITTED (JUN-1991) TO EMBL/GENBANK/DDBJ DATA BANKS.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=K12;  
 RX MEDLINE; 92140374.  
 RA NIRSCHACH M., KRUEZALER F., GERSE R.H., POSTMA P., HIRSCH H.J.;  
 RL MOL. GEN. GENET. 232:332-336(1992).  
 CC -!- PATHWAY: ESSENTIAL STEP IN GLUCONEOGENESIS WHEN PYRUVATE AND  
 CC LACTATE ARE USED AS A CARBON SOURCE.  
 CC -!- CATALYTIC ACTIVITY: ATP + PYRUVATE + H(2)O = AMP +  
 CC PHOSPHENOLPYRUVATE + PHOSPHATE.  
 CC -!- SIMILARITY: TO OTHER PEP-UTILIZING ENZYMES.  
 DR EMBL; M69116; G147146; -.  
 DR EMBL; X59381; G42481; -.  
 DR PIR; S20554; S20554.  
 DR SWISS-2DPAGE; P23538; COLI.  
 DR ECO2DBASE; B083.0; 6TH EDITION.  
 DR ECOGENE; EG10759; PPSA.

DR PROSITE; PS00370; PEP ENZYMES PHOS SITE.  
 DR TRANSFERASE; KINASE; ATP-BINDING; PHOSPHORYLATION.  
 FT MOD RES 472 422 PHOSPHORYLATION (BY SIMILARITY).  
 FT CONFLICT 194 196 AGL -> RM (IN REF. 2).  
 FT CONFLICT 342 344 AHA -> RSRQ (IN REF. 2).  
 FT CONFLICT 346 361 RSMVIRCIHVRVLS -> MERYTLHSQKIIA  
 (IN REF. 2).  
 SQ SEQUENCE 793 AA; 87402 MW; BF0F2A9E CRC32;

Query Match 88.9%; Score 40; DB 7; Length 793;  
 Best Local Similarity 100.0%; Pred. No. 7.43e+00;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 39 sgmgvs 44  
 :|||||  
 QY 2 SGMGVS 7

RESULT 3  
 ID MEDB GIALA STANDARD; PRT; 857 AA.  
 AC Q08014;  
 DT 01-NOV-1995 (REL. 32, CREATED)  
 DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)  
 DE MEDIAN BODY PROTEIN.  
 OS GIARDIA LAMBLIA.  
 OC EUKARYOTA; PROTOZOA; SARCOMASTIGOPHORA; MASTIGOPHORA; DIPLOMONADIDA;  
 OC HEXAMITIDAE.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=PORTLAND-1;  
 RX MEDLINE; 93287123.  
 RA MARSHALL J., HOLBERTON D.V.;  
 RL J. MOL. BIOL. 231:521-530(1993).  
 CC -!- FUNCTION: MAY HAVE A ROLE IN IMMOBILISING THE MICROTUBULES  
 CC BETWEEN CELL DIVISIONS.  
 CC -!- SUBCELLULAR LOCATION: MEDIAN BODY.  
 CC -!- DOMAIN: SHOWS AN ALPHA-HELICAL COILED COIL STRUCTURE (30  
 CC REPEATING HEPTADS).  
 DR EMBL; X64517; G312671; -.  
 KW CYTOSKELETON; MICROTUBULES; COILED COIL; HEPTAD REPEAT PATTERN.  
 SQ SEQUENCE 857 AA; 100583 MW; 5E2BBA84 CRC32;

Query Match 88.9%; Score 40; DB 5; Length 857;  
 Best Local Similarity 71.4%; Pred. No. 7.43e+00;  
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 795 stgmgs 801  
 :::|||||  
 QY 1 TSGMGVS 7

RESULT 4  
 ID SRF3 BACSU STANDARD; PRT; 1274 AA.  
 AC Q08787;  
 DT 01-FEB-1995 (REL. 31, CREATED)  
 DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)  
 DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)  
 DE SURFACTIN SYNTHETASE SUBUNIT 3.  
 GN SRFAC OR SRFAC3.  
 OS BACILLUS SUBTILIS.  
 OC PROKARYOTA; FIRMICUTES; ENDOSPORE-FORMING RODS AND COCCI; BACILLACEAE.  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC STRAIN=168 / JH642;  
 RX MEDLINE; 93360813.  
 RA COSMINA P., RODRIGUEZ F., DE FERRA F., GRANDI G., PEREGO M.,  
 RA VENEMA G., VAN SINDEREN D.;  
 RL MOL. MICROBIOL. 8:821-831(1993).  
 CC -I- FUNCTION: PROBABLY ACTIVATES A LEUCINE.  
 CC -I- PATHWAY: NON-RIBOSOMAL BIOSYNTHESIS OF THE CYCLIC PEPTIDE  
 CC ANTI-BIOTIC SURFACTIN.  
 CC -I- COFACTOR: CONTAINS A COVALENTLY BOUND PHOSPHOPANTHETHEINE.  
 CC -I- SIMILARITY: TO OTHER ENZYMES WHICH ACT VIA AN ATP-DEPENDENT  
 CC COVALENT BINDING OF AMP TO THEIR SUBSTRATE.  
 DR ENBL; X70356; G396483; -.  
 DR SUBTILIST; BG10170; SRFAC.  
 DR PROSITE; PS00455; AMP BINDING.  
 KW ANTI-BIOTIC BIOSYNTHESIS; LIGASE; SPORULATION; PHOSPHOPANTHETHEINE.  
 FT REPEAT 1 1044 DOMAIN 1 (LED-ACTIVATING).  
 FT BINDING 1003 1003 PHOSPHOPANTHETHEINE (POTENTIAL).  
 SQ SEQUENCE 1274 AA; 143817 MW; A3B95100 CRC32;

Query Match 88.9%; Score 40; DB 8; Length 1274;  
 Best Local Similarity 100.0%; Pred. No. 7.43e+00;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 809 sgmgvs 814  
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 Qy 2 SCMGVS 7

## RESULT 5

ID CITB SALTY STANDARD; PRT; 58 AA.  
 AC P37463;  
 DT 01-OCT-1994 (REL. 30, CREATED)  
 DT 01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)  
 DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)  
 DE CITB PROTEIN (FRAGMENT).  
 GN CITB.  
 OS SALMONELLA TYPHIMURIUM.  
 OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;  
 OC ENTEROBACTERIACEAE.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=LT2;  
 RX MEDLINE; 92041761.  
 RA SHIMAMOTO T., IZAWA H., DAIMON H., ISHIGURO N., SHINAGAWA M.,  
 RA SAKANO Y., TSUDA M., TSUCHIYA T.;  
 RL J. BIOCHEM. 110:22-28(1991).  
 DR ENBL; D90203; E42680; -.  
 DR PIR; PQ0098; PQ0098.  
 DR STIGENE; SG10059; CITB.  
 KW CITRATE UTILIZATION.  
 FT NON TER 1 1  
 SQ SEQUENCE 58 AA; 6271 MW; E33DDB8B CRC32;

Query Match 86.7%; Score 39; DB 2; Length 58;  
 Best Local Similarity 83.3%; Pred. No. 1.28e+01;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 4 tsgmgi 9  
 |||||  
 Qy 1 TSCMGV 6

## RESULT 6

ID CELS XENIA STANDARD; PRT; 417 AA.  
 AC P14885;  
 DT 01-APR-1990 (REL. 14, CREATED)  
 DT 01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)  
 DT 01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)  
 DE GELSOLIN (ACTIN-DEPOLYMERIZING FACTOR) (ADF) (BREVIN) (FRAGMENT).  
 OS XENOPUS LAEVIS (AFRICAN CLAWED FROG).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AMPHIBIA; ANURA.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-OVARY;  
 RX MEDLINE; 89008590.  
 RA ANKENBAUER T., KLEINSCHMIDT J.A., VANDEKERCKHOVE J., FRANK W.W.;  
 RL J. CELL BIOL. 107:1489-1498(1988).  
 CC -I- FUNCTION: GELSOLIN IS A CALCIUM-REGULATED, ACTIN-MODULATING  
 CC PROTEIN THAT BINDS TO THE PLUS (OR BARBED) ENDS OF ACTIN MONOMERS  
 CC OR FILAMENTS, PREVENTING MONOMER EXCHANGE (END-BLOCKING OR  
 CC CAPPING). IT CAN PROMOTE THE ASSEMBLY OF MONOMERS INTO FILAMENTS  
 CC (NUCLEATION) AS WELL AS SEVER FILAMENTS ALREADY FORMED.  
 CC -I- IN ADDITION TO ITS ROLE IN ACTIN REGULATION, THIS PROTEIN IS KNOWN  
 CC TO BIND WITH HIGH AFFINITY TO FIBRONECTIN.

DR ENBL; M36652; G214176; -.  
 DR ENBL; X13319; G64716; -.  
 DR HSP; P02640; 1SWO.  
 KW ACTIN-BINDING; REPEAT; CALCIUM.  
 FT NON TER 1 1  
 SQ SEQUENCE 417 AA; 46024 MW; B71940E2 CRC32;

Query Match 86.7%; Score 39; DB 4; Length 417;  
 Best Local Similarity 71.4%; Pred. No. 1.28e+01;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 38 tdgmga 44  
 |||||  
 Qy 1 TSGMGVS 7

## RESULT 7

ID MYFC YEREN STANDARD; PRT; 841 AA.  
 AC P33408;  
 DT 01-FEB-1994 (REL. 28, CREATED)  
 DT 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)  
 DE OUTER MEMBRANE USHER PROTEIN MYFC PRECURSOR.  
 GN MYFC.  
 OS YERSINIA ENTEROCOLITICA.  
 OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;  
 OC ENTEROBACTERIACEAE.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=W1024 / SEROTYPE 0:9;  
 RX MEDLINE; 94018646.  
 RA TRIARTE M., VANOOTECHEM J.-C., DELOR I., DIAZ R., KNUITON S.,  
 RA CORNELIS G.R.;  
 RL MOL. MICROBIOL. 9:507-520(1993).  
 CC -I- FUNCTION: INVOLVED IN THE EXPORT AND ASSEMBLY OF THE MYFA  
 CC FIMBRIAL SUBUNIT.  
 CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE  
 CC (BY SIMILARITY).  
 CC -I- SIMILARITY: TO OTHER FIMBRIAL EXPORT USHER PROTEINS.  
 DR ENBL; Z21953; G402172; -.  
 DR PIR; S39365; S39365.  
 DR PROSITE; PS01151; FIMBRIAL\_USHER.  
 KW OUTER MEMBRANE; TRANSMEMBRANE; FIMBRIA; TRANSPORT; SIGNAL.

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US-08-612-929-22.fsp

7

FT SIGNAL 1 26 POTENTIAL.  
 FT CHAIN 27 841 OUTER MEMBRANE USHER PROTEIN MYFC.  
 FT DISULFID 817 840 POTENTIAL.  
 SQ SEQUENCE 841 AA; 93414 MW; 19A34962 CRC32;

Query Match 86.7%; Score 39; DB 6; Length 841;  
 Best Local Similarity 83.3%; Pred. No. 1.28e+01;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 412 tagmqv 417  
 I:||||  
 Qy 1 TSGMGV 6

RESULT 8  
 ID FLHE SALTY STANDARD; PRT; 130 AA.

AC P40728;  
 DT 01-FEB-1995 (REL. 31, CREATED)  
 DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)  
 DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)  
 DE FLAGELLAR PROTEIN FLHE PRECURSOR.  
 GN FLHE.

OS SALMONELLA TYPHIMURIUM.  
 OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;  
 CN ENTEROBACTERIACEAE.

RE SEQUENCE FROM N.A., AND SEQUENCE OF 17-25.  
 RC STRAIN-KK1004;  
 RX MEDLINE; 95095932.

RA MINAMINO T., IINO T., KITSUKAKE K.;  
 RL J. BACTERIOL. 176:1630-1637(1994).  
 CC -1- FUNCTION: NOT ESSENTIAL FOR FLAGELLAR FORMATION AND FUNCTION.

DR EMBL; D32203; G633117; -;  
 DR STYGENE; SG10528; FLHE.  
 KW FLAGELLA; SIGNAL.

FT SIGNAL 1 16  
 FT CHAIN 17 130 FLAGELLAR PROTEIN FLHE.  
 SQ SEQUENCE 130 AA; 14073 MW; F9805A38 CRC32;

Query Match 84.4%; Score 38; DB 3; Length 130;  
 Best Local Similarity 83.3%; Pred. No. 2.18e+01;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 25 sgmgvt 30  
 I:||||  
 Qy 2 SCMGVS 7

RESULT 9  
 ID YF09 HAEIN STANDARD; PRT; 194 AA.

AC P44231;  
 DT 01-NOV-1995 (REL. 32, CREATED)  
 DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)  
 DE HYPOTHETICAL PROTEIN H11509.

GN H11509.  
 OS HAEMOPHILUS INFLUENZAE.  
 OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;  
 CN PASTEURACEAE.

RE SEQUENCE FROM N.A.  
 RC STRAIN=RD / KW20;  
 RX MEDLINE; 95350630.

RA FLEISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F.,

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8

RA KERLAVAGE A.R., BULT C.J., TOMB J.-F., DOUGHERTY B.A., MERRICK J.M.,  
 RA MCKENNEY K., SUTTON G., FITZHUGH W., FIELDS C.A., GOCAYNE J.D.,  
 RA SCOTT J.D., SHIRLEY R., LIU L.-I., GLODEK A., KELLEY J.M.,  
 RA WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLUM E., COTTON M.D.,  
 RA UTTERBACK T.R., HANNA M.C., NGUYEN D.T., SAUDEK D.M., BRANDON R.C.,  
 RA FINE L.D., FRITZMAN J.L., FUHRMANN J.L., GEOGHAGEN N.S.M.,  
 RA GNEHM C.L., McDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O.,  
 RA VENTER J.C.;  
 RL SCIENCE 269:496-512(1995).  
 DR EMBL; L46140; G1007674; -;  
 DR EMBL; U32827; G926588; -;  
 KW HYPOTHETICAL PROTEIN.  
 SQ SEQUENCE 194 AA; 21817 MW; 71374765 CRC32;

Query Match 84.4%; Score 38; DB 10; Length 194;  
 Best Local Similarity 83.3%; Pred. No. 2.18e+01;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 134 sgmgva 139  
 I:||||  
 Qy 2 SCMGVS 7

RESULT 10  
 ID Y24K STRGR STANDARD; PRT; 238 AA.

AC P12752;  
 DT 01-OCT-1989 (REL. 12, CREATED)  
 DT 01-OCT-1989 (REL. 12, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)  
 DE HYPOTHETICAL 24.7 KD PROTEIN IN PHOTOLYASE 5' REGION.  
 OS STREPTOMYCES GRISEUS.  
 OC PROKARYOTA; FIRMICUTES; ACTINOMYCETALES; STREPTOMYCETACEAE.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 89315214.  
 RA KOBAYASHI T., TAKAO M., OIKAWA A., YASUI A.;  
 RL NUCLEIC ACIDS RES. 17:4731-4744(1989).  
 DR EMBL; X15060; G47082; -;  
 DR PIR; S05572; S05572.

KW HYPOTHETICAL PROTEIN.  
 SQ SEQUENCE 238 AA; 24655 MW; 313A8012 CRC32;

Query Match 84.4%; Score 38; DB 10; Length 238;  
 Best Local Similarity 57.1%; Pred. No. 2.18e+01;  
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 209 asmggit 215  
 I:||||  
 Qy 1 TSGMGVS 7

RESULT 11  
 ID GLTC BACSU STANDARD; PRT; 300 AA.

AC P20668;  
 DT 01-FEB-1991 (REL. 17, CREATED)  
 DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)  
 DE REGULATORY PROTEIN GLTC.

GN GLTC.  
 OS BACILLUS SUBTILIS.

OC PROKARYOTA; FIRMICUTES; ENDOSPORE-FORMING RODS AND COCCI; BACILLACEAE.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 89359102.

RA BOHANNON D.E., SONENSHIN A.L.;  
RL J. BACTERIOL. 171:4718-4727(1989).  
RN [2]  
RP REVISIONS.  
RA SONENSHIN A.L.;  
RL SUBMITTED (FEB-1994) TO EMBL/GENBANK/DBJ DATA BANKS.  
CC -!- FUNCTION: POSITIVE REGULATOR OF GLUTAMATE BIOSYNTHESIS (GLUTAB  
CC GENES). GLUT ALSO REPRESSSES ITS OWN TRANSCRIPTION.  
CC -!- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL  
CC REGULATORS.  
DR EMBL; M28509; G457514; --.  
DR PIR; A33951; A33951.  
DR SUBTILIST; BG10810; GLUTC.  
DR PROSITE; PS00044; HTH LYSR FAMILY.  
KW GLUTAMATE BIOSYNTHESIS; TRANSCRIPTION REGULATION; ACTIVATOR;  
KW DNA-BINDING.  
FT DNA BIND 18 37 H-T-H MOTIF (BY SIMILARITY).  
SQ SEQUENCE 300 AA; 34019 MW; 3CF46232 CRC32;

Query Match 84.4%; Score 38; DB 4; Length 300;  
Best Local Similarity 57.1%; Pred. No. 2.18e+01;  
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 233 seqmgtv 239

Qy :::::1:

Qy 1 TSGMGVS 7

RESULT 12  
ID CTGF MOUSE STANDARD; PRT; 348 AA.  
AC P29268;  
DT 01-DEC-1992 (REL. 24, CREATED)  
DT 01-DEC-1992 (REL. 24, LAST SEQUENCE UPDATE)  
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)  
DE CONNECTIVE TISSUE GROWTH FACTOR PRECURSOR (CTGF) (FISP-12 PROTEIN).  
GN CTGF OR FISP12 OR FISP-12.  
OS MUS MUSCULUS (MOUSE).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; RODENTIA.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 91363290.  
RA RYSECK R.-P., MACDONALD-BRAVO H., MATTEI M.-G., BRAVO R.;  
RL CELL GROWTH DIFFER. 2:225-233(1991).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 91229699.  
RA BRUNNER A., CHINN J., NEUBAUER M.G., PORCHIO A.F.;  
RL DNA CELL BIOL. 10:293-300(1991).  
CC -!- INDUCTION: BY GROWTH FACTORS.  
CC -!- TISSUE SPECIFICITY: TESTIS, SPLEEN, KIDNEY, LUNG, HEART, AND BRAIN  
CC (LOWEST LEVEL IN TESTIS AND HIGHEST IN LUNG).  
CC -!- SIMILARITY: TO INSULIN-LIKE GROWTH FACTOR BINDING PROTEINS AND  
CC TO THE CEF-10/CYR61/CTGF/FISP-12/NOV PROTEIN FAMILY.  
CC -!- SIMILARITY: CONTAINS A C-TERMINAL CYSTINE KNOT-LIKE DOMAIN (CTCK).  
DR EMBL; M70641; G193314; --.  
DR EMBL; M70642; G193316; --.  
DR EMBL; M80263; G201946; --.  
DR PIR; A53228; A53228.  
DR PROSITE; PS00222; IGF\_BINDING.  
KW GROWTH FACTOR BINDING; SIGNAL.  
FT SIGNAL 1 21 POTENTIAL.  
FT CHAIN 22 348 CONNECTIVE TISSUE GROWTH FACTOR.  
FT DOMAIN 255 329 CTCK.

FT DISULFID 255 292 BY SIMILARITY.  
FT DISULFID 272 306 BY SIMILARITY.  
FT DISULFID 283 322 BY SIMILARITY.  
FT DISULFID 286 324 BY SIMILARITY.  
FT DISULFID 291 328 BY SIMILARITY.  
FT CONFLICT 161 161 K -> E (IN REF. 2).  
SQ SEQUENCE 348 AA; 31793 MW; EAB92BE0 CRC32;

Query Match 84.4%; Score 38; DB 2; Length 348;  
Best Local Similarity 71.4%; Pred. No. 2.18e+01;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 211 tcgmgi 217

Qy :::::1:

Qy 1 TSGMGVS 7

RESULT 13  
ID CTGF HUMAN STANDARD; PRT; 349 AA.  
AC P29279;  
DT 01-DEC-1992 (REL. 24, CREATED)  
DT 01-DEC-1992 (REL. 24, LAST SEQUENCE UPDATE)  
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)  
DE CONNECTIVE TISSUE GROWTH FACTOR PRECURSOR.  
GN CTGF.  
OS HOMO SAPIENS (HUMAN).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; PRIMATES.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=UMBILICAL VEIN ENDOTHELIAL CELLS;  
RX MEDLINE; 91373462.  
RA BRADHAM D.M., IGARASHI A., POTTER R.L., GROTEENDORST G.R.;  
RL J. CELL BIOL. 114:1285-1294(1991).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=UMBILICAL VEIN ENDOTHELIAL CELLS;  
RX MEDLINE; 93187114.  
RA IGARASHI A., BRADHAM D.M., OKOCHI H., GROTEENDORST G.R.;  
RL J. DERMATOL. 19:642-643(1992).  
RN [3]  
RP SEQUENCE FROM N.A.  
RA OEHAR B.S., WERNER A., YANG Z., GARNIER J.M., GENTZ R., LUESCHER T.F.;  
RL SUBMITTED (APR-1994) TO EMBL/GENBANK/DBJ DATA BANKS.  
CC -!- FUNCTION: MAJOR CONNECTIVE TISSUE MITOATTRACTANT SECRETED BY  
CC HUMAN VASCULAR ENDOTHELIAL CELLS. THIS IMMEDIATE-EARLY PROTEIN  
CC MAY BIND ONE OF THE PDGF CELL SURFACE RECEPTORS.  
CC -!- SUBUNIT: MONOMER.  
CC -!- ALTERNATIVE PRODUCTS: A SHORTER FORM MAY BE PRODUCED BY  
CC ALTERNATIVE SPLICING OF THE SAME GENE.  
CC -!- SIMILARITY: TO INSULIN-LIKE GROWTH FACTOR BINDING PROTEINS AND  
CC TO THE CEF-10/CYR61/CTGF/FISP-12/NOV PROTEIN FAMILY.  
CC -!- SIMILARITY: CONTAINS A C-TERMINAL CYSTINE KNOT-LIKE DOMAIN (CTCK).  
DR EMBL; M92934; G180924; --.  
DR EMBL; S56201; G266235; --.  
DR EMBL; X78947; G474934; --.  
DR PIR; A40551; A40551.  
DR PIR; S44205; S44205.  
DR MIM; 121009; 11TH EDITION.  
DR PROSITE; PS00222; IGF\_BINDING.  
KW GROWTH FACTOR BINDING; SIGNAL; ALTERNATIVE SPLICING.  
FT SIGNAL 1 21 POTENTIAL.  
FT CHAIN 22 349 CONNECTIVE TISSUE GROWTH FACTOR.  
FT DOMAIN 256 330 CTCK.



Mar 18 10:11

US-08-612-929-22.rsp

11

FT DISULFID 256 293 BY SIMILARITY.  
FT DISULFID 273 307 BY SIMILARITY.  
FT DISULFID 284 323 BY SIMILARITY.  
FT DISULFID 287 325 BY SIMILARITY.  
FT DISULFID 292 329 BY SIMILARITY.  
FT CARBOHYD 28 28 POTENTIAL.  
FT CARBOHYD 225 225 POTENTIAL.  
FT VARSPLIC 172 198 MISSING (IN SHORT FORM).  
SQ SEQUENCE 349 AA; 38069 MW; C21E9662 CRC32;

Query Match 84.4%; Score 38; DB 2; Length 349;  
Best Local Similarity 71.4%; Pred. No. 2.18e+01;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 212 tcgmgis 218  
| |||:  
Qy 1 TSGMGVS 7

RESULT 14  
ID LIG.PHLRA STANDARD; PRT; 361 AA.  
AC P20010;  
DT 01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)  
DT 01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)  
DT 01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)  
DE LIGNINASE III PRECURSOR (EC 1.11.1.-) (LIGNIN PEROXIDASE).  
OS PHLEBIA RADIATA (WHITE-ROT FUNGUS).  
CC EUKARYOTA; FUNGI; BASIDIOMYCOTINA.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=79;  
RX MEDLINE; 90185208.  
RA SALOHEIMO M., BARAJAS V., NIKU-PAAVOLA M.L., KNOWLES J.K.C.;  
RL GENE 85:343-351(1989).  
CC -/- CATALYTIC ACTIVITY: DEPOLYMERIZATION OF LIGNIN. CATALYSES THE  
C (ALPHA)-C (BETA) CLEAVAGE OF THE PROPYL SIDE CHAINS OF LIGNIN.  
CC -/- PATHWAY: FIRST STEP IN LIGNIN DEGRADATION.  
DR PIR; JQ0374; JQ0374.  
DR HSP; P31837; ILGA.  
DR PROSITE; PS00435; PEROXIDASE 1.  
DR PROSITE; PS00436; PEROXIDASE 2.  
KW OXIDOREDUCTASE; PEROXIDASE; HEME; GLYCOPROTEIN; MULTIGENE FAMILY;  
KW LIGNIN DEGRADATION; SIGNAL.  
FT SIGNAL 1 20 POTENTIAL.  
FT CHAIN 21 361 LIGNINASE.  
FT ACT SITE 66 66 BY SIMILARITY.  
FT ACT SITE 70 70 DISTAL HISTIDINE (BY SIMILARITY).  
FT ACT SITE 199 199 PROXIMAL HISTIDINE (HEME AXIAL LIGAND).  
FT CARBOHYD 268 268 POTENTIAL.  
SQ SEQUENCE 361 AA; 38439 MW; F65A5254 CRC32;

Query Match 84.4%; Score 38; DB 5; Length 361;  
Best Local Similarity 83.3%; Pred. No. 2.18e+01;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 124 sgmgva 129  
| |||:  
Qy 2 SGMGVS 7

RESULT 15  
ID PGCA BOVIN STANDARD; PRT; 719 AA.  
AC P13608;  
DT 01-JAN-1990 (REL. 13, CREATED)

Mar 18 10:11

US-08-612-929-22.rsp

12

DT 01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)  
DT 01-AUG-1992 (REL. 23, LAST ANNOTATION UPDATE)  
DE CARTILAGE-SPECIFIC PROTEOGLYCAN CORE PROTEIN (CSPCP) (AGGREGAN)  
DE (FRAGMENT).  
OS BOS TAURUS (BOVINE).  
CC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
CC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 87270630.  
RA OLDBERG A., ANTONSSON P., HEINEGARD D.;  
RL BIOCHEM. J. 243:255-259(1987).  
RN [2]  
RP PARTIAL SEQUENCE.  
RX MEDLINE; 85027710.  
RA PERIN J.P., BONNET F., JOLLES J., JOLLES P.;  
RL FEBS LETT. 176:37-42(1984).  
RN [3]  
RP PARTIAL SEQUENCE.  
RX MEDLINE; 87005253.  
RA PERIN J.P., BONNET F., JOLLES P.;  
RL FEBS LETT. 206:73-77(1986).  
CC -/- FUNCTION: THIS PROTEOGLYCAN IS A MAJOR COMPONENT OF EXTRACELLULAR  
MATRIX OF CARTILAGINOUS TISSUES. A MAJOR FUNCTION OF THIS PROTEIN  
IS TO RESIST COMPRESSION IN CARTILAGE.  
CC -/- PTM: CONTAINS MOSTLY CHONDROITIN SULFATE, BUT ALSO KERATAN SULFATE  
CHAINS, N-LINKED AND O-LINKED OLIGOSACCHARIDES.  
CC -/- SIMILARITY: CONTAINS A C-TYPE LECTIN FAMILY DOMAIN.  
DR EMBL; X16486; G282; -.  
DR PIR; A27752; A27752.  
DR PIR; A29164; A29164.  
DR PIR; B29164; B29164.  
DR PIR; E29164; E29164.  
DR PIR; G27751; G27751.  
DR HSP; P20693; IHLJ.  
DR PROSITE; PS00615; C TYPE LECTIN.  
KW GLYCOPROTEIN; CARTILAGE; PROTEOGLYCAN; LECTIN.  
FT NON TER 1 1  
FT DOMAIN 513 631 C-TYPE LECTIN.  
FT CARBOHYD 353 353 POTENTIAL.  
SQ SEQUENCE 719 AA; 74501 MW; FAF270AE CRC32;

Query Match 84.4%; Score 38; DB 6; Length 719;  
Best Local Similarity 85.7%; Pred. No. 2.18e+01;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 369 taglqvs 375  
| |||:  
Qy 1 TSGMGVS 7

Search completed: Tue Mar 18 10:13:26 1997  
Job time : 9 secs.



Mar 18 10:12

US-08-612-929-22.rpr

3

```

RESULT      2
ENTRY
TITLE      Iq heavy chain precursor V region (IDB5.7) - mouse (fragment)
ORGANISM   #formal name Mus musculus #common name house mouse
DATE       31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change
          12-Apr-1995
ACCESSIONS PT0174
REFERENCE   PT0174
#authors   Perfetti, V.; Borden, P.; Tao, M.H.; Morrison, S.L.; Kabat,
          E.A.
#journal   Mol. Immunol. (1991) 28:505-515
#title     Specificity and variable region cDNA sequence of an isogenic
          monoclonal antidiotype to an anti-alpha (1-6) dextran.
#cross-references MUID:91287738
#accession PT0174
#molecule_type mRNA
#residues_ 1-143 ##label PER
#experimental_source strain BALB/c
COMMENT    IDB5.7 is an antibody to anti-alpha (1-6) dextran.
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
SUMMARY     #length 143 #checksum 3660

Query Match 100.0%; Score 45; DB 5; Length 143;
Best Local Similarity 100.0%; Pred. No. 1.75e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 50 tsgmgvs 56
|||||
Qy 1 TSGMGVS 7

RESULT      3
ENTRY
TITLE      Ig heavy chain V region - mouse
ORGANISM   #formal name Mus musculus #common name house mouse
DATE       06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
          12-Apr-1995
ACCESSIONS S26465
REFERENCE   S26459
#authors   Kavalet, J.
#submission submitted to the EMBL Data Library, April 1991
#accession S26465
#status    preliminary
#molecule_type mRNA
#residues_ 1-113 ##label KAV
#cross-references EMBL:X59115
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
SUMMARY     #length 113 #molecular-weight 12508 #checksum 2993

Query Match 93.3%; Score 42; DB 5; Length 113;
Best Local Similarity 85.7%; Pred. No. 7.98e+00;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 22 tsgmgvs 28
|||||
Qy 1 TSGMGVS 7

RESULT      4
ENTRY
TITLE      flagellin - Borrelia afzelii
ORGANISM   #formal name Borrelia afzelii
DATE       25-Dec-1994 #sequence_revision 25-Dec-1994 #text_change

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Mar 18 10:12

US-08-612-929-22.rpr

4

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25-Dec-1994
ACCESSIONS S39304
REFERENCE   S39302
#authors   Noppa, L.; Burman, N.; Sadziene, A.; Barbour, A.G.;
          Bergstrom, S.
#submission submitted to the EMBL Data Library, September 1993
#accession S39304
#status    preliminary
#residues_ 1-336 ##label NOP
#cross-references EMBL:X75202
SUMMARY     #length 336 #molecular-weight 35737 #checksum 8921

Query Match 88.9%; Score 40; DB 14; Length 336;
Best Local Similarity 71.4%; Pred. No. 2.12e+01;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 43 aagmqvs 49
|||||
Qy 1 TSGMGVS 7

RESULT      5
ENTRY
TITLE      flagellin - Lyme disease spirochete (strain GeHo)
ORGANISM   #formal name Borrelia burgdorferi #common name Lyme disease
          spirochete
DATE       12-Jul-1991 #sequence_revision 12-Jul-1991 #text_change
          18-Nov-1994
ACCESSIONS A38450
REFERENCE   A38450
#authors   Gassmann, G.S.; Jacobs, E.; Deutzmann, R.; Goebel, U.B.
          J. Bacteriol. (1991) 173:1452-1459
#title     Analysis of the Borrelia burgdorferi GeHo fla gene and
          antigenic characterization of its gene product.
#cross-references MUID:91139587
#accession A38450
#molecule_type DNA
#residues_ 1-336 ##label GAS
#cross-references GB:X56334
REFERENCE   S04091
#authors   Gassmann, G.S.; Kramer, M.; Goebel, U.B.; Wallich, R.
          Nucleic Acids Res. (1989) 17:3590
#journal   Nucleotide sequence of a gene encoding the Borrelia
          burgdorferi flagellin.
#cross-references MUID:89263802
#accession S04091
#molecule_type DNA
#residues_ 1-336 ##label GA2
#cross-references EMBL:X14941
#note      translation of nucleotide sequence not given
REFERENCE   A60276
#authors   Collins, C.; Peltz, G.
          Infect. Immun. (1991) 59:514-520
#journal   Immureactive epitopes on an expressed recombinant flagellar
          protein of Borrelia burgdorferi.
#accession A60276
#status    not compared with conceptual translation
#molecule_type mRNA
#residues_ 1-336 ##label COL
#experimental_source strain CA12
#note      the authors say this sequence from strain CA12 differs
          from the sequence from strain GeHo, but the GeHo
          sequence shown for comparison is inconsistent with
          reference A38450

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Mar 18 10:12

US-08-612-929-22.rpr

5

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REFERENCE      A61075
#authors       Gasmann, G.S.; Deutzmann, R.; Vogt, A.; Goebel, U.B.
#journal       FEMS Microbiol. Lett. (1989) 60:101-106
#title         N-terminal amino acid sequence of the Borrelia burgdorferi
               flagellin.
#accession     A61075
#molecule_type protein
#residues      1-15,'X',17-29 ##label GA3

```

#### GENETICS

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#gene          fla
#superfamily   flagellin
#keywords      flagellum

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SUMMARY        #length 336 #molecular-weight 35765 #checksum 9490

```

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Query Match    88.9%; Score 40; DB 6; Length 336;
Best Local Similarity 71.4%; Pred. No. 2.12e+01;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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```

Db 43 aaagvgs 49
      ::|||||
Qy 1 TSCMGVS 7

```

RESULT 6

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ENTRY          S39303 #type complete
TITLE          flagellin - Borrelia garinii
ORGANISM       #formal name Borrelia garinii
DATE           25-Dec-1994 #sequence_revision 25-Dec-1994 #text_change
               25-Dec-1994

```

```

ACCESSIONS     S39303
REFERENCE       S39302
#authors       Noppa, L.; Burman, N.; Sadziene, A.; Barbour, A.G.;
               Bergstrom, S.

```

```

#submission    submitted to the EMBL Data Library, September 1993
#accession     S39303
#status        preliminary
#residues      1-336 ##label NOP
#cross-references EMBL:X75203

```

```

SUMMARY        #length 336 #molecular-weight 35765 #checksum 9778

```

```

Query Match    88.9%; Score 40; DB 14; Length 336;
Best Local Similarity 71.4%; Pred. No. 2.12e+01;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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```

Db 43 aaagvgs 49
      ::|||||
Qy 1 TSCMGVS 7

```

RESULT 7

```

ENTRY          S39305 #type complete
TITLE          flagellin - Lyme disease spirochete
ORGANISM       #formal name Borrelia burgdorferi #common_name Lyme disease
               spirochete
DATE           06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change

```

```

ACCESSIONS     S39305
REFERENCE       S39302
#authors       Noppa, L.; Burman, N.; Sadziene, A.; Barbour, A.G.;
               Bergstrom, S.

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#submission    submitted to the EMBL Data Library, September 1993
#accession     S39305
#status        preliminary
#molecule_type DNA

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Mar 18 10:12

US-08-612-929-22.rpr

6

```

#residues      1-336 ##label NOP
#cross-references EMBL:X75200
SUMMARY        #length 336 #molecular-weight 35789 #checksum 9643

```

```

Query Match    88.9%; Score 40; DB 7; Length 336;
Best Local Similarity 71.4%; Pred. No. 2.12e+01;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

Db 43 aaagvgs 49
      ::|||||
Qy 1 TSCMGVS 7

```

RESULT 8

```

ENTRY          FLLYB3 #type complete
TITLE          flagellin - Lyme disease spirochete (strain B31)
ALTERNATE_NAMES 41K antigen
ORGANISM       #formal name Borrelia burgdorferi #common_name Lyme disease
               spirochete
DATE           31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change
               18-Nov-1994

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```

ACCESSIONS     A41470; S04696; B60118; A60705; S08541
REFERENCE       A41470
#authors       Wallich, R.; Motor, S.E.; Simon, M.M.; Ebnet, K.; Heiberger,
               A.; Kramer, M.D.

```

```

#journal       Infect. Immun. (1990) 58:1711-1719
#title         The Borrelia burgdorferi flagellum-associated 41-kilodalton
               antigen (flagellin): molecular cloning, expression, and
               amplification of the gene.
#cross-references MUID:90256248
#accession     A41470
#molecule_type DNA
#residues      1-336 ##label WA2
#cross-references GB:X16833

```

```

REFERENCE       S04091

```

```

#authors       Gasmann, G.S.; Kramer, M.; Goebel, U.B.; Wallich, R.
#journal       Nucleic Acids Res. (1989) 17:3590
#title         Nucleotide sequence of a gene encoding the Borrelia
               burgdorferi flagellin.
#cross-references MUID:89263802
#accession     S04696
#molecule_type DNA
#residues      1-336 ##label GAS
#cross-references EMBL:X15661

```

```

#note          translation of nucleotide sequence not given

```

```

REFERENCE       A60118
#authors       Luft, B.J.; Jiang, W.; Munoz, P.; Battwyler, R.J.; Gorevic,
               P.D.
#journal       Infect. Immun. (1989) 57:3637-3645
#title         Biochemical and immunological characterization of the surface
               proteins of Borrelia burgdorferi.
#cross-references MUID:90035442
#accession     B60118
#molecule_type protein
#residues      1-9,'A',11-13,'X',15-18 ##label LUF

```

```

REFERENCE       A60705

```

```

#authors       Coleman, J.L.; Benach, J.L.
#journal       J. Clin. Invest. (1989) 84:322-330
#title         Identification and characterization of an endoflagellar
               antigen of Borrelia burgdorferi.
#accession     A60705
#molecule_type protein
#residues      1-10 ##label COL

```

```

CLASSIFICATION #superfamily flagellin

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Mar 18 10:12

US-08-612-929-22.rpr

7

KEYWORDS flagellum; periplasmic space  
SUMMARY #length 336 #molecular-weight 35751 #checksum 54

Query Match 88.9%; Score 40; DB 3; Length 336;  
Best Local Similarity 71.4%; Pred. No. 2.12e+01;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 43 aagmgvs 49  
:::|||||  
Qy 1 TSGMGVS 7

RESULT 9  
ENTRY S37728 #type complete  
TITLE P41 protein - Lyme disease spirochete  
ORGANISM #formal\_name Borrelia burgdorferi #common\_name Lyme disease spirochete  
DATE 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change  
ACCESSIONS S37728  
REFERENCE S37726  
#authors Jauris-Heipke, S.; Fuchs, R.; Motz, M.; Preac-Mursic, V.; Schwab, E.; Soutschek, E.; Will, G.; Willeke, B.  
#journal Med. Microbiol. Immunol. (1993) 182:37-50  
#title Genetic heterogeneity of the genes coding for the outer surface protein C (OspC) and the flagellin of Borrelia burgdorferi.  
#accession S37728 preliminary  
##status preliminary  
##molecule type DNA  
##residues\_ 1-336 ##label JAU  
##cross-references EMBL:X69598  
SUMMARY #length 336 #molecular-weight 35754 #checksum 9781

Query Match 88.9%; Score 40; DB 7; Length 336;  
Best Local Similarity 71.4%; Pred. No. 2.12e+01;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 43 aagmgvs 49  
:::|||||  
Qy 1 TSGMGVS 7

RESULT 10  
ENTRY S37729 #type complete  
TITLE P41 protein - Lyme disease spirochete  
ORGANISM #formal\_name Borrelia burgdorferi #common\_name Lyme disease spirochete  
DATE 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change  
ACCESSIONS S37729  
REFERENCE S37726  
#authors Jauris-Heipke, S.; Fuchs, R.; Motz, M.; Preac-Mursic, V.; Schwab, E.; Soutschek, E.; Will, G.; Willeke, B.  
#journal Med. Microbiol. Immunol. (1993) 182:37-50  
#title Genetic heterogeneity of the genes coding for the outer surface protein C (OspC) and the flagellin of Borrelia burgdorferi.  
#accession S37729 preliminary  
##status preliminary  
##molecule type DNA  
##residues\_ 1-336 ##label JAU  
##cross-references EMBL:X69597  
SUMMARY #length 336 #molecular-weight 35753 #checksum 9281

Mar 18 10:12

US-08-612-929-22.rpr

8

Query Match 88.9%; Score 40; DB 7; Length 336;  
Best Local Similarity 71.4%; Pred. No. 2.12e+01;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 43 aagmgvs 49  
:::|||||  
Qy 1 TSGMGVS 7

RESULT 11  
ENTRY I39171 #type complete  
TITLE cyclin A/CDK2-associated p45 - human  
ORGANISM #formal\_name Homo sapiens #common\_name man  
DATE 23-Feb-1996 #sequence\_revision 23-Feb-1996 #text\_change  
ACCESSIONS I39171  
REFERENCE I39170  
#authors Zhang, H.; Kobayashi, R.; Galaktionov, K.; Beach, D.  
#journal Cell (1995) 82:915-925  
#title p19Skl and p45Skp2 are essential elements of the cyclin A-CDK2 S phase kinase.  
#cross-references MUID:96016087  
#accession I39171 preliminary  
##status preliminary  
##molecule type mRNA  
##residues\_ 1-435 ##label RES  
##cross-references EMBL:U33761; NID:g995825; CDS\_PID:g995826  
GENETICS  
#note gene name Skp2  
SUMMARY #length 435 #molecular-weight 48989 #checksum 8642

Query Match 88.9%; Score 40; DB 11; Length 435;  
Best Local Similarity 100.0%; Pred. No. 2.12e+01;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 46 sgmgvs 51  
|||||  
Qy 2 SGMGVS 7

RESULT 12  
ENTRY S20554 #type complete  
TITLE pyruvate, water dikinase (EC 2.7.9.2) - Escherichia coli  
ALTERNATE\_NAMES phosphoenolpyruvate synthase  
ORGANISM #formal\_name Escherichia coli  
DATE 16-Sep-1992 #sequence\_revision 16-Sep-1992 #text\_change  
ACCESSIONS S20554; S14838  
REFERENCE S20554  
#authors Niersbach, M.; Kreuzaler, F.; Geerse, R.H.; Postma, P.W.; Hirsch, H.J.  
#journal Mol. Gen. Genet. (1992) 231:332-336  
#title Cloning and nucleotide sequence of the Escherichia coli K-12 ppsA gene, encoding PEP synthase.  
#cross-references MUID:92140374  
#accession S20554  
##molecule type DNA  
##residues\_ 1-792 ##label NIE  
##cross-references EMBL:X59381  
GENETICS  
#gene ppsA  
#transfease transferase  
SUMMARY #length 792 #molecular-weight 87434 #checksum 1665

Query Match 88.9%; Score 40; DB 7; Length 792;  
Best Local Similarity 100.0%; Pred. No. 2.12e+01;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 39 sgmgvs 44  
|||||  
Qy 2 SCMGVS 7

RESULT 13  
ENTRY S33821 #type complete  
TITLE median body protein - Giardia lamblia  
ORGANISM #formal name Giardia lamblia  
DATE 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change  
06-Jan-1995  
ACCESSIONS S33821  
REFERENCE S33821  
#authors Marshall, J.; Holberton, D.V.  
#journal J. Mol. Biol. (1993) 231:521-530  
#title Sequence and structure of a new coiled coil protein from a  
microtubule bundle in Giardia.  
#accession S33821  
##status preliminary  
##molecule\_type mRNA  
##residues 1-857 ##label MAR  
##cross-references EMBL:X64517  
SUMMARY #length 857 #molecular-weight 100583 #checksum 6805

Query Match 88.9%; Score 40; DB 10; Length 857;  
Best Local Similarity 71.4%; Pred. No. 2.12e+01;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 795 sgmgvs 801  
:|||||  
Qy 1 TSCMGVS 7

RESULT 14  
ENTRY PQ0098 #type fragment  
TITLE citB protein - Salmonella typhimurium (fragment)  
ORGANISM #formal name Salmonella typhimurium  
DATE 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change  
23-Mar-1993  
ACCESSIONS PQ0098  
REFERENCE J00576  
#authors Shinamoto, T.; Iwawa, H.; Daimon, H.; Ishiguro, N.;  
Shinagawa, M.; Sakano, Y.; Tsuda, M.; Tsuchiya, T.  
#journal J. Biochem. (1991) 110:22-28  
#title Cloning and nucleotide sequence of the gene (citA) encoding a  
citrate carrier from Salmonella typhimurium.  
#cross-references MUID:92041761  
#accession PQ0098  
##molecule\_type DNA  
##residues 1-58 ##label SH1  
##experimental\_source strain LT2

GENETICS  
#gene citB  
SUMMARY #length 58 #checksum 2672

Query Match 86.7%; Score 39; DB 6; Length 58;  
Best Local Similarity 83.3%; Pred. No. 3.41e+01;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 4 tegmgi 9  
|||||  
Qy 1 TSGMGV 6

RESULT 15  
ENTRY A31142 #type fragments  
TITLE gelsolin, ovary - African clawed frog (fragments)  
ORGANISM #formal name Xenopus laevis #common name African clawed frog  
DATE 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change  
08-Jul-1994  
ACCESSIONS A31142; B31142  
REFERENCE A31142  
#authors Ankenbauer, T.; Kleinschmidt, J.A.; Vandekerckhove, J.;  
Franke, W.W.  
#journal J. Cell Biol. (1988) 107:1489-1498  
#title Proteins regulating actin assembly in oogenesis and early  
embryogenesis of Xenopus laevis: gelsolin is the major  
cytoplasmic actin-binding protein.

#cross-references MUID:89008590  
#accession A31142  
##molecule\_type mRNA  
##residues 21-437 ##label AN1  
#accession B31142  
##molecule\_type protein  
##residues 1-20 ##label AN2  
##cross-references EMBL:X13319  
CLASSIFICATION #superfamily gelsolin; gelsolin repeat homology  
KEYWORDS actin binding  
FEATURE 101-419  
SUMMARY #domain gelsolin repeat homology #label GEL2  
#length 437 #checksum 6465

Query Match 86.7%; Score 39; DB 5; Length 437;  
Best Local Similarity 71.4%; Pred. No. 3.41e+01;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 58 tdgmga 64  
|||||  
Qy 1 TSCMGVS 7

Search completed: Tue Mar 18 10:13:56 1997  
Job time : 12 secs.



Mar 18 10:12

US-08-612-929-22.rag

3

CC encoded the protein given in R70190. 3 CDRs (R70198-200) were  
CC identified.  
SQ Sequence 7 AA;

Query Match 100.0%; Score 45; DB 13; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.59e+01;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 tsgmgs 7  
|||||  
Qy 1 TSGMGVS 7

RESULT 2

ID R70190 standard; Protein; 140 AA.

AC R70190;

DT 20-SEP-1995 (first entry)

DE Mouse MAb 3B9 heavy chain.

KW Chimeric antibody; humanized antibody; antibody engineering;

KW monoclonal antibody; MAb; interleukin-4; IL-4; allergy.

OS Mus sp.

FH Key Location/Qualifiers

FT Peptide 1..19

FT /label= Sig\_peptide

FT Region 50..56

FT /label= CDR

FT /note= "complementarity determining region"

FT Region 71..86

FT /label= CDR

FT /note= "complementarity determining region"

FT Region 119..129

FT /label= CDR

FT /note= "complementarity determining region"

PN W09507301-A.

PD 16-MAR-1995.

PF 07-SEP-1994; U10308.

PR 07-SEP-1993; US-117366.

PR 14-OCT-1993; US-136783.

PA (SMIK ) SMITHKLINE BEECHAM CORP.

PA (SMIK ) SMITHKLINE BEECHAM PLC.

PI Gross MS, Holmes SD, Sylvester DR;

DR WPI; 95-123387/16.

DR N-PSDB; Q83491.

PT Chimeric and humanized IL-4 monoclonal antibodies (mAbs), derived

PT from high affinity mAbs - useful in treatment of IL-4-mediated

PT and IgE-mediated allergic conditions

PS Disclosure; Fig.2; 97pp; English.

CC Spleen cells from mice immunized with human IL-4 were used to prepare

CC hybridomas, which were screened for anti-IL-4 MAb secretion. Only

CC clone 3B9 was positive. cDNA clones of the 3B9 light and heavy

CC chains were cloned into pGEM7f+ and transformed into E. coli

CC DH5-alpha. The clones were sequenced (Q83490-91), and used for

CC antibody engineering.

SQ Sequence 140 AA;

Query Match 100.0%; Score 45; DB 13; Length 140;

Best Local Similarity 100.0%; Pred. No. 1.59e+01;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 50 tsgmgs 56  
|||||  
Qy 1 TSGMGVS 7

Mar 18 10:12

US-08-612-929-22.rag

4

RESULT 3

ID R70192 standard; Protein; 141 AA.

AC R70192;

DT 20-SEP-1995 (first entry)

DE Humanized antibody 3B9 heavy chain.

KW Humanized antibody; antibody engineering; monoclonal antibody;

KW MAb; interleukin-4; IL-4; allergy.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Peptide 1..19

FT /label= Sig\_peptide

FT Region 51..57

FT /label= CDR

FT /note= "complementarity determining region"

FT Region 72..87

FT /label= CDR

FT /note= "complementarity determining region"

FT Region 120..130

FT /label= CDR

FT /note= "complementarity determining region"

PN W09507301-A.

PD 16-MAR-1995.

PF 07-SEP-1994; U10308.

PR 07-SEP-1993; US-117366.

PR 14-OCT-1993; US-136783.

PA (SMIK ) SMITHKLINE BEECHAM CORP.

PA (SMIK ) SMITHKLINE BEECHAM PLC.

PI Gross MS, Holmes SD, Sylvester DR;

DR WPI; 95-123387/16.

DR N-PSDB; Q83493.

PT Chimeric and humanized IL-4 monoclonal antibodies (mAbs), derived

PT from high affinity mAbs - useful in treatment of IL-4-mediated

PT and IgE-mediated allergic conditions

PS Disclosure; Fig.4; 97pp; English.

CC A humanized antibody heavy chain variable region and signal

CC sequence is given in R70192. The signal sequence is also

CC provided in R70193. The CDR sequences of the construct are

CC identical to the native CDRs of mouse anti-human IL-4 MAb

CC 3B9 (R70198-200).

SQ Sequence 141 AA;

Query Match 100.0%; Score 45; DB 13; Length 141;

Best Local Similarity 100.0%; Pred. No. 1.59e+01;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 51 tsgmgs 57  
|||||  
Qy 1 TSGMGVS 7

RESULT 4

ID R70191 standard; Protein; 141 AA.

AC R70191;

DT 20-SEP-1995 (first entry)

DE Chimeric antibody 3B9 heavy chain.

KW Chimeric antibody; antibody engineering; monoclonal antibody;

KW MAb; interleukin-4; IL-4; allergy.

OS Homo sapiens; Mus sp.

FH Key Location/Qualifiers

FT Peptide 1..19

FT /label= Sig\_peptide

FT Region 51..57

FT /label= CDR

FT /note= "complementarity determining region"



FT Region 72..87  
 FT /label= CDR  
 FT /note= "complementarity determining region"  
 FT Peptide 120..130  
 FT /label= CDR  
 FT /note= "complementarity determining region"  
 PN WQ9507301-A.  
 PD 16-MAR-1995.  
 PF 07-SEP-1994; U10308.  
 PR 07-SEP-1993; US-117366.  
 PR 14-OCT-1993; US-136783.  
 PA (SMIK ) SMITHKLINE BEECHAM CORP.  
 PA (SMIK ) SMITHKLINE BEECHAM PLC.  
 PI Gross MS, Holmes SD, Sylvester DR;  
 DR WPI; 95-123387/16.  
 DR N-PSDB; Q83492.  
 PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived from high affinity mAbs - useful in treatment of IL-4-mediated PT and IgE-mediated allergic conditions  
 PS Disclosure; Fig.3; 97pp; English.  
 CC A human/mouse chimeric antibody heavy chain variable region was constructed (given in R70191) that contained the mouse anti-human IL-4 Mab 3B9 variable region including 3 CDRs (R70198-200) and a CC human antibody signal peptide (R70193). The construct was used CC for humanized antibody production.  
 SQ Sequence 141 AA;

Query Match 100.0%; Score 45; DB 13; Length 141;  
 Best Local Similarity 100.0%; Pred. No. 1.59e+01;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 51 tsgmgvs 57  
 |||||  
 Qy 1 TSGMGVS 7

RESULT 5  
 ID R58612 standard; Protein; 246 AA.  
 AC R58612;  
 DT 28-APR-1995 (first entry)  
 DE IL-6 binding inhibitor.  
 KW Human interleukin-6 binding inhibitor; IL-6; rheumatoid arthritis; septic shock; multiple myeloma; ss.  
 OS Homo sapiens.  
 PN EP-617126-A.  
 PD 28-SEP-1994.  
 PF 16-FEB-1994; 102346.  
 PR 17-FEB-1993; JP-028173.  
 PA (AJIN ) AJINOMOTO KK.  
 PI Hamuro J, Nakazawa H, Shimamura T;  
 DR WPI; 94-295777/37.  
 DR N-PSDB; Q70612.  
 PT Polypeptide inhibiting binding of human interleukin-6 (IL-6) to its receptor - useful for treating autoimmune disease induced PT or aggravated by IL-6  
 PS Claim 5; Page 18; 26pp; English.  
 CC Q70612 codes for human interleukin-6 binding inhibitor, the CC polypeptide described in R58612. This polypeptide inhibits the CC binding of human IL-6 to its receptor, and can therefore be CC useful in the treatment of a variety of autoimmune diseases; CC specifically in the treatment of rheumatoid arthritis, septic CC shock due to bacterial infection and multiple myeloma.  
 SQ Sequence 246 AA;

Query Match 100.0%; Score 45; DB 11; Length 246;  
 Best Local Similarity 100.0%; Pred. No. 1.59e+01;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 153 tsgmgvs 159  
 |||||  
 Qy 1 TSGMGVS 7

RESULT 6  
 ID R66304 standard; Protein; 111 AA.  
 AC R66304;  
 DT 02-AUG-1995 (first entry)  
 DE Human immunoglobulin variable heavy chain #10.  
 KW Primer; PCR; amplify; human; immunoglobulin; variable; heavy chain;  
 KW cosmid; placenta; vector; pJB81; E.coli; mammalian.  
 OS Homo sapiens.  
 PN WQ9426895-A.  
 PD 24-NOV-1994.  
 PF 10-MAY-1993; J00603.  
 PR 10-MAY-1993; WO-J00603.  
 PA (NISR ) JAPAN TOBACCO INC.  
 PI Honjo T, Matsuda F;  
 DR WPI; 95-006791/01.  
 DR N-PSDB; Q78948.  
 PT DNA fragment comprising human immunoglobulin Vh genes - for the PT production of human immunoglobulin in mammalian hosts  
 PS Claim 19; Page 43-44; 130pp; Japanese.  
 CC Protein sequences (R66295-51) are novel human immunoglobulin heavy chain CC sequences encoded by novel isolated genes. The genes (Q78939-79002) were CC isolated and cloned from a series of cosmid constructs: Y202, Y103, Y21; CC Y6; Y24; 3-31; M84; M118 and M131, by PCR amplification using primers CC Q78917-38. The genes are subdivided into 5 families of Vh genes. The CC fragments cover a region of 800 kb. The DNA fragments were isolated from CC high molecular weight DNA from human placenta. The DNA was partially CC digested with TagI restriction enzyme. The fragments were separated by CC gel electrophoresis and 35-45 kb fractions were collected. The fragments CC were ligated with ClaI-digested cosmid vector pUB81. The ligation CC products were in vitro packed and infected into E.coli 490A. The CC fragments were then subcloned by colony hybridisation. The Vh genes and CC the DNA fragments encoding them are useful in producing human CC immunoglobulin in mammalian hosts.

Query Match 93.3%; Score 42; DB 12; Length 111;  
 Best Local Similarity 85.7%; Pred. No. 3.81e+01;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 49 tsgmgvs 55  
 |||||  
 Qy 1 TSGMGVS 7

RESULT 7  
 ID R88109 standard; peptide; 120 AA.  
 AC R88109;  
 DT 25-JUL-1996 (first entry)  
 DE Murine anti-Protein C Mab HPC-4 Vh gamma mature peptide.  
 KW Epitope; activation; heavy chain; protein C; vitamin K; plasma protein;  
 KW zymogen; cleavage; mouse; humanised antibody; variable region;  
 KW light chain; inhibition; anticoagulant; coagulation; tumour.  
 OS Mus musculus.  
 PN WQ9534652-A1.  
 PD 21-DEC-1995.

PF 09-JUN-1995; U07372.  
PR 10-JUN-1994; US-259321.  
PA (OKLA-) OKLAHOMA MED RES FOUND.  
PI Esmon CT, Rezaie A;  
DR WPI; 96-049681/05.  
DR N-PSDB; T09300.  
PT Calcium-binding monoclonal antibody immunoreactive with Protein C -  
PT thrombin-thrombomodulin, e.g. for treating tumours  
PS Claim 2; Page 29; 41pp; English.  
CC This is the amino acid sequence of the mature peptide from the murine  
CC anti-protein C monoclonal antibody HPC-4 heavy chain variable region.  
CC HPC-4 recognises the activation peptide region (R88106) of the heavy  
CC chain of protein C, a vitamin K-dependent plasma protein zymogen.  
CC Protein C is converted to activated protein C (APC) by cleavage between  
CC the Arg-Leu amino acid contained within the activation peptide sequence.  
CC HPC-4 prevents protein C activation to APC by binding to this region.  
CC The DNA sequences encoding the variable regions of the heavy and light  
CC chains of the antibody (T09299-302) were used to construct humanised  
CC antibodies using the PCR primers T09303-9. The humanised antibodies are  
CC useful as inhibitors of coagulation and can be used for the treatment of  
CC tumours by inhibiting the anticoagulant activity of APC by preventing  
CC conversion of protein C to APC.  
SQ Sequence 120 AA;

Query Match 93.3%; Score 42; DB 17; Length 120;  
Best Local Similarity 85.7%; Pred. No. 3.81e+01;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 31 tsgmgvgv 37  
|||||:  
Qy 1 TSGMGVVS 7

## RESULT 8

ID R88107 standard; Protein; 139 AA.  
AC R88107;  
DE 25-JUL-1996 (first entry)  
DT Murine anti-Protein C MAb HPC-4 VH gamma protein.  
KW Epitope; activation; heavy chain; protein C; vitamin K; plasma protein;  
KW zymogen; cleavage; mouse; humanised antibody; variable region;  
KW light chain; inhibition; anticoagulant; coagulation; tumour.  
OS Mus musculus.  
FH Key Location/Qualifiers  
FT Peptide 1..19  
FT /note= "signal peptide"  
FT Peptide 20..139  
FT /note= "mature peptide"  
PN W09534652-AL.  
PD 21-DEC-1995.  
PF 09-JUN-1995; U07372.  
PR 10-JUN-1994; US-259321.  
PA (OKLA-) OKLAHOMA MED RES FOUND.  
PI Esmon CT, Rezaie A;  
DR WPI; 96-049681/05.  
DR N-PSDB; T09299.  
PT Calcium-binding monoclonal antibody immunoreactive with Protein C -  
PT inhibits Protein C anticoagulant activation by  
PT thrombin-thrombomodulin, e.g. for treating tumours  
PS Claim 2; Page 29; 41pp; English.  
CC This is the amino acid sequence of the heavy chain variable region from  
CC the murine anti-protein C monoclonal antibody HPC-4 which recognises  
CC the activation peptide region (R88106) of the heavy chain of protein C,  
CC a vitamin K-dependent plasma protein zymogen. Protein C is converted to

CC activated protein C (APC) by cleavage between the Arg-Leu amino acid  
CC contained within the activation peptide sequence. HPC-4 prevents protein  
CC C activation to APC by binding to this region. The DNA sequences encoding  
CC the variable regions of the heavy and light chains of the antibody  
CC (T09299-302) were used to construct humanised antibodies using the PCR  
CC primers T09303-9. The humanised antibodies are useful as inhibitors of  
CC coagulation and can be used for the treatment of tumours by inhibiting  
CC the anticoagulant activity of APC by preventing conversion of protein C  
CC to APC.  
SQ Sequence 139 AA;

Query Match 93.3%; Score 42; DB 17; Length 139;  
Best Local Similarity 85.7%; Pred. No. 3.81e+01;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 50 tsgmgvgv 56  
|||||:  
Qy 1 TSGMGVVS 7

## RESULT 9

ID R175747 standard; Protein; 336 AA.  
AC R175747;  
DE 30-JUL-1996 (first entry)  
DT B. burgdorferi strain B31 antigen P41 (P41-B31).  
KW Strain B31; P41 antigen; antigenic domain; chimaeric protein;  
KW treatment; diagnosis; infection; vaccine; Lyme borreliosis;  
KW immunodiagnostic assay; antibody; T-cell reactivity;  
KW chimeric.  
OS Borrelia burgdorferi.  
PN W09512676-AL.  
PD 11-MAY-1995.  
PF 27-OCT-1994; U12352.  
PR 01-NOV-1993; US-148191.  
PR 29-APR-1994; US-235836.  
PA (ASU-) ASSOC UNIVERSITIES INC.  
PI Dunn JJ, Luft BJ;  
DR WPI; 95-215034/28.  
DR N-PSDB; 090744.  
PT Chimeric protein comprising 2 or more antigenic Borrelia  
PT polypeptide(s) - useful in a vaccine against Lyme borreliosis and in  
PT immuno:diagnostic assays  
PS Example 1; Fig 40; 200pp; English.  
CC The present sequence is the B. burgdorferi strain B31, antigen  
CC P41 (P41-B31). Using chemical or enzymatic methods, peptide  
CC fragments of P41-B31 were pred., and analysed by western blot to  
CC assess their ability to bind different anti-P41 monoclonal  
CC antibodies. The information obtd. was used to locate antigenic  
CC domains in P41-B31, the epitopes of which were mapped with the  
CC aid of site directed mutagenesis. Identical analyses were performed  
CC on a selection of antigens purified from a variety of B. burgdorferi  
CC strains, the results from which were utilised in the prepn. of a  
CC pool of antigenic Borrelia polypeptides, and corresponding  
CC polynucleotides. Chimaeric proteins comprising 2 or more antigenic  
CC Borrelia polypeptides, that do not naturally occur in the same  
CC protein, can be used in the treatment and diagnosis of Borrelia  
CC infections, i.e. as a vaccine against Lyme borreliosis, in  
CC immunodiagnostic assays to detect anti-Borrelia antibodies or to  
CC measure T-cell reactivity.  
SQ Sequence 336 AA;

Query Match 88.9%; Score 40; DB 17; Length 336;  
Best Local Similarity 71.4%; Pred. No. 6.77e+01;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 43 aagmgvs 49  
 ::|||  
 Qy 1 TSGMGVS 7

RESULT 10  
 ID R25897 standard; Protein; 336 AA.  
 AC R25897;  
 DT 25-JAN-1993 (first entry)  
 DE Flagellar protein of *Borrelia burgdorferi*.  
 KW Flagella-less; vaccine; immunoassay; Lyme disease; epidemic bovine;  
 KW abortion; avian spirochetosis; relapsing fever; flagellin.  
 OS *Borrelia burgdorferi*.  
 PN W09212235-A.  
 PD 23-JUL-1992.  
 PF 10-JAN-1992; U00181.  
 PR 11-JAN-1991; US-641143.  
 PA (TEXA) UNIV TEXAS.  
 PI Barbour AG, Bundoc V;  
 DR WPI; 92-268660/32.  
 DR N-PSDB; Q27078.  
 PT New flagella-less *Borrelia* and derived antigens - useful for  
 PT vaccinating against and diagnosing *Borrelia* infections e.g. Lyme  
 PT disease or relapsing fever  
 PS Example 1; Fig 1; 88pp; English.  
 CC The sequence shows a *Borrelia burgdorferi* flagellin protein whose  
 CC sequence was deduced from that of the flagellin gene (fla gene)  
 CC which was prep. by screening a genomic library of strain HB19 of *B.*  
 CC *burgdorferi* in lambda FIX II with an oligonucleotide probe having a  
 CC DNA sequence based on a conserved sequence of fla genes from two  
 CC other strains of *B. burgdorferi* (Gassman, et al., 1989). The fla  
 CC gene may be mutagenised to form an inactive fla gene e.g. by deletion  
 CC of the entire coding region, or mutagenesis of the RBS, etc. so that  
 CC functional flagellar protein is not produced. This mutated gene may  
 CC be reintroduced into *Borrelia* species and cultures of flagellaless  
 CC *Borrelia* microbes produced. Antigens to the flagellaless *Borrelia*  
 CC sp. and vaccines can be used for thir prevention and treatment of  
 CC Lyme disease, epidemic bovine abortion, avian spirochetosis or  
 CC relapsing fever. Since the transformed microorganism lacks the  
 CC flagella antigen associated with autoantibody, it can be used to  
 CC immunise individuals against Lyme disease without the risk of vaccine  
 CC induced autoantibody formation.  
 SQ Sequence 336 AA;

Query Match 88.9%; Score 40; DB 5; Length 336;  
 Best Local Similarity 71.4%; Pred. No. 6.77e+01;  
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 43 aagmgvs 49  
 ::|||  
 Qy 1 TSGMGVS 7

RESULT 11  
 ID R13142 standard; Protein; 341 AA.  
 AC R13142;  
 DT 27-SEP-1991 (first entry)  
 DE *B. burgdorferi* strain pKo p41 protein.  
 KW Lyme borreliosis; vaccine; flagellin.  
 OS *Borrelia burgdorferi*.  
 PN W09109870-A.  
 PD 11-JUL-1991.  
 PF 21-DEC-1990; E02282.

PR 22-DEC-1989; DE-942728.  
 PR 13-JUN-1990; DE-018988.  
 PA (MIKR-) MIKROGEN MOLEKULARB.  
 PI Fuchs R, Wilske B, Preac-Mursic V, Motz M, Soutschek E.  
 DR WPI; 91-222844/30.  
 PT New *Borrelia burgdorferi* proteins - useful as immunoassay  
 PT reagents and antigens for vaccine prodn.  
 PS Claim 6; Page 48; 68pp; German.  
 CC p41(flagellin) is a 41kD protein isolated from *B. burgdorferi*. The  
 CC p41 coding sequence was isolated from a *B. burgdorferi* cDNA library  
 CC and is used for recombinant production of the protein. p41 is  
 CC immunologically active and is useful as an immunoassay reagent for  
 CC detecting antibodies directed against *Borrelia* spp., esp. for early  
 CC diagnosis of Lyme borreliosis.  
 CC See Q12744-7, Q13297-8, R13139-R13142.  
 SQ Sequence 341 AA;

Query Match 88.9%; Score 40; DB 3; Length 341;  
 Best Local Similarity 71.4%; Pred. No. 6.77e+01;  
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 48 aagmgvs 54  
 ::|||  
 Qy 1 TSGMGVS 7

RESULT 12  
 ID R24102 standard; Protein; 1074 AA.  
 AC R24102;  
 DT 14-NOV-1992 (first entry)  
 DE Marek's disease virus MD20 polypeptide.  
 KW Antibodies; vaccine; recombinant; poultry; passive immunotherapy;  
 KW diagnostic immunoassay; anti-idiotypic; antigen.  
 OS Marek's disease virus.  
 PN EP-486106-A.  
 PD 20-MAY-1992.  
 PF 13-NOV-1991; 202947.  
 PR 16-NOV-1990; US-615211.  
 PA (ALAU) AKZO NV.  
 PI Morgan RW;  
 DR WPI; 92-168713/21.  
 DR N-PSDB; Q24789.  
 PT DNA encoding Marek's disease virus polypeptides MD18 and MD20 -  
 PT and antibodies and vaccine useful for the protection of poultry  
 PT against MDV infection  
 PS Claim 8; Page 18; 31pp; English.  
 CC The protein sequence of MDV MD20 was deduced from the DNA sequence  
 CC obt'd. by screening a lambda EMBL 3 library made by infecting chicken  
 CC embryo fibroblasts with a tissue-culture adapted passage of Marek's  
 CC disease virus (MDV) strain GA, and incubating until a 90 percent  
 CC cytopathic effect had developed. Vectors and host cells contg. the  
 CC MDV MD20 gene and MDV polypeptides can be used in a vaccine to protect  
 CC poultry against Marek's disease. Antibodies or antiserum raised by  
 CC the polypeptides may be used in passive immunotherapy, diagnostic  
 CC immunoassays and in the generation of anti-idiotypic antibodies for  
 CC use in a test kit for Marek's disease. The vaccine may also contain  
 CC immunogens related to other poultry pathogens, e.g. infectious  
 CC bronchitis-virus, Newcastle disease-virus or infectious bursal  
 CC disease-virus to produce a multivalent vaccine.  
 CC See also R24102.  
 SQ Sequence 1074 AA;

Query Match 88.9%; Score 40; DB 4; Length 1074;  
 Best Local Similarity 71.4%; Pred. No. 6.77e+01;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 99 asgmva 105  
:|||||  
Qy 1 TSCMGVS 7

## RESULT 13

ID R34714 standard; Protein; 1274 AA.

AC R34714;

DT 17-AUG-1993 (first entry)

DE Bacillus subtilis srfA operon ORF3 prod.

KW Multienzyme complex; surfactin synthetase; MCSS; ORF; surfactant.

OS Bacillus subtilis.

FH Key Location/Qualifiers

FT Peptide 146..152

FT /note= "repeat sequence"

FT Peptide 613..623

FT /note= "repeat sequence"

FT Peptide 857..877

FT /note= "repeat sequence"

PN EP-540074-A.

PD 05-MAY-1993.

PF 03-OCT-1992; 203037.

PR 09-OCT-1991; IT-M12683.

PR 02-SEP-1992; IT-M12044.

PA (ENIE) ENIRICERCH SPA.

PI Carrera P, Cosmina P, De FERRA E, Grandi G, Perego M;

PI Rodriguez F;

DR WPI; 93-145447/18.

DR N-PSDB; Q40706.

PT Multi-enzyme complex surfactin synthetase DNA - is isolated from

PT Bacillus subtilis, and used for prodn. of surfactin for use in

PT pharmaceutical prods.

PS Claim 15; Page 43-45; 70pp; English.

CC The Bacillus subtilis chromosomal DNA region comprises the srfA

CC operon which encodes the multienzyme complex surfactin synthetase

CC (MCSS). Analysis of the sequence showed four regions potentially

CC coding for proteins, a zone upstream of the first ORF contg. the

CC srfA operon promoter and a presumed terminator positioned downstream

CC of the stop codon of the fourth ORF. ORF3 encodes a protein

CC (shown) contg. a 1008 amino acid region (module 7) which can be

CC aligned with the modules of ORFs 1 and 2 to show highly conserved

CC sequences. The last 243 amino acids of the protein show no homology

CC with any modules or sequences of antibiotic peptide synthetases.

CC See also R34712-21.

SQ Sequence 1274 AA;

Query Match 88.9%; Score 40; DB 7; Length 1274;

Best Local Similarity 100.0%; Pred. No. 6.77e+01;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 809 sqmgvs 814

:|||||

Qy 2 SQMGVS 7

## RESULT 14

ID R49994 standard; Protein; 1128 AA.

AC R49994;

DT 23-SEP-1994 (first entry)

DE Mouse carboxypeptidase-like bone-specific protein OSF-5.

KW Mouse OSF-5; bone-related carboxypeptidase-like protein;

KW growth factor; adhesion molecule; osteogenesis; bone induction;

KW bone metabolism disorder; osteoporosis; osteopetrosis;

KW Paget's disease.

OS Mus musculus (osteoblastic cell line MC3T3E1).

FH Key Location/Qualifiers

FT Peptide 1..25

FT /label= signal\_sequence

FT Region 116..159

FT /label= Repeat region

FT /note= "contains 4 tandem copies of 11mer repeat"

FT Region 116..126

FT /label= Repeat unit

FT /note= "Lysine- and Proline-rich repeat; shows weak

FT homology with receptors for prolactin, FGF,

FT GABA, serotonin and Histone H1"

FT Domain 423..531

FT /label= Factor VIII-like domain

FT /note= "homologous with phospholipid binding domain

FT of blood coagulation factor VIII"

FT Domain 544..1027

FT /label= Carboxypeptidase-like domain

FT /note= "acts as a controlling element for peptide

FT hormones and cytokines during bone

FT metabolism"

PN EP-588118-A.

PD 23-MAR-1994.

PF 25-AUG-1993; 113604.

PR 28-AUG-1992; JP-230029.

PR 03-DEC-1992; JP-324033.

PA (FARH) HOECHST JAPAN LTD.

PA (FARH) HOECHST JAPAN KK.

PI Amann E, Kawai S, Okazaki M, Takeshita S;

PI WPI; 94-093794/12.

DR N-PSDB; Q58708.

PT New bone-related carboxypeptidase OSF-5 - used to obtain prods.

PT for the diagnosis and treatment of bone metabolic diseases, e.g.

PT osteoporosis, or Paget's disease

PS Claim 1; Page 13-19; 26pp; English.

CC OSF-5 is a bone-specific carboxypeptidase which acts as an adhesion

CC molecule or growth factor; it takes part in osteogenesis at the site

CC of bone induction. OSF-5 can be used to treat bone metabolic diseases,

CC e.g. osteoporosis, Paget's disease, osteomalacia, hyperostosis or

CC osteopetrosis.

SQ Sequence 1128 AA;

Query Match 86.7%; Score 39; DB 9; Length 1128;

Best Local Similarity 83.3%; Pred. No. 8.99e+01;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 831 tsqmgj 836

:|||||

Qy 1 TSCMGV 6

## RESULT 15

ID R31612 standard; Protein; 22 AA.

AC R31612;

DT 24-MAY-1993 (first entry)

DE Fragment XXXI homologous to chicken nov protein fragment.

KW avian nephroblastoma; avian myeloblastoma virus;

KW stringent hybridisation.

OS Homo sapiens.

PN W09300430-A.

PD 07-JAN-1993.

PF 25-JUN-1992; F00589.

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PR 25-JUN-1991; FR-007807;  
PA (CNRS ) CENT NAT RECH SCI.  
PI Martinie C, Perbal B;  
DR WPI; 93-036377/04.  
PT Nucleotide sequences hybridising to regions of chicken nov gene -  
PT useful as probes for detecting complementary sequences to  
PT evaluate development and/or differentiation of tumours  
PS Disclosure; Page 42; 67pp; French.  
CC The invention includes nucleotide sequences which encode amino acid  
CC sequences with at least 80% homology to sequence XXX (R31611), i.e  
CC to part of the chicken nov protein encoded by the 4th. exon. Such  
CC sequences preferably encode the amino acid sequence XXXI (R31612).  
SQ Sequence 22 AA;

Query Match 84.4%; Score 38; DB 6; Length 22;  
Best Local Similarity 71.4%; Pred. No. 1.19e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 9 tcgmgis 15  
| | | | |  
Qy 1 TSGMGVS 7

Search completed: Tue Mar 18 10:14:23 1997  
Job time : 10 secs.





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5

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RESULT 4
ID KV30 MOUSE STANDARD; PRT; 111 AA.
AC P01667;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (PC 7183).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN SEQUENCE.
RX MEDLINE; 79073152.
RA WEIGERT M., GATMAITAN L., LOH E., SCHILLING J., HOOD L.E.;
RL NATURE 276:785-790(1978).
DR PIR; B01937; KVM583.
DR HSP; P01679; ICG8.
KW IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11952 MW; 041902B8 CRC32;

Query Match 79.4%; Score 744; DB 5; Length 111;
Best Local Similarity 97.3%; Pred. No. 1.80e-142;
Matches 108; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 1 divltqspaslavslgqraticskasqsvdydgsymwvyqqkpgppklliyaaanles 60
QY 21 DIVLTQSPASLAVSLGQRATISCKASQSVDYDGSYNNWYQQKPGPPKLLIYAAANLES 80

Db 61 giparfsgsgtdftlnihpveedaatyccqsnedpftfgsktleik 111
QY 81 GIPARFSGSGTDFTLNIHPVEEDAATYCCQSNEDPFTFGGKLEIK 131

RESULT 5
ID KV30 MOUSE STANDARD; PRT; 111 AA.
AC P01667;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (PC 6308).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN SEQUENCE.
RX MEDLINE; 79073152.
RA WEIGERT M., GATMAITAN L., LOH E., SCHILLING J., HOOD L.E.;
RL NATURE 276:785-790(1978).
DR PIR; C01937; KVM508.
DR HSP; P01679; ICG8.
KW IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60

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6

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FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12071 MW; F7865271 CRC32;

Query Match 79.2%; Score 742; DB 5; Length 111;
Best Local Similarity 97.3%; Pred. No. 5.27e-142;
Matches 108; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 1 divltqspaslavslgqraticskasqsvdydgsymwvyqqkpgppklliyaaanles 60
QY 21 DIVLTQSPASLAVSLGQRATISCKASQSVDYDGSYNNWYQQKPGPPKLLIYAAANLES 80

Db 61 giparfsgsgtdftlnihpveedaatyccqsnedpftfgsktleik 111
QY 81 GIPARFSGSGTDFTLNIHPVEEDAATYCCQSNEDPFTFGGKLEIK 131

RESULT 6
ID KV30 MOUSE STANDARD; PRT; 111 AA.
AC P01669;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (PC 7769).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN SEQUENCE.
RX MEDLINE; 79073152.
RA WEIGERT M., GATMAITAN L., LOH E., SCHILLING J., HOOD L.E.;
RL NATURE 276:785-790(1978).
DR PIR; E01937; KVM569.
DR HSP; P01679; IACY.
KW IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 9CB705B9 CRC32;

Query Match 78.1%; Score 732; DB 5; Length 111;
Best Local Similarity 96.4%; Pred. No. 1.15e-139;
Matches 107; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 1 divltqspaslavslgqraticskasqsvdydgsymwvyqqkpgppklliyaaanles 60
QY 21 DIVLTQSPASLAVSLGQRATISCKASQSVDYDGSYNNWYQQKPGPPKLLIYAAANLES 80

Db 61 giparfsgsgtdftlnihpveedaatyccqsnedpftfgsktleik 111
QY 81 GIPARFSGSGTDFTLNIHPVEEDAATYCCQSNEDPFTFGGKLEIK 131

RESULT 7
ID KV30 MOUSE STANDARD; PRT; 111 AA.

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AC P01664;  
DT 21-JUL-1986 (REL. 01, CREATED)  
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)  
DE IG KAPPA CHAIN V-III REGION (CBPC 101).  
OS MUS MUSCULUS (MOUSE).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; RODENTIA.  
RN [1]  
RP SEQUENCE.  
RX MEDLINE; 79012520.  
RA MCKEAN D.J., BELL M., POTTER M.;  
RL PROC. NATL. ACAD. SCI. U.S.A. 75:3913-3917(1978).  
CC -!- THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.  
DR PIR; A01936; KWSCL.  
DR HSSP; P01679; IIGB.  
KW IMMUNOGLOBULIN V REGION.  
FT DOMAIN 1 23 FRAMEWORK 1.  
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING 1.  
FT DOMAIN 39 53 FRAMEWORK 2.  
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING 2.  
FT DOMAIN 61 92 FRAMEWORK 3.  
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING 3.  
FT DOMAIN 102 111 FRAMEWORK 4.  
FT DISULFID 23 92 BY SIMILARITY.  
FT NON\_TER 111 111  
SQ SEQUENCE 111 AA; 11964 MW; A2AC84C7 CRC32;

Query Match 77.9%; Score 730; DB 5; Length 111;  
Best Local Similarity 95.5%; Pred. No. 3.38e-139;  
Matches 106; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 1 divltqspaslavslqqratisckasqsdvdygdsymnywqgqppklliyaasnl 60  
|||||  
Qy 21 DIVLTQSPASLAVSLQQRATISCKASQSDVDYDGSYNNWYQQKPCQPPKLLIYAASNL 80  
|||||  
Db 61 giparfsgsgtdftlnihpveedaatyccqsnedpytfgggtkleik 111  
|||||  
Qy 81 GIPARFSGSGTDTLNIHPVEEDAATYCCQSNEDPPTFGGGTKLEIK 131  
|||||

RESULT 8  
ID KV3P MOUSE STANDARD; PRT; 110 AA.  
AC P01668;  
DT 21-JUL-1986 (REL. 01, CREATED)  
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)  
DE IG KAPPA CHAIN V-III REGION (PC 7210).  
OS MUS MUSCULUS (MOUSE).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; RODENTIA.  
RN [1]  
RP SEQUENCE.  
RX MEDLINE; 79073152.  
RA WEIGERT M., GATHAITAN L., LOH E., SCHILLING J., HOOD L.E.;  
RL NATURE 276:785-790(1978).  
DR PIR; D01937; KWS10.  
DR HSSP; P01679; IIGB.  
KW IMMUNOGLOBULIN V REGION.  
FT DOMAIN 1 23 FRAMEWORK 1.  
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING 1.  
FT DOMAIN 39 53 FRAMEWORK 2.  
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING 2.  
FT DOMAIN 61 92 FRAMEWORK 3.

FT DOMAIN 93 100 COMPLEMENTARITY-DETERMINING 3.  
FT DOMAIN 101 110 FRAMEWORK 4.  
FT DISULFID 23 92 BY SIMILARITY.  
FT NON\_TER 110 110  
SQ SEQUENCE 110 AA; 11950 MW; BF45B542 CRC32;

Query Match 76.7%; Score 719; DB 5; Length 110;  
Best Local Similarity 95.5%; Pred. No. 1.26e-136;  
Matches 106; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

Db 1 divltqspaslavslqqratisckasqsdvdygdsymnywqgqppklliyaasnl 60  
|||||  
Qy 21 DIVLTQSPASLAVSLQQRATISCKASQSDVDYDGSYNNWYQQKPCQPPKLLIYAASNL 80  
|||||  
Db 61 giparfsgsgtdftlnihpveedaatyccqsnedpytfgggtkleik 110  
|||||  
Qy 81 GIPARFSGSGTDTLNIHPVEEDAATYCCQSNEDPPTFGGGTKLEIK 131  
|||||

RESULT 9  
ID KV3P MOUSE STANDARD; PRT; 111 AA.  
AC P01670;  
DT 21-JUL-1986 (REL. 01, CREATED)  
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)  
DE IG KAPPA CHAIN V-III REGION (PC 6684).  
OS MUS MUSCULUS (MOUSE).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; RODENTIA.  
RN [1]  
RP SEQUENCE.  
RX MEDLINE; 79073152.  
RA WEIGERT M., GATHAITAN L., LOH E., SCHILLING J., HOOD L.E.;  
RL NATURE 276:785-790(1978).  
DR PIR; A01938; KWS84.  
DR HSSP; P01679; IACY.  
KW IMMUNOGLOBULIN V REGION.  
FT DOMAIN 1 23 FRAMEWORK 1.  
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING 1.  
FT DOMAIN 39 53 FRAMEWORK 2.  
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING 2.  
FT DOMAIN 61 92 FRAMEWORK 3.  
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING 3.  
FT DISULFID 23 92 BY SIMILARITY.  
FT NON\_TER 111 111  
SQ SEQUENCE 111 AA; 12039 MW; F4B1FA93 CRC32;

Query Match 71.9%; Score 674; DB 5; Length 111;  
Best Local Similarity 88.3%; Pred. No. 3.88e-126;  
Matches 98; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

Db 1 divltqspaslavslqqratisckasqsdvdygdsymnywqgqppklliyaasnl 60  
|||||  
Qy 21 DIVLTQSPASLAVSLQQRATISCKASQSDVDYDGSYNNWYQQKPCQPPKLLIYAASNL 80  
|||||  
Db 61 giparfsgsgtdftlnihpveedaatyccqsnedpytfgggtkleik 111  
|||||  
Qy 81 GIPARFSGSGTDTLNIHPVEEDAATYCCQSNEDPPTFGGGTKLEIK 131  
|||||

RESULT 10  
ID KV3T MOUSE STANDARD; PRT; 111 AA.  
AC P01672;

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US-08-612-929-2.rsp

9

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DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (PC 7940).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUETHERIA; RODENTIA.
RN [1]
RP SEQUENCE.
RX MEDLINE; 79073152.
RA WEIGERT M., GATMAITAN L., LOH E., SCHILLING J., HOOD L.E.;
RL NATURE 276:785-790(1978).
DR PIR; C01938; KVM540.
DR HSSP; P01679; IACY.
KW IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12038 MW; 4856B39D CRC32;

Query Match 71.5%; Score 670; DB 5; Length 111;
Best Local Similarity 88.3%; Pred. No. 3.30e-125;
Matches 98; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

Db 1 divltqpsaslavlsgqratisckasvdygdsgymnwtyqqkpgppklllylaenles 60
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 21 DIVLTQPSASLAVSLGQRATISCKASQSDVDGDSYMNWYQQKPGPPKLLIYAASNLES 80

Db 61 gvpafegsgtdftlnihpveedavtyyccqhsrelpftfgggtkleik 111
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 81 GIPARFSGSGTDFTLNIHPVEEDAATYYCQSNEDPPTFGGGTKLEIK 131

RESULT 11
ID KV3H MOUSE STANDARD; PRT; 111 AA.
AC P01660;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (PC 3741 AND TEPC 111).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUETHERIA; RODENTIA.
RN [1]
RP SEQUENCE (PC 3741).
RX MEDLINE; 79073152.
RA WEIGERT M., GATMAITAN L., LOH E., SCHILLING J., HOOD L.E.;
RL NATURE 276:785-790(1978).
RN [2]
RP SEQUENCE (TEPC 111).
RX MEDLINE; 79012520.
RA MCKEAN D.J., BELL M., POTTER M.;
RL PROC. NATL. ACAD. SCI. U.S.A. 75:3913-3917(1978).
CC -/- THE PC 3741 AND TEPC 111 SEQUENCES ARE IDENTICAL.
DR PIR; A01934; KVM637.
DR HSSP; P01679; ICGH.
KW IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12038 MW; 4856B39D CRC32;
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US-08-612-929-2.rsp

10

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FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12099 MW; 76502E89 CRC32;

Query Match 70.8%; Score 663; DB 5; Length 111;
Best Local Similarity 86.5%; Pred. No. 1.40e-123;
Matches 96; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Db 1 divltqpsaslavlsgqratisckasvdygdsgymnwtyqqkpgppklllylaenles 60
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 21 DIVLTQPSASLAVSLGQRATISCKASQSDVDGDSYMNWYQQKPGPPKLLIYAASNLES 80

Db 61 gvpafegsgtdftlnihpveedavtyyccqhsrelpftfgggtkleik 111
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 81 GIPARFSGSGTDFTLNIHPVEEDAATYYCQSNEDPPTFGGGTKLEIK 131

RESULT 12
ID KV3S MOUSE STANDARD; PRT; 111 AA.
AC P01671;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (PC 7175).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUETHERIA; RODENTIA.
RN [1]
RP SEQUENCE.
RX MEDLINE; 79073152.
RA WEIGERT M., GATMAITAN L., LOH E., SCHILLING J., HOOD L.E.;
RL NATURE 276:785-790(1978).
DR PIR; B01938; KVM575.
DR HSSP; P01679; IACY.
KW IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12010 MW; AA8039B3 CRC32;

Query Match 70.4%; Score 660; DB 5; Length 111;
Best Local Similarity 86.5%; Pred. No. 6.98e-123;
Matches 96; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

Db 1 divltqpsaslavlsgqratisckasvdygdsgymnwtyqqkpgppklllylaenles 60
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 21 DIVLTQPSASLAVSLGQRATISCKASQSDVDGDSYMNWYQQKPGPPKLLIYAASNLES 80

Db 61 gvpafegsgtdftlnihpveedavtyyccqhsrelpftfgggtkleik 111
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 81 GIPARFSGSGTDFTLNIHPVEEDAATYYCQSNEDPPTFGGGTKLEIK 131
```

RESULT 13  
ID KV3C MOUSE STANDARD; PRT; 112 AA.  
AC P01659;  
DT 21-JUL-1986 (REL. 01, CREATED)  
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)  
DE IG KAPPA CHAIN V-III REGION (TEPC 124).  
OS MUS MUSCULUS (MOUSE).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; RODENTIA.  
RN [1]  
RP SEQUENCE.  
RX MEDLINE; 73140225.  
RA MCKEAN D.J., POTTER M., HOOD L.E.;  
RL BIOCHEMISTRY 12:760-771 (1973).  
DR PIR; A01933; KVM532.  
DR HSP; P01679; KVM532.  
KW IMMUNOGLOBULIN V REGION.  
FT DOMAIN 1 23  
FT DOMAIN 24 38  
FT DOMAIN 39 53  
FT DOMAIN 54 60  
FT DOMAIN 61 92  
FT DOMAIN 93 101  
FT DOMAIN 102 111  
FT DISULFID 23 92  
FT NON\_TER 112 112  
SQ SEQUENCE 112 AA; 12339 MW; 4504DD0E CRC32;

Query Match 70.2%; Score 658; DB 5; Length 112;  
Best Local Similarity 74.1%; Pred. No. 2.03e-122;  
Matches 83; Conservative 20; Mismatches 9; Indels 0; Gaps 0;

Db 1 divltqpaslavlgqratiscrasvsnvymfzwyzzkzppklliyraenlzs 60  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Qy 21 DIVLTQSPASLAVSLGORATISCKASQSDVDGDSYNNWYQKPGQPKLLIYAASNL 80  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 61 giparfsgsrbftltpvzabdvatycfzszbapwtfsggkkleir 112  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Qy 81 GIPARFSGSGTDFTLNHPVEEDAATYQCQSNEDPPTFGGKLEIKR 132

RESULT 14  
ID KV3J MOUSE STANDARD; PRT; 111 AA.  
AC P01662;  
DT 21-JUL-1986 (REL. 01, CREATED)  
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)  
DE IG KAPPA CHAIN V-III REGION (ABPC 22 AND PC 9245).  
OS MUS MUSCULUS (MOUSE).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; RODENTIA.  
RN [1]  
RP SEQUENCE (ABPC 22).  
RX MEDLINE; 79012520.  
RA MCKEAN D.J., BELL M., POTTER M.;  
RL PROC. NATL. ACAD. SCI. U.S.A. 75:3913-3917 (1978).  
RN [2]  
RP SEQUENCE (PC 9245).  
RX MEDLINE; 79073152.  
RA WEIGERT M., GATMAITAN L., LOH E., SCHILLING J., HOOD L.E.;  
RL NATURE 276:785-790 (1978).  
CC -!- THE ABPC22 AND PC9241 SEQUENCES ARE IDENTICAL.

DR PIR; A01935; KVM5M6.  
DR HSP; P01679; IACY.  
KW IMMUNOGLOBULIN V REGION.  
FT DOMAIN 1 23  
FT DOMAIN 24 38  
FT DOMAIN 39 53  
FT DOMAIN 54 60  
FT DOMAIN 61 92  
FT DOMAIN 93 101  
FT DOMAIN 102 111  
FT DISULFID 23 92  
FT NON\_TER 111 111  
SQ SEQUENCE 111 AA; 12041 MW; 711C554A CRC32;

Query Match 70.1%; Score 657; DB 5; Length 111;  
Best Local Similarity 84.7%; Pred. No. 3.47e-122;  
Matches 94; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

Db 1 nivltqpaslavlgqratiscrasvsnvymfzwyzzkzppklliyraenlzs 60  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Qy 21 DIVLTQSPASLAVSLGORATISCKASQSDVDGDSYNNWYQKPGQPKLLIYAASNL 80  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 61 gyparfsgsrbftltpdvdaatycqnnedpytfggkkleik 111  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Qy 81 GIPARFSGSGTDFTLNHPVEEDAATYQCQSNEDPPTFGGKLEIK 131

RESULT 15  
ID KV3K MOUSE STANDARD; PRT; 111 AA.  
AC P01663;  
DT 21-JUL-1986 (REL. 01, CREATED)  
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)  
DE IG KAPPA CHAIN V-III REGION (PC 4050).  
OS MUS MUSCULUS (MOUSE).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; RODENTIA.  
RN [1]  
RP SEQUENCE.  
RX MEDLINE; 79073152.  
RA WEIGERT M., GATMAITAN L., LOH E., SCHILLING J., HOOD L.E.;  
RL NATURE 276:785-790 (1978).  
DR PIR; A01935; KVM5M6.  
DR HSP; P01679; IACY.  
KW IMMUNOGLOBULIN V REGION.  
FT DOMAIN 1 23  
FT DOMAIN 24 38  
FT DOMAIN 39 53  
FT DOMAIN 54 60  
FT DOMAIN 61 92  
FT DOMAIN 93 101  
FT DOMAIN 102 111  
FT DISULFID 23 92  
FT NON\_TER 111 111  
SQ SEQUENCE 111 AA; 12005 MW; 5EBF3264 CRC32;

Query Match 69.4%; Score 650; DB 5; Length 111;  
Best Local Similarity 82.9%; Pred. No. 1.47e-120;  
Matches 92; Conservative 11; Mismatches 8; Indels 0; Gaps 0;

Db 1 nivltqpaslavlgqratiscrasvsnvymfzwyzzkzppklliyraenlzs 60  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Qy 21 DIVLTQSPASLAVSLGORATISCKASQSDVDGDSYNNWYQKPGQPKLLIYAASNL 80  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Mar 18 09:38

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13

Db 61 gyparfsgsrtfdltitdpveaddaatyycqgnedpltfagqklelk 111  
Qy 81 GIPARFSGSGCTDFTLNIHPVEEDAATYCOQSNEDPPTFGGCKLEIK 131

Search completed: Tue Mar 18 10:00:08 1997  
Job time : 34 secs.



```
Best Local Similarity 96.9%; Pred. No. 2.87e-95;
Matches 127; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 1 metdtdllwllwpqstgdlvtqspaelmslqgratiscasqslvdydgsymnw 60
|||||
Qy 1 METDTLLWLLWVPGSTGDLVTQSPASLAVSLQGRATISCKASQSDVDGDSYNNWY 60
|||||

Db 61 qkqgqpklliyaaanlesgiparfsgsgtdftlnihpveedaatyccasedpp 120
|||||
Qy 61 QKQPGQPKLLIYAASNLSEGPAPFSGSGCTDFTLNHPVEEDAATYCCQSNEDPP 120
|||||

Db 121 tfgggtkleik 131
|||||
Qy 121 TFGGGTKLEIK 131

RESULT 2
ENTRY KWMS6 #type complete
TITLE Ig kappa chain precursor V regions (M63, AB22, PC9245,
PC4050) - mouse
ORGANISM #formal name Mus musculus #common name house mouse
DATE 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change
31-Dec-1993
ACCESSIONS B90412; B90374; B93822; C93822; C93204; D93204; A01935
REFERENCE A90412
#authors Burstein, Y.; Schechter, I.
#journal Biochemistry (1978) 17:2392-2400
#title Primary structures of N-terminal extra peptide segments
linked to the variable and constant regions of
immunoglobulin light chain precursors: implications on the
organization and controlled expression of immunoglobulin
genes.
#cross-references MUID:78235887
#contents M63
#accession B90412
#molecule_type protein
#residues 1-35 ##label BUR
REFERENCE A90374
#authors McKean, D.; Potter, M.; Hood, L.
#journal Biochemistry (1973) 12:760-771
#title Mouse immunoglobulin chains. Pattern of sequence variation
among kappa chains with limited sequence differences.
#cross-references MUID:73140225
#contents M63
#accession B90374
#molecule_type protein
#residues 21-46, 'Q', 48-53, 'B', 55-57, '2', 59-86, 'F', 88-131 ##label
MCK
#note this sequence has since been revised in reference A93822
REFERENCE A93822
#authors McKean, D.J.; Bell, M.; Potter, M.
#journal Proc. Natl. Acad. Sci. U.S.A. (1978) 75:3913-3917
#title Mechanisms of antibody diversity: multiple genes encode
structurally related mouse kappa variable regions.
#cross-references MUID:79012520
#contents M63; AB22
#accession B93822
#molecule_type protein
#residues 1-53; 69-107 ##label MC2
#accession C93822
#molecule_type protein
#residues 21-119, 'Y', 121-131 ##label MC3
REFERENCE A93204
#authors Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
```

```
#journal Nature (1978) 276:785-790
#title Rearrangement of genetic information may produce
immunoglobulin diversity.
#cross-references MUID:79073152
#contents PC9245; PC4050
#accession C93204
#molecule_type protein
#residues 21-119, 'Y', 121-131 ##label WEI
#accession D93204
#molecule_type protein
#residues 21-119, 'L', 121-123, 'A', 125-129, 'L', 131 ##label WE2
COMMENT The M63 precursor sequence is shown.
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
FEATURE
1-20 #domain signal sequence #status experimental #label SIG
SUMMARY #length 131 #molecular-weight 14291 #checksum 5945

Query Match 86.7%; Score 812; DB 2; Length 131;
Best Local Similarity 86.3%; Pred. No. 5.42e-83;
Matches 113; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

Db 1 metdtdllwllwpqstgdlvtqspaelmslqgratiscasqslvdydgsymnw 60
|||||
Qy 1 METDTLLWLLWVPGSTGDLVTQSPASLAVSLQGRATISCKASQSDVDGDSYNNWY 60
|||||

Db 61 qkqgqpklliyaaanlesgiparfsgsgtdftlnihpveedaatyccqnnedpw 120
|||||
Qy 61 QKQPGQPKLLIYAASNLSEGPAPFSGSGCTDFTLNHPVEEDAATYCCQSNEDPP 120
|||||

Db 121 tfgggtkleik 131
|||||
Qy 121 TFGGGTKLEIK 131

RESULT 3
ENTRY KWMS32 #type complete
TITLE Ig kappa chain precursor V regions (MOPC 321, TEPC 124) -
mouse
ORGANISM #formal name Mus musculus #common name house mouse
DATE 31-May-1979 #sequence_revision 31-May-1979 #text_change
04-Nov-1994
ACCESSIONS A90412; A90373; A90374; A01933
REFERENCE A90412
#authors Burstein, Y.; Schechter, I.
#journal Biochemistry (1978) 17:2392-2400
#title Primary structures of N-terminal extra peptide segments
linked to the variable and constant regions of
immunoglobulin light chain precursors: implications on the
organization and controlled expression of immunoglobulin
genes.
#cross-references MUID:78235887
#contents MOPC 321
#accession A90412
#molecule_type protein
#residues 1-37 ##label BUR
#note this precursor was synthesized in a cell-free system
directed by mRNA isolated from myeloma polyomes
REFERENCE A90373
#authors McKean, D.; Potter, M.; Hood, L.
#journal Biochemistry (1973) 12:749-759
#title Mouse immunoglobulin chains. Partial amino acid sequence of a
kappa chain.
#cross-references MUID:73140224
#contents MOPC 321
```

```
#accession A90373
##molecule_type protein
##residues 21-132 ##label MCK
##note the partial sequence of the C region of this Bence Jones
protein was also determined; it differs from that
reported for mouse MOPC 21 only in the transposition
of two nearby residues

REFERENCE
#authors McKean, D.; Potter, M.; Hood, L.
#journal Biochemistry (1973) 12:760-771
#title Mouse immunoglobulin chains. Pattern of sequence variation
among kappa chains with limited sequence differences.
#cross-references MUID:73140225
#contents TEPC 124
#accession A90374
##molecule_type protein
##residues 21-131 ##label MC2
##note the sequence is compatible with that of MOPC 321 except
in having 47-Glx, 51-Trp, and 118-Ala

COMMENT The MOPC 321 sequence is shown.
COMMENT Residues 1-20 are the signal sequence.
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
FEATURE
36-114 #domain immunoglobulin homology #label IMM
SUMMARY #length 132 #molecular-weight 14523 #checksum 370
```

```
Query Match 86.3%; Score 809; DB 2; Length 132;
Best Local Similarity 77.3%; Pred. No. 1.28e-82;
Matches 102; Conservative 21; Mismatches 9; Indels 0; Gaps 0;

Db 1 metdtllllwllwpqstgdivltqpaslavslgqratiscrasksvntynqsfmzwy 60
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 1 METDTILLWLLWVPGSGDIVLTQSPASLAVSLGQRATISCKASQSDVDGDSYNNWY 60
::|||:||||| ||||:||||| ||||:||||| ||||:||||| ||||:||||| ||||:||||:

Db 61 zdkpgqpkllylvrasmzsqiparfsgsgtdftlnihpveedatyyccqherypl 120
::|||:||||| ||||:||||| ||||:||||| ||||:||||| ||||:||||| ||||:||||:
Qy 61 QQKPGQPPLLIIYAASNLGSIPIARFSGSGTDFTLNIHPVEEDAAITYCQSQSNEPDP 120
||||:||||| ||||:||||| ||||:||||| ||||:||||| ||||:||||| ||||:||||:

Db 121 tfqggtkleikr 132
||||:|||||
Qy 121 TFGGGTKLEIKR 132
||||:|||||
```

```
RESULT 4
ENTRY S55027 #type fragment
TITLE immunoglobulin light chain variable region precursor - mouse
ORGANISM (fragment)
#formal name Mus musculus #common name house mouse
DATE 23-Aug-1995 #sequence_revision 19-Oct-1995 #text_change
19-Oct-1995
ACCESSION S55027
REFERENCE S55027
#authors Jeffrey, P.D.; Schildbach, J.F.; Chang, C.Y.; Kussie, P.H.;
Margolies, M.N.; Sheriff, S.
#journal J. Mol. Biol. (1995) 248:344-360
#title Structure and specificity of the anti-digoxin antibody 40-50.
#accession S55027
##status preliminary
##molecule_type mRNA
##residues 1-131 ##label JEF
##cross-references EMBL:L31404
SUMMARY #length 131 #checksum 6089
```

Query Match 83.2%; Score 780; DB 12; Length 131;

```
Best Local Similarity 84.7%; Pred. No. 5.34e-79;
Matches 111; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

Db 1 metdtllllwllwpqstgdivltqpaslavslgqratiscrasksvatgagyhwhw 60
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 1 METDTILLWLLWVPGSGDIVLTQSPASLAVSLGQRATISCKASQSDVDGDSYNNWY 60
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

Db 61 qdkpgqpkllylasilesgvparfsgsgtdftlnihpveedatyyccqherypl 120
||||:||||| ||||:||||| ||||:||||| ||||:||||| ||||:||||| ||||:||||:
Qy 61 QQKPGQPPLLIIYAASNLGSIPIARFSGSGTDFTLNIHPVEEDAAITYCQSQSNEPDP 120
||||:||||| ||||:||||| ||||:||||| ||||:||||| ||||:||||| ||||:||||:

Db 121 tfqggtkleikr 131
||||:|||||
Qy 121 TFGGGTKLEIKR 131
||||:|||||
```

```
RESULT 5
ENTRY PN0446 #type fragment
TITLE Ig kappa chain precursor V-II region - human (fragment)
ORGANISM #formal name Homo sapiens #common name man
DATE 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
30-Apr-1995
ACCESSION PN0446
REFERENCE PN0444
#authors Kaluza, B.; Betzl, G.; Shao, H.; Diamantstein, T.; Weidle,
U.H.
#journal Gene (1992) 122:321-328
#title A general method for chimerization of monoclonal antibodies
by inverse polymerase chain reaction which conserves
authentic N-terminal sequences.
```

```
#accession PN0446
##molecule_type mRNA
##residues 1-140 ##label KAL
##cross-references GB:102345
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
immunoglobulin
KEYWORDS
1-20 #domain signal sequence #status predicted #label SIG\
21-140 #product Ig light chain kappa-2 V region #status
predicted #label MAT
SUMMARY #length 140 #checksum 3597
```

```
Query Match 82.3%; Score 771; DB 5; Length 140;
Best Local Similarity 84.8%; Pred. No. 7.07e-78;
Matches 112; Conservative 6; Mismatches 12; Indels 2; Gaps 1;

Db 1 metdtllllwllwpqstgdivltqpaslavslgqratiscrasksvatgagyhwhw 60
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 1 METDTILLWLLWVPGSGDIVLTQSPASLAVSLGQRATISCKASQSDVDGDSYNNWY 60
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

Db 61 qdkpgqpkllylvsnlesgvparfsgsgtdftlnihpveedatyyccqherypl 118
||||:||||| ||||:||||| ||||:||||| ||||:||||| ||||:||||| ||||:||||:
Qy 61 QQKPGQPPLLIIYAASNLGSIPIARFSGSGTDFTLNIHPVEEDAAITYCQSQSNEPDP 120
||||:||||| ||||:||||| ||||:||||| ||||:||||| ||||:||||| ||||:||||:

Db 119 tfqggtkleikr 130
||||:|||||
Qy 121 TFGGGTKLEIKR 132
||||:|||||
```

```
RESULT 6
ENTRY S19971 #type fragment
TITLE Ig kappa chain V region (CD4 mAb clone M-T310 and others) -
mouse (fragment)
ORGANISM #formal name Mus musculus #common name house mouse
```

```
DATE          06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change
ACCESSIONS    S19971; S19973
REFERENCE      S19963
#authors      Weissenhorn, W.; Riethmuller, G.; Weiss, E.M.; Rieber, E.P.
#submission   submitted to the EMBL Data Library, March 1992
#description   Structural characterization of CD4 mAb.
#accession    S19971
##molecule_type mRNA
##residues    1-112 ##label WEI
##cross-references EMBL:X65091
##experimental_source clone M-T310
#accession    S19973
##molecule_type mRNA
##residues    1-112 ##label WEI
##cross-references EMBL:X65092
##experimental_source M-T404
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
SUMMARY       #length 112 #checksum 4782

Query Match      80.9%; Score 758; DB 5; Length 112;
Best Local Similarity 96.4%; Pred. No. 2.94e-16;
Matches 108; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 1 divltqspaslpmslqgratiscasqsdgdydgsymwvqqkpgppklliyaasnles 60
    |||||
Qy 21 DIVLTQSPASLAVSLGQRATISCKASQSDVDGDSYNNWYQQKPGPPKLLIYAASNLES 80
    |||||

Db 61 giparfsgsgtdftlnihpveedaatyccqsnedpftfgggtkleikr 112
    |||||
Qy 81 GIPARFSGSGTDFTLNIHPVEEDAATYYCQSNEDPFTFGGGTKLEIKR 132
    |||||

RESULT 7
ENTRY   KWMS43      #type complete
TITLE   Ig kappa chain V region (PC7043) - mouse
ORGANISM #formal name Mus musculus #common name house mouse
DATE    01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change
        05-Apr-1995
ACCESSIONS A01937
REFERENCE  A93204
#authors   Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
#journal   Nature (1978) 276:785-790
#title     Rearrangement of genetic information may produce
           immunoglobulin diversity.
#cross-references MUID:79073152
#accession A01937
##molecule_type protein
##residues 1-111 ##label WEI
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
FEATURE      23-92
SUMMARY      #disulfide bonds #status predicted
           #length 111 #molecular-weight 12002 #checksum 438

Query Match      79.6%; Score 746; DB 2; Length 111;
Best Local Similarity 98.2%; Pred. No. 9.16e-75;
Matches 109; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 1 divltqspaslpmslqgratiscasqsdgdydgsymwvqqkpgppklliyaasnles 60
    |||||
Qy 21 DIVLTQSPASLAVSLGQRATISCKASQSDVDGDSYNNWYQQKPGPPKLLIYAASNLES 80
    |||||

Db 61 giparfsgsgtdftlnihpveedaatyccqsnedpftfgggtkleik 111
    |||||
```

```
Qy 81 GIPARFSGSGTDFTLNIHPVEEDAATYYCQSNEDPFTFGGGTKLEIK 131
    |||||

RESULT 8
ENTRY   KWMS83      #type complete
TITLE   Ig kappa chain V region (PC7183) - mouse
ORGANISM #formal name Mus musculus #common name house mouse
DATE    30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change
        30-Sep-1993
ACCESSIONS B01937; A01937
REFERENCE  A93204
#authors   Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
#journal   Nature (1978) 276:785-790
#title     Rearrangement of genetic information may produce
           immunoglobulin diversity.
#cross-references MUID:79073152
#accession B01937
##molecule_type protein
##residues 1-111 ##label WEI
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS     immunoglobulin
FEATURE      23-92
SUMMARY      #disulfide bonds #status predicted
           #length 111 #molecular-weight 11952 #checksum 9

Query Match      79.4%; Score 744; DB 2; Length 111;
Best Local Similarity 97.3%; Pred. No. 1.62e-74;
Matches 108; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 1 divltqspaslpmslqgratiscasqsdgdydgsymwvqqkpgppklliyaasnles 60
    |||||
Qy 21 DIVLTQSPASLAVSLGQRATISCKASQSDVDGDSYNNWYQQKPGPPKLLIYAASNLES 80
    |||||

Db 61 giparfsgsgtdftlnihpveedaatyccqsnedpftfgggtkleik 111
    |||||
Qy 81 GIPARFSGSGTDFTLNIHPVEEDAATYYCQSNEDPFTFGGGTKLEIK 131
    |||||

RESULT 9
ENTRY   KWMS08      #type complete
TITLE   Ig kappa chain V region (PC6308) - mouse
ORGANISM #formal name Mus musculus #common name house mouse
DATE    30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change
        30-Sep-1993
ACCESSIONS C01937; A01937
REFERENCE  A93204
#authors   Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
#journal   Nature (1978) 276:785-790
#title     Rearrangement of genetic information may produce
           immunoglobulin diversity.
#cross-references MUID:79073152
#accession C01937
##molecule_type protein
##residues 1-111 ##label WEI
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS     immunoglobulin
FEATURE      23-92
SUMMARY      #disulfide bonds #status predicted
           #length 111 #molecular-weight 12071 #checksum 2195

Query Match      79.2%; Score 742; DB 2; Length 111;
Best Local Similarity 97.3%; Pred. No. 2.88e-74;
Matches 108; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```



Mar 18 09:59

US-08-612-929-2.rpr

9

```

Db 1 divltqpsaslavlgratiasckasgvdgdsymwyqgkppklliytaasles 60
|||||
Qy 21 DIVLTQSPASLAVSLGORATISCKASQSDVDGDSYNNWYQKQKPPKLLIYAASNLES 80
|||||

Db 61 giparfsgsgtdftlinhpveeedaatyccgsnedpwtfgsgtkleik 111
|||||
Qy 81 GIPARFSGSGTDFTLINHPVEEEDAATYYCQSNEDPPTFGGKTLEIK 131
|||||

RESULT 10
ENTRY KWMS69 #type complete
TITLE Ig kappa chain V region (PC7769) - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change
30-Sep-1993
ACCESSIONS E01937; A01937
REFERENCE A93204
#authors Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
#journal Nature (1978) 276:785-790
#title Rearrangement of genetic information may produce immunoglobulin diversity.
#cross-references MUID:79073152
#accession E01937
#molecule_type protein
##residues 1-111 ##label WEI
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS immunoglobulin
FEATURE
23-92 #disulfide_bonds #status predicted
SUMMARY #length 111 #molecular_weight 12011 #checksum 662

Query Match 78.1%; Score 732; DB 2; Length 111;
Best Local Similarity 96.4%; Pred. No. 5.04e-73;
Matches 107; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 1 divltqpsaslavlgratiasckasgvdgdsymwyqgkppkllifaasles 60
|||||
Qy 21 DIVLTQSPASLAVSLGORATISCKASQSDVDGDSYNNWYQKQKPPKLLIYAASNLES 80
|||||

Db 61 giparfsgsgtdftlinhpveeedaatyccgsnedpwtfgsgtkleik 111
|||||
Qy 81 GIPARFSGSGTDFTLINHPVEEEDAATYYCQSNEDPPTFGGKTLEIK 131
|||||

RESULT 11
ENTRY KWMSCL #type complete
TITLE Ig kappa chain V region (CBPC 101) - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change
05-Apr-1995
ACCESSIONS A01936
REFERENCE A93822
#authors McKean, D.J.; Bell, M.; Potter, M.
#journal Proc. Natl. Acad. Sci. U.S.A. (1978) 75:3913-3917
#title Mechanisms of antibody diversity: multiple genes encode structurally related mouse kappa variable regions.
#cross-references MUID:79012520
#accession A01936
#molecule_type protein
##residues 1-111 ##label MCK
COMMENT This chain was isolated from a myeloma protein.
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
FEATURE
23-92 #disulfide_bonds #status predicted

```

Mar 18 09:59

US-08-612-929-2.rpr

10

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SUMMARY #length 111 #molecular_weight 11964 #checksum 1507

Query Match 77.9%; Score 730; DB 2; Length 111;
Best Local Similarity 95.5%; Pred. No. 8.94e-73;
Matches 106; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 1 divltqpsaslavlgratiasckasgvdgdsymwyqgkppklliytaasles 60
|||||
Qy 21 DIVLTQSPASLAVSLGORATISCKASQSDVDGDSYNNWYQKQKPPKLLIYAASNLES 80
|||||

Db 61 giparfsgsgtdftlinhpveeedaatyccgsnedpwtfgsgtkleik 111
|||||
Qy 81 GIPARFSGSGTDFTLINHPVEEEDAATYYCQSNEDPPTFGGKTLEIK 131
|||||

RESULT 12
ENTRY S19976 #type fragment
TITLE Ig kappa chain V region (M-T413) - mouse (fragment)
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change
12-Apr-1995
ACCESSIONS S19976
REFERENCE S19963
#authors Weissenhorn, W.; Riethmueller, G.; Weiss, E.M.; Rieber, E.P.
#submission Submitted to the EMBL Data Library, March 1992
#description Structural characterization of CD4 mAb.
#accession S19976
#status preliminary
#molecule_type mRNA
##residues 1-112 ##label WEI
##cross-references EMBL:X65093
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
SUMMARY #length 112 #checksum 4816

Query Match 77.7%; Score 728; DB 5; Length 112;
Best Local Similarity 93.8%; Pred. No. 1.58e-72;
Matches 105; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Db 1 divltqpsaslavlgratiasckasgldydadsymhwyqgkppklliytaasles 60
|||||
Qy 21 DIVLTQSPASLAVSLGORATISCKASQSDVDGDSYNNWYQKQKPPKLLIYAASNLES 80
|||||

Db 61 giparfsgsgtdftlinhpveeedaatyccgsiqdpytfgggtkleikr 112
|||||
Qy 81 GIPARFSGSGTDFTLINHPVEEEDAATYYCQSNEDPPTFGGKTLEIKR 132
|||||

RESULT 13
ENTRY S06731 #type complete
TITLE Ig kappa chain precursor - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
12-Apr-1995
ACCESSIONS S06731
REFERENCE S06731
#authors Alanen, A.; Weiss, S.
#journal Eur. J. Immunol. (1989) 19:1961-1963
#title Sequence and linkage of the V(kappa)21A and G germ-line gene segments in the mouse.
#cross-references MUID:90060210
#accession S06731
#status preliminary
#molecule_type DNA
##residues 1-120 ##label MIA

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WAP5REL (TM)

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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Mar 18 10:01:42 1997; MasPar time 4.25 Seconds  
319,919 Million cell updates/sec

Tabular output not generated.

Title: >US-08-612-929-2  
Description: (1-132) from US08612929.pep  
Perfect Score: 937  
Sequence: 1 MEYDTILLVLLWVFGTGTG.....QQSNEDPPTFGGKLEIKR 132

Scoring table: PAM 150  
Gap 11

Searched: 88003 seqs, 10295656 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: a-geneseq25  
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13  
14:part14 15:part15 16:part16 17:part17 18:part18

Statistics: Mean 30.011; Variance 164.394; scale 0.183

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	937	100.0	132	13	Mouse MAB 3B9 light c	9.23e-62
2	910	97.1	131	6	Anti-CD4 antibody MT	1.12e-59
3	905	96.6	131	1	Anti-Leu 3a light cha	2.72e-59
4	895	95.5	131	1	Amino acids sequence	1.61e-58
5	819	87.4	131	6	p12-k2.	1.15e-52
6	816	87.1	131	6	p64-k4 protein produc	1.96e-52
7	801	85.5	131	1	Light chain variable	2.78e-51
8	790	84.3	131	6	Antibody 4A2 light ch	1.95e-50
9	789	84.2	132	3	kappa light chain var	2.33e-50
10	776	82.8	132	3	Mouse 4C10 anti-Idiot	2.32e-49
11	767	81.9	130	14	Anti-idiotypic antibod	1.14e-48
12	747	79.7	111	10	Mouse anti-HIV mu5.5	3.90e-47

13	747	79.7	111	11	R60302	Anti HIV antibody lig	3.90e-47
14	734	78.3	111	1	P90541	Immunoglobulin L chai	3.87e-46
15	727	77.6	146	14	R74966	Anti-idiotypic antibod	1.33e-45
16	719	76.7	120	9	R48618	Sequence of the monoc	5.46e-45
17	708	75.6	131	13	R70202	Humanized antibody 3B	3.80e-44
18	705	75.2	111	6	R33305	MaE11 light chain.	6.45e-44
19	701	74.8	131	13	R75355	Humanized antibody 3B	1.30e-43
20	700	74.7	106	6	R33309	MaE15 light chain.	1.56e-43
21	670	71.5	111	9	R47494	Murine anti-CD18 Ab 6	3.06e-41
22	665	71.0	112	3	R13089	Murine 1B4 light chai	7.38e-41
23	657	70.1	260	15	R77617	Anti-C5 MAB N19/8 scF	3.01e-40
24	655	69.9	112	14	R80272	V1 region from an ant	4.28e-40
25	653	69.7	112	14	R75431	Human thyroid stimula	6.09e-40
26	653	69.7	112	2	R10539	Chimeric MAb 9.2.27 1	6.09e-40
27	651	69.5	111	15	R85236	Murine 206 antibody v	8.65e-40
28	650	69.4	113	16	R79892	Anti-EGFR antibody li	1.03e-39
29	649	69.3	111	13	R65172	Murine NM-01 variable	1.23e-39
30	648	69.2	110	11	R60564	Anti-carcinoembryonic	1.47e-39
31	647	69.1	121	9	R48615	Sequence of the monoc	1.75e-39
32	646	68.9	218	15	R75459	Mouse antibody F4-7 1	2.08e-39
33	646	68.9	218	15	R75457	Mouse antibody FB3-2	2.08e-39
34	645	68.8	113	16	R79893	Anti-EGFR antibody li	2.48e-39
35	645	68.8	113	16	R79882	Anti-EGFR antibody li	2.48e-39
36	645	68.8	121	6	R33346	Sequence of the varia	2.48e-39
37	644	68.7	120	9	R48620	Sequence of the light	2.96e-39
38	643	68.6	112	14	R79158	Human IgE receptor-bi	3.53e-39
39	641	68.4	239	16	R79866	Anti-EGFR single chai	5.01e-39
40	639	68.2	212	10	R52659	Porphyrin antibody li	7.12e-39
41	637	68.0	599	16	R90837	3B1 single chain anti	1.01e-38
42	635	67.8	110	10	R60810	Light chain variable	1.44e-38
43	635	67.8	112	15	R79156	Human IgE receptor-bi	1.44e-38
44	635	67.8	113	16	R79891	Anti-EGFR antibody li	1.44e-38
45	633	67.6	133	10	R59511	Sequence of the light	2.04e-38

## ALIGNMENTS

RESULT 1  
ID R70189 standard; Protein; 132 AA.  
AC R70189;  
DT 20-SEP-1995 (first entry)  
DE Mouse MAB 3B9 light chain.  
KW Chimeric antibody; humanized antibody; antibody engineering;  
KW monoclonal antibody; MAB; interleukin-4; IL-4; allergy.  
OS Mus sp.  
FH Key Location/Qualifiers  
FT Peptide 1..20  
FT /label= Sig\_peptide  
FT Region 44..58  
FT /label= CDR  
FT /note= \*complementarity determining region\*  
FT Region 74..80  
FT /label= CDR  
FT /note= \*complementarity determining region\*  
FT Region 113..121  
FT /label= CDR  
FT /note= \*complementarity determining region\*  
PN W09507301-A.  
PD 16-MAR-1995.  
PF 07-SEP-1994; U10308.  
PR 07-SEP-1993; US-117366.  
PR 14-OCT-1993; US-136783.  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
PA (SMIK ) SMITHKLINE BEECHAM PLC.

Mar 18 10:00

US-08-612-929-2.rag

3

PI Gross MS, Holmes SD, Sylvester DR;  
DR WPI; 95-123387/16.  
DR N-PSDB; Q83490.  
PT Chimeric and humanised IL-4 monoclonal antibodies (mabs), derived  
PT from high affinity mabs - useful in treatment of IL-4-mediated  
PT and IgE-mediated allergic conditions  
PS Disclosure; Fig.1; 97pp; English.  
CC Spleen cells from mice immunized with human IL-4 were used to prepare  
CC hybridomas, which were screened for anti-IL-4 MAb secretion. Only  
CC clone 3B9 was positive. cDNA clones of the 3B9 light and heavy  
CC chains were cloned into pCEW1f+ and transformed into E. coli  
CC DH5-alpha. The clones were sequenced (Q83490-91), and used for  
CC antibody engineering.  
SQ Sequence 132 AA;

Query Match 100.0%; Score 937; DB 13; Length 132;  
Best Local Similarity 100.0%; Pred. No. 9,23e-62;  
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 metdtilllwllwvpgstgdivltqspaslavslgqratisckasqsvdydgsymny 60  
|||||  
Qy 1 METDTILLWVLLWVPGSTGDIVLTQSPASLAVSLGQRATISCKASQSDYDGDSTYNNY 60  
|||||

Db 61 qkpgqppklliyaasnlesgiparfsgsgtdftlnihpveedaatyccgsedpp 120  
|||||  
Qy 61 QQKPGQPPLLIYAASNLESIGIPARFSGSGTGDTFTLNHPVEEDAATYCCQSNEDPP 120  
|||||

Db 121 tfgggtkleik 132  
|||||  
Qy 121 TFGGGTKLEIK 132  
|||||

RESULT 2

ID R32123 standard; Protein; 131 AA.  
AC R32123;  
DT 02-JUN-1993 (first entry)  
DE Anti-CD4 antibody MT 3.10 light chain variable region.  
KW Immunosuppression; tissue transplantation; graft; I chain; V region;  
KW T-helper cell inhibition; transplant rejection; Mab;  
KW interleukin-2 receptor.  
FH Key Location/Qualifiers  
FT Peptide 1..20  
FT /label= signal 21..120  
FT Region  
FT /label= Variable  
FT Region 121..131  
FT /label= J1  
PN DE4143214-A.  
PD 28-JAN-1993.  
PF 30-DEC-1991; 143214.  
PR 25-JUL-1991; DE-124759.  
PR 30-DEC-1991; DE-143214.  
PA (BOEF) BOEHRINGER MANNHEIM GMBH.  
PI Kaluza B, Riettmüller G, Scheuer W, Weidle U;  
DR WPI; 93-037582/05.  
DR N-PSDB; Q36609.  
PT Synergistic antibody compsn. for use as immunosuppressant -  
PT comprises monoclonal anti-CD4 antibodies and monoclonal anti-IL2R  
PT alpha- or anti-IL2R beta antibodies  
PS Claim 5; Page 11; 18pp; German.  
CC This sequence is the light chain variable region of a preferred  
CC anti-CD4 monoclonal antibody for use in the claimed synergistic  
CC composition. Mab MT 3.10 is deposited as clone 3.101/sB10 (ECACC  
CC 90090702). The anti-CD4 antibody is used with at least one anti-IL2R

Mar 18 10:00

US-08-612-929-2.rag

4

CC alpha or beta antibody. Individually the antibodies are strongly  
CC inhibiting and when used together their immunosuppressive properties  
CC are improved; they synergistically inhibit T-helper cell  
CC proliferation to effectively inhibit transplant rejection at low  
CC doses without significantly reducing the general immune response.  
CC See also Q36608-Q36616.  
SQ Sequence 131 AA;

Query Match 97.1%; Score 910; DB 6; Length 131;  
Best Local Similarity 96.9%; Pred. No. 1.12e-59;  
Matches 127; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 1 metdtilllwllwvpgstgdivltqspaslavslgqratisckasqsvdydgsymny 60  
|||||  
Qy 1 METDTILLWVLLWVPGSTGDIVLTQSPASLAVSLGQRATISCKASQSDYDGDSTYNNY 60  
|||||

Db 61 qkpgqppklliyaasnlesgiparfsgsgtdftlnihpveedaatyccgsedpp 120  
|||||  
Qy 61 QQKPGQPPLLIYAASNLESIGIPARFSGSGTGDTFTLNHPVEEDAATYCCQSNEDPP 120  
|||||

Db 121 tfgggtkleik 131  
|||||  
Qy 121 TFGGGTKLEIK 131  
|||||

RESULT 3

ID R04132 standard; protein; 131 AA.  
AC R04132;  
DT 06-SEP-1990 (first entry)  
DE Anti-Leu 3a light chain variable region gene product, 206 Vx.  
KW HIV; AIDS; anti-Leu3A; vaccine; ds.  
OS Mus musculus.  
PN EP-365209-A.  
PD 25-APR-1990.  
PF 11-OCT-1989; 010415.  
PR 17-OCT-1988; US-260558.  
PA (BECT) Becton Dickinson Co.  
PI Hinton R, Oi VT;  
DR WPI; 90-126329/17.  
DR N-PSDB; Q04039.  
PT New chimeric variants of murine antibody anti-leucine -  
PT contg. human antibody regions, and DNA encoding sequences.  
PS Claim 1; Fig 2; 12pp; English.  
CC Variants of murine monoclonal anti-CD4 antibody, anti-leu3A can be  
CC used to form chimeric mouse-variable, human-constant region Abs  
CC suggested as being useful as a vaccine to HIV.  
SQ Sequence 131 AA;

Query Match 96.6%; Score 905; DB 1; Length 131;  
Best Local Similarity 96.2%; Pred. No. 2.72e-59;  
Matches 126; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Db 1 metdtilllwllwvpgstgdivltqspaslavslgqratisckasqsvdydgsymny 60  
|||||  
Qy 1 METDTILLWVLLWVPGSTGDIVLTQSPASLAVSLGQRATISCKASQSDYDGDSTYNNY 60  
|||||

Db 61 qkpgqppklliyaasnlesgiparfsgsgtdftlnihpveedaatyccgsedpp 120  
|||||  
Qy 61 QQKPGQPPLLIYAASNLESIGIPARFSGSGTGDTFTLNHPVEEDAATYCCQSNEDPP 120  
|||||

Db 121 tfaggtkleik 131  
|||||  
Qy 121 TFGGGTKLEIK 131  
|||||

Mar 18 10:00

US-08-612-929-2.rag

5

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RESULT 4
ID P90543 standard; protein; 131 AA.
AC P90543;
DE 20-OCT-1989 (first entry)
KW Amino acids sequence of a V chi region gene.
OS V cji region; immunoglobulin; L chain variable region; HIV.
PN Mus musculus
PD EP-327000-A.
PF 09-AUG-1989; 101583.
PR 30-JAN-1988; JP-20255.
PR 08-JUL-1988; JP-171385.
PA The Chemo-Sero-Therapeutic Research Institute.
PI Maeda H, Eda Y, Kimachi K, Tokiyoshi S, Matsuhashita S, Hattori T,
PI Takatsuki K;
DR WP1; 89-229050/32.
DR N-PSDB; N90495.
PT Chimeric anti-human immune virus antibodies - contg. mouse variable
PT regions and human constant regions for diagnosis, treatment and
PT prevention of AIDS
PS Disclosure; Fig 8; 33pp; English.
CC The sequence is encoded by a V chi region gene (see N90495).
CC The sequence from Asp 21 encodes the L chain variable region.
SQ Sequence 131 AA;

Query Match 95.5%; Score 895; DB 1; Length 131;
Best Local Similarity 97.7%; Pred. No. 1.61e-58;
Matches 128; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 1 metdtllwllwvpgstgdlvtqspaslvslqgratiscraskvsgvdydgdsymw 60
QY 1 METDTLLWVLLWVPGSTGDIVLTQSPASLVSLGQRATISCKASQSDVDYDGSYNNWY 60

Db 61 qkqpgqpklliyaaaslesgiparfsgsgtdftlnihpveeedaatyycqgsnedpf 120
QY 61 QKPGQPPLLIYAASNLESIGIPARFSGSGTDFTLNIHPVEEEDAATYYCQGSNEDPP 120

Db 121 tfgggtkleik 131
QY 121 TFGGGTKLEIK 131

Query Match 95.5%; Score 895; DB 1; Length 131;
Best Local Similarity 97.7%; Pred. No. 1.61e-58;
Matches 128; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 1 metdtllwllwvpgstgdlvtqspaslvslqgratiscraskvsgvdydgdsymw 60
QY 1 METDTLLWVLLWVPGSTGDIVLTQSPASLVSLGQRATISCKASQSDVDYDGSYNNWY 60

Db 61 qkqpgqpklliyaaaslesgiparfsgsgtdftlnihpveeedaatyycqgsnedpf 120
QY 61 QKPGQPPLLIYAASNLESIGIPARFSGSGTDFTLNIHPVEEEDAATYYCQGSNEDPP 120

Db 121 tfgggtkleik 131
QY 121 TFGGGTKLEIK 131

RESULT 5
ID R28668 standard; protein; 131 AA.
AC R28668;
DE 30-MAR-1993 (first entry)
DE p12-k2.
KW Human; antibody; interleukin-6; receptor; IL-6R; light chain; L; H;
KW heavy chain; variable region; mouse; monoclonal; hybridoma; AUK12-20;
KW plasmid; p12-k2; p12-h2.
OS Synthetic.
FH Key Location/Qualifiers
FT Peptide 1..20
FT /note= "Signal peptide"
FT Protein 21..131
FT /note= "Mature peptide"
PN W09219759-A.
PD 12-NOV-1992.
PF 24-APR-1992; J00544.
PR 25-APR-1991; JP-095476.
PR 19-FEB-1992; JP-032084.
PA (CHUS ) CHUGAI SEIYAKU KK.
PI Bendig MM, Jones ST, Saldanha JW, Sato K, Tsuchiya M;
DR WP1; 92-398882/48.
DR N-PSDB; Q30757.
PT Reconstituted human antibody to human interleukin-6 receptor -
PT has low antigenicity and contains mouse V-region complementarity
PT determining regions
PS Disclosure; Page 124-125; 207pp; Japanese.
CC The sequences given in R29008-09 were encoded by plasmids which were
CC used in example to illustrate the production of a human antibody which
CC recognises human interleukin-6 receptor (IL-6R). The antibody
CC comprises light (L) chain and heavy (H) chain variable regions which
CC were derived from a mouse monoclonal antibody produced from the

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Mar 18 10:00

US-08-612-929-2.rag

6

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DR WP1; 92-398882/48.
DR N-PSDB; Q30753.
PT Reconstituted human antibody to human interleukin-6 receptor -
PT has low antigenicity and contains mouse V-region complementarity
PT determining regions
PS Disclosure; Page 118; 207pp; Japanese.
CC The sequences given in R28668-69 were encoded by plasmid sequences
CC which were used in example to illustrate the production of a human
CC antibody which recognises human interleukin-6 receptor (IL-6R). The
CC antibody comprises light (L) chain and heavy (H) chain variable
CC regions which were derived from a mouse monoclonal antibody produced
CC from the hybridoma AUK12-20 which contained the plasmids p12-k2 and
CC p12-h2.
SQ Sequence 131 AA;

Query Match 87.4%; Score 819; DB 6; Length 131;
Best Local Similarity 87.0%; Pred. No. 1.15e-52;
Matches 114; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

Db 1 mesdtllwllwvpgstgdlvtqspaslvslqgratiscraskvsgvdydgdsymw 60
QY 1 METDTLLWVLLWVPGSTGDIVLTQSPASLVSLGQRATISCKASQSDVDYDGSYNNWY 60

Db 61 qkqpgqpklliyaaaslesgiparfsgsgtdftlnihpveeedaatyycqgsrenpy 120
QY 61 QKPGQPPLLIYAASNLESIGIPARFSGSGTDFTLNIHPVEEEDAATYYCQGSNEDPP 120

Db 121 tfgggtkleik 131
QY 121 TFGGGTKLEIK 131

RESULT 6
ID R29008 standard; protein; 131 AA.
AC R29008;
DE 30-MAR-1993 (first entry)
DE p64-k4 protein product.
KW Human; antibody; interleukin-6; receptor; IL-6R; light chain; L; H;
KW heavy chain; variable region; mouse; monoclonal; hybridoma; AUK64-7;
KW plasmid; p64-k4; p64-h2.
OS Synthetic.
FH Key Location/Qualifiers
FT Peptide 1..20
FT /note= "Signal peptide"
FT Protein 21..131
FT /note= "Mature peptide"
PN W09219759-A.
PD 12-NOV-1992.
PF 24-APR-1992; J00544.
PR 25-APR-1991; JP-095476.
PR 19-FEB-1992; JP-032084.
PA (CHUS ) CHUGAI SEIYAKU KK.
PI Bendig MM, Jones ST, Saldanha JW, Sato K, Tsuchiya M;
DR WP1; 92-398882/48.
DR N-PSDB; Q30757.
PT Reconstituted human antibody to human interleukin-6 receptor -
PT has low antigenicity and contains mouse V-region complementarity
PT determining regions
PS Disclosure; Page 124-125; 207pp; Japanese.
CC The sequences given in R29008-09 were encoded by plasmids which were
CC used in example to illustrate the production of a human antibody which
CC recognises human interleukin-6 receptor (IL-6R). The antibody
CC comprises light (L) chain and heavy (H) chain variable regions which
CC were derived from a mouse monoclonal antibody produced from the

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CC hybridoma AUK64-7 which contained the plasmids p64-k4 and p64-h2.  
SQ Sequence 131 AA;

Query Match	87.1%;	Score 816;	DB 6;	Length 131;
Best Local Similarity	85.5%;	Pred. No. 1.96e-52;		
Matches 112:	Conservative	11;	Mismatches 8;	Indels 0;
	Gaps	0;		

```
Db      1 m e e d t l l l w l l l v p g s t g d i v l q s p a s l a v s l g q r a t i s c r a s e s v d y g n s f m h w y 60
        ||:::||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:||
Ov      1 M E E D T I L L W V L L V P G S T G D I V L Q S P A S L A V S L G O R A T I S C R A S O S V D Y D G S Y M N H Y 60
```

```

61 qqkqgppklllyrasnlesgiparfsgsgrtdftltinpveaddvatvycqgsnedpp 120
|||||
61 ookcpobkllvaasniescipafesgscstetninpveefdaatvycqgsnedpp 120
|||||

```

Db 121 tfgagtklelk 131  
|||:||||:|  
Qv 121 TFGGgTKLEIK 131

RESULT	7
ID	R05089 standard; protein; 131 AA.
AC	R05089;
DT	04-OCT-1990 (first entry)
DE	Light chain variable domain of human chorion gonadotrophin-binding prot.
KW	Human chorionic gonadotropin; antibodies; choriocarcinoma; abortion;
KW	tumour detection; complementary determining regions;
KW	pregnancy prevention; light chain.
OS	Mus musculus.

Key	Location/Qualifiers
FT	Binding-site 44..58
FT	/label=CDR
FT	Binding-site 74..80
FT	/label=CDR
FT	Binding-site 113..120
FT	/label=CDR
PN	EP-370581-A.
PD	30-MAY-1990.
PF	21-NOV-1989; 202951.
PR	25-NOV-1988; NL-002902.
PA	(ALKU) AKZO NV.
PI	van Wezenbeek PM;
DR	WPI; 90-165307/22.
DR	N-PSDB; Q04694.
PT	Polypeptide(s) which specifically bind human chorionic gonadotropin -
PT	contg. antigen-binding domains comprising complementary
PT	determining domains.
PS	Disclosure; p; English.
CC	Together with the heavy chain variable domain (R05090) the sequence forms
CC	a hCG-binding antibody fragment (PhCG). For the production of Abs
CC	the variable region was fused to a constant region of human origin.
CC	The product can be used to prevent pregnancy or for combatting
CC	choriocarcinomas or other hCG-producing tumours.
CC	They also have diagnostic applications as immune reagents for in vivo
CC	diagnosis, eg for localisation of tumours and for in vitro diagnosis for
CC	detection of hCG in body fluids.
SQ	Sequence 131 AA;

Query Match 85.5%; Score 801; DB 1; Length 131;  
Best Local Similarity 82.4%;  
Pred. No. 2.78e-51;  
Matches 108; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

```
Db 1 mekdtllllwllwpgsgdivltqspaslavslqqratvscraseevdnqisfmwf 60
|| ||:|||||||||||||||||||||||||||:||||:|:||||:|:||||:
```

OV 1 METDTILLWVLLWVPGSTGDIVLTQSPASLA VSLGQRATISCKASQSVVDYDGSYMNWY 60

```
Db      61 qakpgppklliyaasiqsgsvparfsgsgstdfslnihpmeeddtamfcqqikevpp 120
        |||||
Ow      61 ookpgoppkllyaaSNIESGIPARESGSGTDTLNHPVEEDAAVYCOOSNEDPP 120
```

Qy 61 QQKPQQPKLLIYAASNLSESGIPARFSGSGTDTLNIHPVEEDAATYYCQSQSNEDPP 120

Db 121 tfgggtkkleik 131

Db 121 tfgggtkleik 131  
| | | | | | | |  
Qy 121 TFGGgTKLEIK 131

## RESULT

RESOLUTION

ID	R30881 standard; Protein; 131 AA.
AC	R30881;
DT	10-MAY-1993 (first entry)
DE	Antibody 4A2 light chain constant region.
FE	Fd'; fragment; human; 4A2; constant region; Fab'; F(ab') <sub>2</sub> ; antibody;
KW	light chain; primer.
OS	Mus musculus.

992

PF	15-JUN-1992; U04976.
PR	14-JUN-1991; US-714175.
PA	(XOMA ) XOMA CORP.
PI	Better MD, Carroll S, Horwitz AH;
DR	WPI: 93-017909/02.
DR	P-FSDB; Q34575.
PT	Polynucleotide sequences encoding Fab' and F(ab') <sub>2</sub> fragments -
PT	used to produce, e.g. antibody-ricin A chain immuno:toxin(s)
PT	Disclosure; Fig 10; 92pp; English.
PS	This sequence represents the light chain constant domain (CL) from
CC	mouse antibody 4A2. This sequence was used in conjunction
CC	with the Fd' sequences given in Q34567-72 to produce chimeric Fd'
CC	vectors.
SQ	Sequence 131 AA;

Query Match 84.3%; Score 790; DB 6; Length 131;  
Best Local Similarity 84.0%; Pred. No. 1.95e-50;  
Matches 110; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

```

Db      1 mesdtlllwlwpgsgdivltqsgaslawslqratiscrasseveygtslmqwy 60
      ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
      1 mntmrttllvlllwmrctctnvl tgcgacst avsi cdpatt scfka scsmvncnsvmny 60

```

**Db**     qkqpgtpbklliyaanvesvypar fsqsgstdfslnhpveedi amvfqqgarkvpw 120  
         ||||| :||||:||||| :||||| :||||| | :||||| -  
**Ov**     ooxpgopkllyaa snfsgtgar fssgsctdt ln lhpveedaaty coosnepp 120

Db 121 tfgggtkleik 131  
 |||||  
 Ov 121 tEGCGTKLEIK 131

## RESULT

RESULT	9
ID	R10920 standard; Protein; 132 AA.
AC	R10920;
DT	08-MAY-1991 (first entry)
DE	kappa light chain variable region of T84.66 monoclonal antibody
KW	MAB T84.66; kappa light chain; carcinoembryonic antigen; CEA;
OS	human adenocarcinoma; mouse-human chimaeric antibody.
KS	Mus musculus.
FH	Key
FT	Location/Qualifiers
ET	Peptide 21..38
	/label= tryptic peptide

PT diseases  
PS Disclosure; Page 30-31; 46pp; English.  
CC The sequence is that of the 4C10 anti-idiotype Ab light chain V region  
CC which was used in the construction of a murine/human monoclonal  
CC anti-idiotype antibody (MA1A). The MA1A elicits an anti-ganglioside  
CC response and produces antibodies which induce cytotoxic destruction  
CC of cancer cells bearing the gangliosides. It can be used for treating  
CC cancers partic. melanomas. It can also be used as an immunomodulator to  
CC enhance anti-cancer immunity, suppress organ transplant rejection and  
CC suppress autoimmune disease. The MA1A can also be used in the diagnosis  
CC of cancers.  
SQ Sequence 132 AA;

Query Match	82.8%;	Score 776;	DB 7;	Length 132;
Best Local Similarity	83.3%;	Pred.No. 2.32e-49;		
Matches	110;	Conservative 10;	Mismatches 11;	Indels 1; Gaps 1;
Db	1	metctllwlllwpvgtdgdlvtgspaslavslgratmcraesvdsyvnafmhwy 60      :     :     :     :     :     :     :     :     :     :		
Qy	1	METDTLLWLLWPVGSTGDIIVLTGPASLAVSLGRATISCKASQSDYDGDYSNNWY 60      :     :     :     :     :     :     :     :     :     :		
Db	61	qkqpgppklliyraklesqiparfsgsestfdtltlnpveadadvatyvcqsenedpt 120      :     :     :     :     :     :     :     :     :     :		
Qy	61	QQKQPQPKLLIYAANLESIPARFSGSGGTDFTLNHPVEEDAAITYCQSNEPPP 120      :     :     :     :     :     :     :     :     :     :		
Db	121	wfgggwkleik 132      :		
Qy	121	-TFGGGTLEIK 131      :		

RESULT	11	
ID	R74967	standard; Protein; 130 AA.
AC	R74967;	
DE	02-FEB-1996	(first entry)
DT	Anti-idiotypic antibody Idio20 clone 20KB1.	
KW	Antibody; cancer; CDR; heavy chain; light chain; immunoglobulin;	
KW	complementarity determining region.	
OS	Mus sp.	
FH	Key	Location/Qualifiers
FT	Peptide	1..20
FT	/label= signal_peptide	
PN	J07101999-A.	
PD	18-APR-1995.	
PF	06-OCT-1993; 272950.	
PR	06-OCT-1993; JP-272950.	
PA	(HAGI/) HAGIWARA Y.	
WPI	95-182987/24.	
DR	N-PSDB; Q90432.	
PT	Novel anti-idiotypic antibody against an human anticancer monoclonal	
PT	antibody - and DNA sequences encoding the antibody, useful in	
PT	pharmacology, medicine and biochemical fields.	
PS	Example 5; Page 20; 28pp; Japanese.	
CC	R74960-R74969 are clones of the anti-idiotypic antibodies Idio3, Idio17,	
CC	Idio20, Idio27 and Idio33 against a human anticancer monoclonal antibody.	
CC	These antibodies and DNA encoding them are useful in pharmacological,	
CC	medical and biochemical fields of research.	
SQ	Sequence	130 AA;

```

Query Match      81.9%; Score 767; DB 14; Length 130;
Best Local Similarity 83.2%; Pred. No. 1.14e-48;
Matches 109; Conservative 9; Mismatches 12; Indels 1; Gaps 1;

Db 1 metcdllllwllwpqgtgdvltqpsalavlgqratsyrasksvstegsyymhwn 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

FT	/note= "sequenced as peptide fragment"	
FT	Region	44..57
FT	/label= complementarity determining region	
FT	Region	70..80
FT	/label= complementarity determining region	
FT	Region	110..121
FT	/label= complementarity determining region	
PN	W09101990-A.	
PD	21-FEB-1991.	
PF	19-JUL-1990; U04049.	
PR	26-JUL-1989; US-385102.	
PA	(CITY ) CITY OF HOPE.	
PI	Shively JE, Riggs AD, Neumaier M;	
PI	WPI; 91-073486/10.	
DR	N-PSDB; Q10834.	
PT	Novel anti-CEA antibody - comparable to ATCC Accession No. BH	
PT	8747, produced by recombinant DNA, used in diagnosis of tumours	
PS	Claim 4; Page 18; 24pp; English.	
CC	The light chain variable region of murine MA8 84.66 was cloned and	
CC	sequenced. It was used to produce mouse V-human C antibodies with high	
CC	affinity for CEA. Chimaeric murine-human anti-CEA Abs are used to	
CC	diagnose human colon adenocarcinomas.	
CC	See also Q11098 and Q10835-Q10848.	
SQ	Sequence	132 AA;

Query Match	84.2%;	Score 789;	DB 3;	Length 132;
Best Local Similarity	82.6%;	Pred. No. 2,33e-50;		
Matches	109;	Conservative 12;	Mismatches 11;	Indels 0; Gaps 0;
Db	1 metcdllwlllwpgetgdlvtgspaslvelglgratmcrcagesvdifvgflhw 60      :     :     :     :     :     :     :     :     : 1 METDTILLWLLWPSTGTDVILVTSPASLAVSIGQRATISCKASQSDVDYDGSYMWNY 60			
Qy	61 qkqpgppkllyraenlesgiprfsgtqrtdftliidpveadvatyyccqtnepy 120      :     :     :     :     :     :     :     :     :			
Db	61 QKPGPPKLIIYAENLESIGIPARFSGSGGTDFTLIHPVEEEDAATYYCQSNEDPP 120      :     :     :     :     :     :     :     :     :			
Qy	121 tfgggtkleir 132      :     :     :     :     :     :     :     :     :			
Db	121 TFGGGTKLEIKR 132      :     :     :     :     :     :     :     :     :			

RESULT	10
ID	R37716 standard; Protein; 132 AA.
AC	R37716;
DT	30-SEP-1993 (first entry)
DE	Mouse 4C10 anti-idiotypic Ab light chain V region.
KW	MAIA; monoclonal antibody; hybridoma; organ transplant rejection; immuno-modulator; cancer; treatment; diagnosis; melanoma; anti-cancer immunity; enhancement; suppression. Mus musculus.
OS	Mus musculus.
FH	Key Location/Qualifiers
FT	Misc difference 31
FE	/note= "Thr -> Ser, from PCR substituted gene"
PN	W09310221-A.
PD	27-MAY-1993.
PF	12-NOV-1992; U10166.
PR	13-NOV-1991; US-791934.
PA	(REGC ) UNIV CALIFORNIA.
P1	Hastings A, Irie RF, Morrison SL.
DR	WPI; 93-182538/22.
PT	Chimeric murine-human anti-idiotypic monoclonal antibodies - useful as immuno-modulators for treating and diagnosing cancers, and for suppressing organ transplant rejection and auto-immune

Qy 1 METDTLLWLLWVDCSTGDIVLTQSPASLASVIGQRATISCKASQSDYDGDSDYNNWY 60

Db 61 cqrpgqprlllylvnldsgvparsfgsgtqdfntlnhpveeedaatyycqhi-egay 119  
||:||||:|||| ||:||||:||||:||||:||||:||||:||||:||||: ||:

Qy 61 QQRPGQPKLLIYAASNLESIGPARFSGSGTQDFTLNHPVEEEDAATYYCQSNEDPP 120

Db 120 tfgggtkleik 130  
|||||

Qy 121 TFGGGTKLEIK 131

## RESULT 12

ID R55123 standard; Protein; 111 AA.

AC R55123;

DT 27-JAN-1995 (first entry)

DE Mouse anti-HIV mu5.5 light chain variable region.

KW Immunoglobulin; heavy chain; anti-HIV antibody; neutralisation;

KW human immunodeficiency virus; variable region; VH chain; murine.

OS Mus musculus.

FH Key Location/Qualifiers

FT Region 1..23

FT /label= FR1

FT /label= FR2 24..38

FT /label= CDR1

FT /label= FR2 39..53

FT /label= FR2 54..60

FT /label= CDR2 61..92

FT /label= FR3 93..101

FT /label= CDR3 102..111

FT /label= FR4

PN J06125783-A.

PD 10-MAY-1994.

PF 28-DEC-1991; JP-359808.

PR (KAGA-) 2H KAGAKU KESSEI-RYOHO KENKYUSHO.

DR WPI; 94-187942/23.

DR N-PSDB; 065554.

PT Mouse-human chimeric anti-HIV antibody heavy and light chains -

PT and recombinant antibody consisting of the H- and L-chains,

PT useful in AIDS therapy

PS Example 3; Fig 4; 22pp; Japanese.

CC Murine monoclonal antibodies mu 39.1 and mu 5.5 both neutralise HIV.

CC The heavy and light chain variable regions from these antibodies

CC were sequenced (R55120-R55123). The murine anti-HIV CDRe were

CC introduced into human framework regions to construct chimeric

CC antibodies (R55124-R55127).

SQ Sequence 111 AA;

Query Match 79.7%; Score 747; DB 10; Length 111;

Best Local Similarity 98.2%; Pred. No. 3.90e-47;

Matches 109; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 1 divltqspaslasvlgqratisckasqsdvtdgdsgymnwYQQRPGQPKLLIYAASNLES 60  
|||||

Qy 21 DIVLTQSPASLASVIGQRATISCKASQSDYDGDSDYNNWYQQRPGQPKLLIYAASNLES 80

Db 61 gparfsgsgtdftlnhpveeedaatyycqsnedpwtfgggtkleik 111  
|||||

Qy 81 GIPARFSGSGTDFTLNHPVEEEDAATYYCQSNEDPPTFGGGTKLEIK 131

## RESULT 13

ID R60302 standard; Protein; 111 AA.

AC R60302;

DT 09-MAR-1995 (first entry)

DE Anti HIV antibody light chain variable region.

KW Antibody; heavy chain; light chain; human immunodeficiency virus;

KW HIV; acquired immune deficiency syndrome; AIDS; treatment;

OS Mus musculus.

FH Key Location/Qualifiers

FT Region 1..23

FT /label= Framework region 1.

FT /label= CDR1. 24..38

FT /label= CDR1. 39..53

FT /label= Framework region 2.

FT /label= CDR2. 54..60

FT /label= Framework region 3.

FT /label= CDR3. 93..101

FT /label= CDR3. 102..111

FT /label= Framework region 4.

PN W09415969-A.

PD 21-JUL-1994.

PF 14-JAN-1993; J00039.

PR 14-JAN-1993; AU-032671.

PR 14-JAN-1993; WO-J00039.

PA (KAGA) CEMO SERO THERAPEUTIC RES INST.

PI Eda Y, Kimachi K, Maeda H, Osatomi K, Shioaki K;

PI Tokiyoshi S;

DR WPI; 94-249145/30.

DR N-PSDB; Q70372.

PT Recombinant chimeric anti HIV antibody - useful for the treatment

PT and prevention of HIV

PS Claim 15; Figure 4; 51pp; Japanese.

CC The recombinant antibody light chain has neutralising activity

CC against HIV. Chimeric antibodies comprising both mouse and human

CC sequences are useful in the treatment/prevention of AIDS caused by

CC HIV.

SQ Sequence 111 AA;

Query Match 79.7%; Score 747; DB 11; Length 111;

Best Local Similarity 98.2%; Pred. No. 3.90e-47;

Matches 109; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 1 divltqspaslasvlgqratisckasqsdvtdgdsgymnwYQQRPGQPKLLIYAASNLES 60  
|||||

Qy 21 DIVLTQSPASLASVIGQRATISCKASQSDYDGDSDYNNWYQQRPGQPKLLIYAASNLES 80

Db 61 gparfsgsgtdftlnhpveeedaatyycqsnedpwtfgggtkleik 111  
|||||

Qy 81 GIPARFSGSGTDFTLNHPVEEEDAATYYCQSNEDPPTFGGGTKLEIK 131

## RESULT 14

ID P90541 standard; protein; 111 AA.

AC P90541;

DT 20-OCT-1989 (first entry)

DE Immunoglobulin L chain variable region.

KW Immunoglobulin; L chain variable region; HIV.

OS Mus musculus



Mar 18 10:00

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13

PN EP-327000-A.  
PD 09-AUG-1989.  
PF 30-JAN-1989; 101583.  
PR 30-JAN-1988; JP-20255.  
PR 08-JUL-1988; JP-171385.  
PA (\*\*\*\*) The Chemo-Sero-Therapeutic Research Institute.  
PI Maeda H, Eda Y, Kimachi K, Tokiyoshi S, Matsushita S, Hattori T,  
PI Takatsuki K;  
DR WPI; 89-229050/32.  
DR N-PSDB; N90491, N90492, N90493.  
PT Chimeric anti-human immune virus antibodies - contg. mouse variable  
PT regions and human constant regions for diagnosis, treatment and  
PT prevention of AIDS  
PS Claim 5; page 15; 33pp; English.  
CC The sequence is an L chain variable region from an immunoglobulin with  
CC anti-HIV neutralising activity. See N90491-3, and N90495.  
SQ Sequence 111 AA;

Query Match 78.3%; Score 734; DB 1; Length 111;  
Best Local Similarity 97.3%; Pred. No. 3.87e-46;  
Matches 108; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 1 divltqpaslavlqgratiscasqsdvdgdyymwyqkpgqppklliyaasnles 60  
|||||  
QY 21 DIVLTQSPASLAVSLGQRATISCKASQSDVDGDSYNNWYQKPGQPPKLLIYAASNLES 80  
|||||  
Db 61 giparfsgsgtrdftlnihpveedaatyccqnedpftfgsgtkleik 111  
|||||  
QY 81 GIPARFSGSGTDFTLNIHPVEEDAATYCCQSNEDPFTFGGTKLEIK 131  
|||||

RESULT 15

ID R74966 standard; Protein; 146 AA.  
AC R74966;  
DT 02-FEB-1996 (first entry)  
DE Anti-idiotype antibody Idio17 clone 17KB1.  
KW Antibody; cancer; CDR; heavy chain; light chain; immunoglobulin;  
KW complementarity determining region.  
OS Mus sp.  
FH Key Location/Qualifiers  
FT Peptide 1..13  
FT /label= signal\_peptide  
PN J0710199-A.  
PD 18-APR-1995.  
PF 06-OCT-1993; 272950.  
PR 06-OCT-1993; JP-272950.  
PA (HAGI/) HAGIWARA Y.  
DR WPI; 95-182987/24.  
DR N-PSDB; Q90431.  
PT Novel anti-idiotype antibody against an human anticancer monoclonal  
PT antibody - and DNA sequences encoding the antibody, useful in  
PT pharmacology, medicine and biochemical fields.  
PS Example 5; Page 19; 28pp; Japanese.  
CC R74960-R74969 are clones of the anti-idiotype antibodies Idio3, Idio17,  
CC Idio20, Idio27 and Idio33 against a human anticancer monoclonal antibody.  
CC These antibodies and DNA encoding them are useful in pharmacological,  
CC medical and biochemical fields of research.  
SQ Sequence 146 AA;

Query Match 77.6%; Score 727; DB 14; Length 146;  
Best Local Similarity 83.2%; Pred. No. 1.33e-45;  
Matches 104; Conservative 7; Mismatches 13; Indels 1; Gaps 1;

Db 1 lwvlllwpqsgtdvltqpaslavlqgrasivyraskavatsgyymhwnqkpgqp 60

Mar 18 10:00

US-08-612-929-2.rag

14

QY 8 LWVLLWPGSGTGDIVLTQSPASLAVSLGQRATISCKASQSDVDGDSYNNWYQKPGQP 67  
|||||  
Db 61 prlliylnlesgvparfsgsgtdftlnihpveedaatyccqhir-gaytfgggk 119  
|||||  
QY 68 PKLLIYAASNLESIGIPARFSGSGTDFTLNIHPVEEDAATYCCQSNEDPPTFGGGTK 127  
|||||  
Db 120 leikr 124  
|||||  
QY 128 LEIKR 132

Search completed: Tue Mar 18 10:02:18 1997  
Job time : 36 secs.

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TVAIQAELV (TM)  
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Mar 18 10:02:35 1997; MasPar time 4.29 Seconds  
604.294 Million cell updates/sec

Tabular output not generated.

Title: >US-08-612-929-4  
Description: (1-140) from US08612929, pep  
Perfect Score: 1018  
Sequence: 1 MNRITSSLLLIIPAVILSQ.....TVFYWFVDMGAGTTVTSS 140

Scoring table: PAM 150  
Gap 11

Searched: 52205 seqs, 18531385 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: swiss-prot33  
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10

Statistics: Mean 43.053; Variance 81.506; scale 0.528

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	602	59.1	147	4	HV2H_HUMAN IG HEAVY CHAIN PRECUR	2.25e-100
2	561	55.1	121	4	HV2E_HUMAN IG HEAVY CHAIN V-II R	1.24e-91
3	556	54.6	125	4	HV2D_HUMAN IG HEAVY CHAIN V-II R	1.43e-90
4	548	53.8	120	4	HV2B_HUMAN IG HEAVY CHAIN V-II R	7.17e-89
5	530	52.1	126	4	HV2A_HUMAN IG HEAVY CHAIN V-II R	4.68e-85
6	516	50.7	144	4	HV43_MOUSE IG HEAVY CHAIN PRECUR	4.27e-82
7	499	49.0	119	4	HV2C_HUMAN IG HEAVY CHAIN V-II R	1.64e-78
8	499	49.0	137	4	HV46_MOUSE IG HEAVY CHAIN PRECUR	1.64e-78
9	487	47.8	115	4	HV44_MOUSE IG HEAVY CHAIN PRECUR	5.49e-76
10	459	45.1	116	4	HV45_MOUSE IG HEAVY CHAIN PRECUR	4.04e-70
11	442	43.4	116	4	HV60_MOUSE IG HEAVY CHAIN PRECUR	1.47e-66
12	440	43.2	135	4	HV02_XENLA IG HEAVY CHAIN PRECUR	3.69e-66
13	427	41.9	122	4	HV3G_HUMAN IG HEAVY CHAIN V-III	1.85e-63

14	418	41.1	116	4	HV61_MOUSE IG HEAVY CHAIN PRECUR	1.36e-61
15	417	41.0	117	4	HV62_MOUSE IG HEAVY CHAIN PRECUR	2.18e-61
16	416	40.9	119	4	HV38_MOUSE IG HEAVY CHAIN V REGI	3.51e-61
17	410	40.3	136	4	HV16_MOUSE IG HEAVY CHAIN PRECUR	6.11e-60
18	402	39.5	136	4	HV01_XENLA IG HEAVY CHAIN PRECUR	2.73e-58
19	401	39.4	119	4	HV3I_HUMAN IG HEAVY CHAIN V-III	4.38e-58
20	399	39.2	123	4	HV24_MOUSE IG HEAVY CHAIN V REGI	1.13e-57
21	397	39.0	122	4	HV2I_MOUSE IG HEAVY CHAIN V REGI	2.92e-57
22	396	38.9	123	4	HV18_MOUSE IG HEAVY CHAIN V REGI	4.69e-57
23	395	38.8	123	4	HV19_MOUSE IG HEAVY CHAIN V REGI	7.53e-57
24	393	38.6	146	4	HV2I_HUMAN IG HEAVY CHAIN PRECUR	1.94e-56
25	392	38.5	121	4	HV3J_HUMAN IG HEAVY CHAIN V-III	3.11e-56
26	390	38.3	123	4	HV23_MOUSE IG HEAVY CHAIN V REGI	8.02e-56
27	390	38.3	123	4	HV22_MOUSE IG HEAVY CHAIN V REGI	8.02e-56
28	383	37.6	122	4	HV20_MOUSE IG HEAVY CHAIN V REGI	2.19e-54
29	380	37.3	117	4	HV03_CACR IG HEAVY CHAIN PRECUR	9.00e-54
30	379	37.2	117	4	HV2G_HUMAN IG HEAVY CHAIN V-II R	1.44e-53
31	379	37.2	122	4	HV3H_HUMAN IG HEAVY CHAIN V-III	1.44e-53
32	377	37.0	117	4	HV3O_HUMAN IG HEAVY CHAIN V-III	3.70e-53
33	373	36.6	119	4	HV40_MOUSE IG HEAVY CHAIN V REGI	2.43e-52
34	370	36.3	116	4	HV05_CARAU IG HEAVY CHAIN PRECUR	9.95e-52
35	370	36.3	123	4	HV25_MOUSE IG HEAVY CHAIN V REGI	9.95e-52
36	369	36.2	119	4	HV37_MOUSE IG HEAVY CHAIN V REGI	1.59e-51
37	368	36.1	117	4	HV13_MOUSE IG HEAVY CHAIN V REGI	2.55e-51
38	367	36.1	129	4	HV2F_HUMAN IG HEAVY CHAIN V-II R	4.07e-51
39	367	36.1	144	4	HV26_MOUSE IG HEAVY CHAIN PRECUR	4.07e-51
40	365	35.9	119	4	HV3N_HUMAN IG HEAVY CHAIN V-III	1.04e-50
41	362	35.6	115	4	HV3F_HUMAN IG HEAVY CHAIN V-III	4.24e-50
42	361	35.5	118	4	HV39_MOUSE IG HEAVY CHAIN V REGI	6.78e-50
43	361	35.5	136	4	HV2C_RABIT IG HEAVY CHAIN PRECUR	6.78e-50
44	360	35.4	126	4	HV3K_HUMAN IG HEAVY CHAIN V-III	1.08e-49
45	359	35.3	117	4	HV12_MOUSE IG HEAVY CHAIN V REGI	1.73e-49

#### ALIGNMENTS

RESULT 1  
ID HV2H\_HUMAN STANDARD; PRT; 147 AA.  
AC P04438;  
DT 13-AUG-1987 (REL. 05, CREATED)  
DT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)  
DE 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)  
DE IG HEAVY CHAIN PRECURSOR V-II REGION (SESS).  
OS HOMO SAPIENS (HUMAN).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; PRIMATES.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 84298107.  
RA TAKAHASHI N., NOMA T., HONJO T.;  
RL PROC. NATL. ACAD. SCI. U.S.A. 81:5194-5198 (1984).  
DR PIR; A02090; GZHU.S.  
DR HSP; P01772; IGBB.  
KW IMMUNOGLOBULIN V REGION; SIGNAL.  
FT SIGNAL 1 19  
FT CHAIN 20 147 IG HEAVY CHAIN V-II REGION (SESS).  
FT DOMAIN 20 118 V SEGMENT.  
FT DOMAIN 119 132 D SEGMENT.  
FT DOMAIN 133 147 J SEGMENT.  
FT NON TER 147 147  
SQ SEQUENCE 147 AA; 16323 MW; 0994FF54 CRC32;  
Query Match 59.1%; Score 602; DB 4; Length 147;  
Best Local Similarity 66.7%; Pred. No. 2.25e-100;





RESULT 8  
 ID HV46 MOUSE STANDARD; PRT; 137 AA.  
 AC P01822;  
 DT 21-JUL-1986 (REL. 01, CREATED)  
 DT 01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)  
 DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)  
 DE IG HEAVY CHAIN PRECURSOR V REGION (MOPC 315).  
 OS MUS MUSCULUS (MOUSE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; RODENTIA.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 89238351.  
 RA RINFRET A., HORNE C., DORRINGTON K.J., KLEIN M.;  
 RL MOL. IMMUNOL. 26:431-434(1989).  
 RN [2]  
 RP SEQUENCE OF 1-31.  
 RX MEDLINE; 78094475.  
 RA JILKA R.L., PESTKA S.;  
 RL PROC. NATL. ACAD. SCI. U.S.A. 74:5692-5696(1977).  
 RN [3]  
 RP SEQUENCE OF 1-21.  
 RX MEDLINE; 79148758.  
 RA SCHECHTER I., WOLF O., ZEMELL R., BURSTEIN Y.;  
 RL FED. PROC. 38:1839-1845(1979).  
 RN [4]  
 RP SEQUENCE OF 19-136.  
 RX MEDLINE; 74170779.  
 RA FRANCIS S.H., LESLIE R.G.Q., HOOD L., EISEN H.N.;  
 RL PROC. NATL. ACAD. SCI. U.S.A. 71:1123-1127(1974).  
 RN [5]  
 RP REVISION TO 53.  
 RX MEDLINE; 77244979.  
 RA HOOD L., MARCOLIES M.N., GIVOL D., ZAKUT R.;  
 RL UNPUBLISHED RESULTS, CITED BY:  
 RL PADLAN E.A., DAVIES D.R., PECHT I., GIVOL D., WRIGHT C.;  
 RL COLD SPRING HARB. SYMP. QUANT. BIOL. 41:627-637(1977).  
 CC -!- THIS ALPHA CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT HAS  
 CC ANTI-DINITROPHENYL ACTIVITY.  
 DR EMBL; M27638; G602707; -;  
 DR EMBL; X07880; G295908; -;  
 DR PIR; P10102; AVMS35.  
 DR HSP; P01789; 2FGH.  
 KW IMMUNOGLOBULIN V REGION; SIGNAL.  
 FT SIGNAL 1 18  
 FT CHAIN 19 137 IG HEAVY CHAIN V REGION (MOPC 315).  
 FT DOMAIN 19 48 FRAMEWORK 1.  
 FT DOMAIN 49 54 COMPLEMENTARITY-DETERMINING 1.  
 FT DOMAIN 55 68 FRAMEWORK 2.  
 FT DOMAIN 69 84 COMPLEMENTARITY-DETERMINING 2.  
 FT DOMAIN 85 116 FRAMEWORK 3.  
 FT DOMAIN 117 126 COMPLEMENTARITY-DETERMINING 3.  
 FT DOMAIN 127 137 FRAMEWORK 4.  
 FT DISULFID 40 114 BY SIMILARITY.  
 FT CONFLICT 15 15 G -> GG (IN G295908).  
 FT CONFLICT 15 15 G -> H (IN REF. 2).  
 FT CONFLICT 77 78 GY -> YG (IN REF. 4).  
 FT CONFLICT 102 102 N -> D (IN REF. 4).  
 FT CONFLICT 123 123 MISSING (IN REF. 4).  
 FT NON TER 137 137  
 SQ SEQUENCE 137 AA; 15399 MW; 155A5E8D CRC32;

Query Match 49.0%; Score 499; DB 4; Length 137;  
 Best Local Similarity 55.7%; Pred. No. 1.64e-78;  
 Matches 78; Conservative 27; Mismatches 32; Indels 3; Gaps 3;  
 Db 1 mkvlellylltaipg-insdvqlqesgpglvkpsqslscsvtgyisi-tegyfwnwlrq 58  
 QY 1 MNRLLTSSLLLLVPAVILSQVTLKESGPGILQPSQTLSTLTCFSGFSLSGMSGVSWIRQ 60  
 Db 59 fpmklewlgfikydgengynpelnkrvsitrdtsenqffliknsvttedatycagdn 118  
 QY 61 PSCKGLEMLAHIVDDDKRYNPSIKSLRLTISKDTSSNQVFLKITSVDTDATATVYCARRE 120  
 Db 119 dhly-yfdywgqgttlvtss 137  
 QY 121 TVFYFDFVWAGAGTTTVVSS 140  
 RESULT 9  
 ID HV44 MOUSE STANDARD; PRT; 115 AA.  
 AC P01820;  
 DT 21-JUL-1986 (REL. 01, CREATED)  
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DT 01-AUG-1992 (REL. 23, LAST ANNOTATION UPDATE)  
 DE IG HEAVY CHAIN PRECURSOR V REGION (PJ14).  
 OS MUS MUSCULUS (MOUSE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; RODENTIA.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 81012133.  
 RA SAKANO H., MAKI R., KUROSAWA Y., ROEDER W., TONEGAWA S.;  
 RL NATURE 286:676-683(1980).  
 DR PIR; A02095; HVMS14.  
 DR HSP; P01772; IFDE.  
 KW IMMUNOGLOBULIN V REGION; SIGNAL.  
 FT SIGNAL 1 19  
 FT CHAIN 20 115 IG HEAVY CHAIN V REGION (PJ14).  
 FT NON TER 115 115  
 SQ SEQUENCE 115 AA; 12447 MW; 6E782F62 CRC32;  
 Query Match 47.8%; Score 487; DB 4; Length 115;  
 Best Local Similarity 62.3%; Pred. No. 5.49e-76;  
 Matches 71; Conservative 21; Mismatches 16; Indels 6; Gaps 6;  
 Db 5 allfclvtfpccileqvlkpsqslscsvtgyisi-tegyfwnwlrqppqk 62  
 QY 7 SLL-LIV-PAVILSQVTLKESGPGILQPSQTLSTLTCFSGFSLSGMSGVSWIRQPSCK 64  
 Db 63 glewlgml-wgdgstdynsalrleiskdnksqvlkmsalqtdtdtaryyca 115  
 QY 65 GLEWLAHIWDDDKR-YNPSIKSLRLTISKDTSSNQVFLKITSVDTDATATVYCA 117  
 RESULT 10  
 ID HV45 MOUSE STANDARD; PRT; 116 AA.  
 AC P01821;  
 DT 21-JUL-1986 (REL. 01, CREATED)  
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)  
 DE IG HEAVY CHAIN PRECURSOR V REGION (MC101).  
 OS MUS MUSCULUS (MOUSE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; RODENTIA.  
 RN [1]

RP	SEQUENCE FROM N.A.	
RX	MEDLINE; 82075900.	
RA	KATAOKA T., NIKAIIDO T., MIYATA T., MORIYAKI K., HONJO T.;	
RL	J. BIOL. CHEM. 257:277-285(1982).	
DR	PIR; A02096; GIMS10.	
DR	PIR; A02096; GIMS10.	
DR	HSP; P01772; IFDL.	
KW	IMMUNOGLOBULIN V REGION; SIGNAL.	
FT	SIGNAL	1 19
FT	CHAIN	20 116
FT	NON TER	116 116
SQ	SEQUENCE	116 AA; 12593 MW; 982C2581 CRC32;
	Query Match	45.1%; Score 459; DB 4; Length 116;
	Best Local Similarity	57.9%;
	Matches	66; Conservative 24; Mismatches 20; Indels 4; Gaps 4;

[illegible]

RESULT	11
ID	HV60 MOUSE STANDARD; PRT; 116 AA.
AC	P18531;
DT	01-NOV-1990 (REL. 16, CREATED)
DT	01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
DT	01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE	IG HEAVY CHAIN PRECURSOR V REGION (M315).
OS	MUS MUSCULUS (MOUSE).
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC	EUTHERIA; RODENTIA..
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=BALB/CJ;
RX	MEDLINE; 89279149.
RA	LEVY N.S., MALPIERO U.V., LEBEQUE S.G., GEARHART P.J.;
RL	J. EXP. MED. 169:2007-2019(1989).
DR	PIR; JT0509; HVM531.
DR	HSP; P01825; IBAF.
KW	IMMUNOGLOBULIN V REGION; SIGNAL.
FT	SIGNAL 1 18
FT	CHAIN 19 116 IG HEAVY CHAIN V REGION (M315).
FT	DOMAIN 19 48 FRAMEWORK 1.
FT	DOMAIN 49 53 COMPLEMENTARITY--DETERMINING 1.
FT	DOMAIN 54 67 FRAMEWORK 2.
FT	DOMAIN 68 84 COMPLEMENTARITY--DETERMINING 2.
FT	DOMAIN 85 116 FRAMEWORK 3.
FT	DISULFID 40 114 BY SIMILARITY.
FT	NON TER 116 116
SO	SEQUENCE 116 AA: 13095 MW: 810F3E97 CRC32:

```
Query Match      43.4%; Score 442; DB 4; Length 116;
Best Local Similarity 55.9%; Pred. No. 1.42e-66;
Matches         66; Conservative   24; Mismatches 26; Indels    2; Gaps    2;

Db              1 mkvlslylkaipg-ilsvdqlqespglvkpsqsisltsvtgsy-i-tgyyywnwirq 58
               l:- :- :|||:|||||:- :|||:|||||:- |: ||| :|||| 
Qy             1 MWRLTSSLLIIPAVVLVSQTIVKESGFILOPSOTLSLTCSFGSLSTGCWVSHIRQ 60

Db             59 fpaeklemwavisydgannvnpslknsisritdstknaffklinsvttedatvcvar 116
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01: |||||: | | : |||||||:|:||||| | ||||: | | | |||||||||
61 PSCKGLEWLAHVTDDKRYNPSLKSRLLSKTSNQVFIKITSVDATATTYCAR 118

Qy      RESULT 12
ID       HV02 XENIA    STANDARD;   PRT;   135 AA.
AC       P20957;
DT       01-FEB-1991 (REL. 17, CREATED)
DT       01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
DE       01-FEB-1991 (REL. 17, LAST ANNOTATION UPDATE)
DT       IG HEAVY CHAIN PRFCURSOR V REGION (XIG14) (FRAGMENT).
OS       XENOPUS LAEVIS (AFRICAN CLAWED FROG).
OC       EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AMPHIBIA; ANURA.
[1]
RN       SEQUENCE FROM N.A.
RP       MEDLINE; 88176921.
RX       RA SCHWAGER J., MIKORYAK C.A., STEINER L.A.;
RL       PROC. NAT'L. ACAD. SCI. U.S.A. 85:2245-2249(1988).
DR       EMBL; J03632; G214330; -.
DR       PIR; B31933; B31933.
DR       HSSP; P01607; IFCV.
KW       IMMUNOGLOBULIN V REGION; SIGNAL.
FT       NON TER      1      1
FT       SIGNAL      <1      18
FT       CHAIN      19      135
FT       FT         135      135
SQ       SEQUENCE 135 AA; 15080 MW; D8327985 CRC32;

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[illegible]

RESULT 13

ID	HV3G HUMAN	STANDARD;	PRT;	122 AA.
AC	P01758;			
DT	21-JUL-1986	(REL. 01, CREATED)		
DT	21-JUL-1986	(REL. 01, LAST SEQUENCE UPDATE)		
DT	21-JUL-1986	(REL. 01, LAST ANNOTATION UPDATE)		
DE	IG HEAVY CHAIN V-III REGION	(CAM).		
OS	HOMO SAPIENS (HUMAN).			
OC	EUKARYOTA; METAZOA; CHORDATA;	VERTEBRATA; TETRAPODA; MAMMALIA;		
OC	EUTHERIA; PRIMATES.			
RN	[1]			
RP	SEQUENCE.			
RX	MEDLINE; 81013859.			
RA	LEHMAN D.W., PUTNAM F.W.;			
RL	PROC. NATL. ACAD. SCI. U.S.A. 77:3239-3243(1980).			
CC	-! THIS MU CHAIN WAS ISOLATED FROM THE PLASMA OF A PATIENT WITH			
CC	MACROGLOBULINEMIA.			
DR	PIR; A02051; M3HUM.			
DR	HSSP; P01607; 2FGM.			

KW	IMMUNOGLOBULIN V REGION.			PYRROLIDONE CARBOXYLIC ACID.	
FT	MOD RES	1			
FT	NON TER	122	122		
SQ	SEQUENCE	122 AA; 13668 MW; 4AF2E3D8 CRC32;			
	Query Match	41.9%; Score 427; DB 4; Length 122;			
	Best Local Similarity	47.6%; Pred. No. 1.85e-63;			
	Matches	59; Conservative 31; Mismatches 29; Indels 5; Gaps			
Dd	1 qvelvesggvvygzrlrslcaasgfttsnyam--hwvrqpqkgglewvavisybgbbk 58				
	: : : : :    :     :         :     : :				
Qy	20 QVTKESGGGLDPQSOTLSLCSFSGFSLSTSGMGVSIRQRSKGLEUAAHI-TWDDDK 78				
	:   :   :   :   : :   : :   :   :   :   :   :   :				
Dd	59 yyabsvkrfttiardbsktllylmalsraebtavycardplygybrafnymqqgtlv 118				
	:   :   :   :   : :   : :   :   :   :   :   :   :				
Qy	79 RYMPSLKRLTISKDTSSNQVFILTSVDTDATATYYCARRETVE---YWYDFWMGAGTTV 136				
	:   :   :   :   : :   : :   :   :   :   :   :   :				
Dd	119 tvss 122				
Qy	137 TVSS 140				

	RESULT	14	
ID	HV61 MOUSE STANDARD;	PRT; 116 AA.	
AC	P1853Z;		
DT	01-NOV-1990 (REL. 16, CREATED)		
DT	01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)		
DT	01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)		
DE	IG HEAVY CHAIN PRECURSOR V REGION (I843).		
OS	MUS MUSCULUS (MOUSE).		
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;		
OC	EUTHERIA; RODENTIA.		
RN	(1)		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=BALB/CJ;		
RX	MEDLINE; 89279149.		
RA	LEVY N.S., MALPIERO U.V., LEBECQUE S.G., GEARHART P.J.;		
RL	J. EXP. MED. 169:2007~2019(1989).		
CC	-/- THIS SEQUENCE BELONGS TO THE VH3660 SUBFAMILY.		
DR	PIR; JT0508; HVMS1B.		
DR	HSP; P01825; IBAF.		
KW	IMMUNOGLOBULIN V REGION; SIGNAL.		
FT	SIGNAL 1 18		
FT	CHAIN 19 116 IG HEAVY CHAIN V REGION (I843).		
FT	DOMAIN 19 48 FRAMEWORK 1.		
FT	DOMAIN 49 53 COMPLEMENTARITY-DETERMINING 1.		
FT	DOMAIN 54 67 FRAMEWORK 2.		
FT	DOMAIN 68 84 COMPLEMENTARITY-DETERMINING 2.		
FT	DOMAIN 85 116 FRAMEWORK 3.		
FT	DISULFD 40 114 BY SIMILARITY.		
FT	NON_TER 116 116		
SQ	SEQUENCE 116 AA; 13158 MW; 10E4EE67 CRC32;		

Query Match 41.1%; Score 418; DB 4; Length 116;  
Best Local Similarity 54.4%; Pred. No. 1.36e-61;  
Matches 62; Conservative 23; Mismatches 25; Indels 4; Gaps 3;

	62
Db	4 lllcllcfafgqilddvqlqesgpdllvkpcqelallctvtgyai--tsqyvwheirfpqan
	: --VUSQTLKESGCGCGLQLQSLSLUCSGFSLTSGMGVSIRPQSGK
QY	8 LLLL-IVPAY--VUSQTLKESGCGCGLQLQSLSLUCSGFSLTSGMGVSIRPQSGK
	63 klemwgyihysgntsynpelksisrldtsknqffllqvattedatyyycar
Db	65 GLEWLAHIYDDDKRRYNPSLKSRLLTIKSDTSNQNVFKITSVDTAADTYTCAR
QY	65 GLEWLAHIYDDDKRRYNPSLKSRLLTIKSDTSNQNVFKITSVDTAADTYTCAR

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RESULT 15
ID HV62 MOUSE STANDARD; PRT; 117 AA.
AC P18533;
DT 01-NOV-1990 (REL. 16, CREATED)
DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE 1G HEAVY CHAIN PRECURSOR V REGION (733).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RR STRAIN=BALB/CJ;
RX MEDLINE; 89279149.
RA LEVY N.S., MALIPIERO U.V., LEBECQUE S.G., GEARHART P.J.;
RL J. EXP. MED. 169:2007-2019(1989).
RR PIR: JTO510; HVM573.
DR HSP; P01825; 1BAF.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 18
FT CHAIN 19 117 1G HEAVY CHAIN V REGION (733).
FT DISULFID 40 115 BY SIMILARITY.
FT NON TER 117 117
SQ SEQUENCE 117 AA; 13223 MW; 47664D8E CRC32;

Query Match 41.0%; Score 417; DB 4; Length 117;
Best Local Similarity 51.7%; Pred. No. 2,18e-61;
Matches 61; Conservative 26; Mismatches 30; Indels 1; Gaps 1;

Db 1 mkmftllylttvpq-ilsdvlqesgplvkpsgialctctgtisittgnyrswirq 59
: : | | : | : | : | | | | : | | : | | : | : | : | | | |
Qy 1 MNRITSSLLLIIPAVQLSVQVTKESGFIQLPQSQTLSLTCFSFGSLSTSGMGVSWIRQ 60
: : | | : | : | : | | | | : | | : | | : | : | : | | | |

Db 60 fpnklewigivysaltsynpskpartitdrkknqfflemaltaedatcyycar 117
: : | | : | : | | | | | | | | | | | | : | : | | | | | | | |
Qy 61 PSCKGLEWLAHIYWDKDEYNPILKSRITISKDTSYSSNQVFLKITSVDVTDATATYYCAR 118

Search completed: Tue Mar 18 10:02:50 1997
Job time : 15 secs.

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Search completed: Tue Mar 18 10:02:50 1997  
Job time : 15 secs.







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Query Match 67.5%; Score 687; DB 5; Length 138;
Best Local Similarity 70.1%; Pred. No. 1.27e-66;
Matches 96; Conservative 19; Mismatches 20; Indels 2; Gaps 1;

Db 2 stllltipwlsqitlksqgtlvkptqtlktcsfsgfslstsgvgvqirgpgkt 61
   1:||||:|:||||:||||:|:|:||||:||||:|:|:||||:||||:|:|:||||:|
Qy 6 SULLLIPAVVLSQVTLKESGPGILQPSQTLSTLTCFSFGSLTSGMGVSWIRQPSGKG 65

Db 62 lewliaywdddkryspalksrlitktcdqngvltmndpvdtdatycahrpgiavt 121
   1:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
Qy 66 LEWLIHYWDDDKRYNPSIKSLRLITSKDTSNQVFLKITSVDTDATYYCARRETFYW 125

Db 122 ggnfdywgqgtlvtpvs 138
   11 11 11 11 11
Qy 126 --YFDVWGAGTTVTVSS 140

RESULT 6
ENTRY S09959 #type fragment
TITLE Ig heavy chain V-D-J region (31-9D) - mouse (fragment)
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 23-Mar-1993

ACCESSIONS S09959
REFERENCE S09955
#authors Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jaton, J.C.; Izui, S.
#journal Eur. J. Immunol. (1990) 20:771-777
#title Variable region sequences of pathogenic anti-mouse red blood cell autoantibodies from autoimmune NZB mice.
#cross-references MUID:90249328
#accession S09959
#molecule_type mRNA
#residues 1-121 #label REI
#cross-references EMBL:X51847
#length 121 #checksum 7852
SUMMARY

Query Match 66.2%; Score 674; DB 12; Length 121;
Best Local Similarity 77.7%; Pred. No. 5.05e-65;
Matches 94; Conservative 13; Mismatches 14; Indels 0; Gaps 0;

Db 1 qvtlksghvlgpqtllstlcsvgsfalsahmgvgwrrpsgkglewlaniwnddky 60
   1:||||:|:||||:||||:|:|:||||:||||:|:|:||||:||||:|:|:|
Qy 20 QVTIKESGPGILQPSQTLSTLTCFSFGSLTSGMGVSWIRQPSGKLEWLIHYWDDDKR 79

Db 61 ynsvlksrltvsdktenqvfllksavtdtdatycaciqvgdwfcdwgagtpvts 120
   1:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
Qy 80 YNPSLKSRLITSKDTSNQVFLKITSVDTDATYYCARRETFYWFYFDVWGAGTTVTVS 139

Db 121 s 121
   1
Qy 140 S-140

RESULT 7
ENTRY S18555 #type complete
TITLE Ig heavy chain - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 22-Apr-1995
ACCESSIONS S18555
REFERENCE S18551
#authors Shin, E.K.; Matsuda, F.; Nagaoka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, E.; Honjo, T.
```

```
#journal EMBO J. (1991) 10:3641-3645
#title Physical map of the 3' region of the human immunoglobulin heavy chain locus: clustering of antibody-related variable segments in one haplotype.
#cross-references MUID:92037524
#accession S18555
#status preliminary
#molecule_type DNA
#residues 1-119 #label SHI
#cross-references EMBL:X62111
GENETICS
#introns 16/1
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
SUMMARY #length 119 #molecular-weight 13230 #checksum 1886

Query Match 65.8%; Score 670; DB 5; Length 119;
Best Local Similarity 72.3%; Pred. No. 1.57e-64;
Matches 86; Conservative 21; Mismatches 12; Indels 0; Gaps 0;

Db 1 mdtlclstllltipswlsqitlksqgtlvkptqtlktctfsgfslstsgvgvqirg 60
   1:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Qy 1 MRRRLTSLLLLIPAVVLSQVTLKESGPGILQPSQTLSTLTCFSFGSLTSGMGVSWIRQ 60

Db 61 ppgkalewliaywdddkryspalksrlitktcdqngvltmndpvdtdatycahr 119
   1:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Qy 61 PSQKGLEWLIHYWDDDKRYNPSIKSLRLITSKDTSNQVFLKITSVDTDATYYCARR 119

RESULT 8
ENTRY A49442 #type fragment
TITLE Ig heavy chain V region (50.1) - mouse (fragment)
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jul-1995
ACCESSIONS A49442
REFERENCE A49442
#authors Stura, E.A.; Stanfield, R.L.; Fieser, G.G.; Silver, S.; Roguska, M.; Hincapie, L.M.; Simmerman, H.K.B.; Profy, A.T.; Wilson, I.A.
#journal Proteins (1992) 14:499-508
#title Crystallization, sequence, and preliminary crystallographic data for an antipeptide Fab 50.1 and peptide complexes with the principal neutralizing determinant of HIV-1 gp120.
#accession A49442
#status preliminary; not compared with conceptual translation
#molecule_type DNA
#residues 1-107 #label STU
#length 107 #checksum 9363
SUMMARY

Query Match 62.6%; Score 637; DB 12; Length 107;
Best Local Similarity 88.8%; Pred. No. 1.76e-60;
Matches 87; Conservative 4; Mismatches 6; Indels 1; Gaps 1;

Db 1 pgilqpsqtlstlcsfsgfslstsgvgvswirgsgkglewlahifwdgdkrynpelkar 60
   1:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
Qy 28 PGIQPSQTLSTLTCFSFGSLTSGMGVSWIRQPSGKLEWLIHYWDDDKRYNPSIKSR 87

Db 61 lkiskdtemqvflkitavtdtdatycaciqvg-egylw 97
   1:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
Qy 88 LTSKDTSSNQVFLKITSVDTDATYYCARRETFYW 125

RESULT 9
ENTRY B25913 #type fragment
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9

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RESULT 12
ENTRY
TITLE Ig heavy chain V region (M60) - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 21-Dec-1990 #sequence_revision 13-Sep-1991 #text_change
22-Apr-1995
ACCESSIONS A36005
REFERENCE A36005
#authors Schroeder Jr., H.W.; Wang, J.Y.
#journal Proc. Natl. Acad. Sci. U.S.A. (1990) 87:6146-6150
#title Preferential utilization of conserved immunoglobulin heavy
chain variable gene segments during human fetal life.
#cross-references MUID:90349571
#accession A36005
#status preliminary
#molecule_type mRNA
#residues 1-121 #label SCH
#cross-references G8:M34071
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
SUMMARY #length 121 #molecular-weight 13557 #checksum 6899

Query Match 56.2%; Score 572; DB 5; Length 121;
Best Local Similarity 68.6%; Pred. No. 1.51e-52;
Matches 83; Conservative 18; Mismatches 20; Indels 0; Gaps 0;

Db 1 evtlresgpkvptqtlitctlygfslstsgmcsvwrqpgkalewllaldwdddy 60
:|||||::: 1:|||||::: ||||| ||||| ||||| ||||| |||||
Qy 20 QVTIKESGPGILQPSQTLSLTCFSFGSLSTSGMGSWIRQPSGKGLEWLAHYWDDDKR 79
|:|||||::: ||| 1:|:| |||||::: |||||::: |||||::: |||||
Db 61 ystslkrltkiskdknqvltmtmdpvdtdatyycvhrhprt1-afdwgggtkvav 119
|:|||||::: ||| 1:|:| |||||::: |||||::: |||||::: |||||
Qy 80 YNPSLKSRLTISKDTSSNQVFIKITSVDTADTATYYCARRETVFYWFDWGAGTTTV 139
|:|||||::: ||| 1:|:| |||||::: |||||::: |||||::: |||||

Db 121 s 121
Qy 140 S 140

RESULT 13
ENTRY
TITLE G1HUHE #type complete
ORGANISM Ig heavy chain V-II region (He) - human
DATE #formal_name Homo sapiens #common_name man
#sequence_revision 07-May-1981 #text_change 16-Feb-1996
ACCESSIONS A02093
REFERENCE A02093
#authors Cunningham, B.A.; Pflumm, M.N.; Rutishauser, U.; Edelman,
G.M.
#journal Proc. Natl. Acad. Sci. U.S.A. (1969) 64:997-1003
#title Subgroups of amino acid sequences in the variable regions of
immunoglobulin heavy chains.
#cross-references MUID:70114712
#accession A02093
#molecule_type protein
#residues 1-121 #label CUN
COMMENT This gamma-1 chain was isolated from a myeloma protein.
GENETICS
#gene GDB:IGHV8
#map_position 14q32.33
#cross-references GDB:C00-128-528
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
FEATURE 1
#modified site blocked amino end (Gln) (probably
pyrrolidone carboxylic acid) #status experimental
#length 121 #molecular-weight 13483 #checksum 9601

SUMMARY
```

Mar 18 10:02

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10

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Query Match 55.1%; Score 561; DB 2; Length 121;
Best Local Similarity 60.7%; Pred. No. 3.29e-51;
Matches 74; Conservative 27; Mismatches 19; Indels 2; Gaps 2;

Db 1 qvtlkengptlvkptetltctlgslstsgmcsvwrqpgkalewllawlywdddk 60
|||||::: 1:|||||::: ||||| ||||| ||||| ||||| |||||
Qy 20 QVTIKESGPGILQPSQTLSLTCFSFGSLSTSGMGSWIRQPSGKGLEWLA-HIYWDDDK 78
|:|||||::: ||| 1:|:| |||||::: |||||::: |||||::: |||||
Db 61 rfpslksrltkvtrdtsknqvltmtmdpvdtdatyycvhrhprt1-afdwgggtkvav 119
|:|||||::: ||| 1:|:| |||||::: |||||::: |||||::: |||||
Qy 79 RNPISLKSRLTISKDTSSNQVFIKITSVDTADTATYYCARRETVFYWFDWGAGTTTV 138
|:|||||::: ||| 1:|:| |||||::: |||||::: |||||::: |||||

Db 120 ss 121
Qy 139 SS 140

RESULT 14
ENTRY
TITLE MHHUMC #type complete
ORGANISM Ig heavy chain V-II region (McE) - human
DATE #formal_name Homo sapiens #common_name man
14-Nov-1983 #sequence_revision 22-Nov-1983 #text_change
16-Feb-1996
ACCESSIONS A02092
REFERENCE A02092
#authors Gerber-Jenson, B.; Kazin, A.; Kehoe, J.M.; Scheffel, C.;
Erickson, B.W.; Litman, G.W.
#journal J. Immunol. (1981) 126:1212-1216
#title Molecular basis for the temperature-dependent insolubility of
cryoglobulins. X. The amino acid sequence of the heavy
chain variable region of McE.
#cross-references MUID:81118242
#accession A02092
#molecule_type protein
#residues 1-125 #label GER
#note this chain was derived from a monoclonal IgM
cryoimmunoglobulin

GENETICS
#gene GDB:IGHV8
#cross-references GDB:G00-128-528
#map_position 14q32.33
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS pyroglytamic acid
FEATURE 1
#modified_site pyrrolidone carboxylic acid (Gln) #status
experimental
SUMMARY #length 125 #molecular-weight 13783 #checksum 9697

Query Match 54.6%; Score 556; DB 2; Length 125;
Best Local Similarity 64.0%; Pred. No. 1.33e-50;
Matches 80; Conservative 21; Mismatches 20; Indels 4; Gaps 3;

Db 1 qitlkesgptlvkptetltctfsgfslstsgmcsvwrqpgkalewllawlywdddr 60
|:|||||::: 1:|||||::: ||||| ||||| ||||| ||||| |||||
Qy 20 QVTIKESGPGILQPSQTLSLTCFSFGSLSTSGMGSWIRQPSGKGLEWLAHYWDDDKR 79
|:|||||::: ||| 1:|:| |||||::: |||||::: |||||::: |||||
Db 61 ypslrsrltkgtktsrnqvltmtmdpvdsgtyfcahrppwfrftgnlgfdwgqgtl 120
|:|||||::: ||| 1:|:| |||||::: |||||::: |||||::: |||||
Qy 80 YNPSLKSRLTISKDTSSNQVFIKITSVDTADTATYYCARRET-VFY-WY--FDWGAGCTT 135
|:|||||::: ||| 1:|:| |||||::: |||||::: |||||::: |||||

Db 121 vtvs 125
Qy 136 VTSS 140
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Search completed: Tue Mar 18 10:03:53 1997  
Job time : 45 secs.



PI Gross MS, Holmes SD, Sylvester DR;  
DR WPI; 95-123387/16.  
DR N-PSDB; Q83491.  
PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived  
PT from high affinity mAbs - useful in treatment of IL-4-mediated  
PT and IgE-mediated allergic conditions  
PS Disclosure; Fig.2; 97pp; English.  
CC Spleen cells from mice immunized with human IL-4 were used to prepare  
CC hybridomas, which were screened for anti-IL-4 Mab secretion. Only  
CC clone 3B9 was positive. cDNA clones of the 3B9 light and heavy  
CC chains were cloned into pGEM7f+ and transformed into E. coli  
CC DH5-alpha. The clones were sequenced (Q83490-91), and used for  
CC antibody engineering.  
SQ Sequence 140 AA;

Query Match 100.0%; Score 1018; DB 13; Length 140;  
Best Local Similarity 100.0%; Pred. No. 1.29e-71;  
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 1 mnr1tssllllivpaylsgvtlksqgqilqpsqtlsltcfsqfslstsgmgvswirg 60  
|||||  
Qy 1 MNR1TSSLLLLIVPAYLISQVTLKESGPGILQPSQTLSTLTCFSFGFSLSTSGMGVSWIRQ 60  
Db 61 psgkglewlahiywdddkrynpelkrltiskdtsnqvflikitsvtdadtatycarretvfywy 120  
|||||  
Qy 61 PSKGLEWLAHIYWDKRYNPISKSRLLTISKDTSNQVFLKITSVDYDTADTATYTCARRE 120  
Db 121 tvfywyfdwagagtvtvss 140  
|||||  
Qy 121 TVFYWYFDWAGAGTTVTVSS 140

## RESULT 2

ID R70191 standard; Protein; 141 AA.  
AC R70191;  
DT 20-SEP-1995 (first entry)  
DE Chimeric antibody 3B9 heavy chain.  
KW Chimeric antibody; antibody engineering; monoclonal antibody;  
KW Mab; interleukin-4; IL-4; allergy.  
OS Homo sapiens; Mus sp.  
FH Key Location/Qualifiers  
FT Peptide 1..19  
FT /label= Sig\_peptide  
FT Region 51..57  
FT /label= CDR  
FT /note= "complementarity determining region"  
FT Region 72..87  
FT /label= CDR  
FT /note= "complementarity determining region"  
FT Peptide 120..130  
FT /label= CDR  
FT /note= "complementarity determining region"  
PN W09507301-A.  
PD 16-MAR-1995.  
PF 07-SEP-1994; U10308.  
PR 07-SEP-1993; US-117366.  
PR 14-OCT-1993; US-136783.  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
PA (SMIK ) SMITHKLINE BEECHAM PLC.  
PI Gross MS, Holmes SD, Sylvester DR;  
DR WPI; 95-123387/16.  
DR N-PSDB; Q83492.  
PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived  
PT from high affinity mAbs - useful in treatment of IL-4-mediated

PT and IgE-mediated allergic conditions  
PS Disclosure; Fig.3; 97pp; English.  
CC A human/mouse chimeric antibody heavy chain variable region was  
CC constructed (given in R70191) that contained the mouse anti-human  
CC IL-4 Mab 3B9 variable region including 3 CDRs (R70198-200) and a  
CC human antibody signal peptide (R70193). The construct was used  
CC for humanized antibody production.  
SQ Sequence 141 AA;

Query Match 88.8%; Score 904; DB 13; Length 141;  
Best Local Similarity 95.5%; Pred. No. 2.48e-62;  
Matches 128; Conservative 1; Mismatches 3; Indels 2; Gaps 1;  
Db 10 slllwisgav---gvtlksqgqilqpsqtlsltcfsqfslstsgmgvswirpsqgkl 67  
|||||  
Qy 7 SLLLIIVPAYVLISQVTLKESGPGILQPSQTLSTLTCFSFGFSLSTSGMGVSWIRQPSGKGL 66  
Db 68 ewlahiywdddkrynpelkrltiskdtsnqvflikitsvtdadtatycarretvfywy 127  
|||||  
Qy 67 EWLAHIYWDKRYNPISKSRLLTISKDTSNQVFLKITSVDYDTADTATYTCARRETVIFYWY 126  
Db 128 fdwagagtvtvss 141  
|||||  
Qy 127 FDWAGAGTTVTVSS 140

## RESULT 3

ID R54092 standard; Protein; 143 AA.  
AC R54092;  
DT 29-DEC-1994 (first entry)  
DE Sequence of mouse VH showing the sequences of recombinant  
DE anti-FHV-1 antibody CDRs 1, 2 and 3.  
KW Feline herpes virus; FHV-1; monoclonal antibody; CDR;  
KW complementarity determining region.  
OS Mus musculus.  
FH Key Location/Qualifiers  
FT Peptide 1..19  
FT /label= leader  
FT Region 20..47  
FT /label= FR1  
FT Region 48..56  
FT /label= CDR1  
FT Region 57..70  
FT /label= FR2  
FT Region 71..86  
FT /label= CDR2  
FT Region 87..118  
FT /label= FR3  
FT Region 119..132  
FT /label= CDR3  
FT Region 133..143  
FT /label= FR4  
PN W09412661-A.  
PD 09-JUN-1994.  
PF 25-NOV-1993; J01724.  
PR 28-NOV-1992; JP-341255.  
PA (KAGA ) CHEMO SERO THERAPEUTIC RES INST.  
PA Kimachi K, Maeda H, Nishiyama K, Tokiyoshi S;  
DR WPI; 94-200288/24.  
DR N-PSDB; Q64166.  
PT Feline monoclonal antibody and recombinant antibodies specific  
PT for FHV-1 - for detection, treatment and prevention of FHV-1  
PT infection.  
PS Disclosure; Page 17-18; 53pp; Japanese.

CC The inventors claim a monoclonal antibody against feline herpes  
CC virus (FHV-1). They also claim a recombinant antibody against FHV-1  
CC and fragments of VH and VL CDR1, CDR2 and CDR3. The antibodies are  
CC used in the detection, treatment and prevention of FHV-1. The  
CC sequences of the CDRs in the VH of the recombinant anti-FHV-1  
CC antibody are given in R54092. The sequences of the CDRs in the VL of  
CC the recombinant anti-FHV-1 antibody are given in R54093. These CDR  
CC sequences are claimed.  
SQ Sequence 143 AA;

Query Match 80.5%; Score 819; DB 10; Length 143;  
Best Local Similarity 81.9%; Pred. No. 1.97e-55;  
Matches 118; Conservative 8; Mismatches 13; Indels

[illegible]

Db      121 iyfdydgaw-fpfwgqgtlvtvsa 143  
         | | | | | | | | :  
Ov      121 TVF-Y---WYEDVWGAGTTVTVSS 140

## RESULT 4

ID	R70192	standard; Protein; 141 AA.
AC	R70192;	
DT	20-SEP-1995	(first entry)
DE	Humanized antibody 3B9 heavy chain.	
KW	Humanized antibody; antibody engineering; monoclonal antibody;	
KW	Mab; interleukin-4; IL-4; allergy.	
OS	Homo sapiens.	
FH	Key	Location/Qualifiers
FT	Peptide	1..19
FT	/label= Sig_peptide	
FT	Region	51..57
FT	/label= CDR	
FT	/note= "complementarity determining region"	
FT	Region	72..87
FT	/label= CDR	
FT	/note= "complementarity determining region"	
FT	Region	120..130
FT	/label= CDR	
FT	/note= "complementarity determining region"	
PN	W09507301-A.	
PD	16-MAR-1995.	
PF	07-SEP-1994; U10308..	
PR	07-SEP-1993; US-117366.	
PR	14-OCT-1993; US-136783.	
PA	(SMIK ) SMITHKLINE BEECHAM CORP.	
PA	(SMIK ) SMITHKLINE BEECHAM PIC.	
PI	Gross MS, Holmes SD, Sylvestre DR;	
DR	WPI; 95-123387/16.	
DR	N-PSDB; Q83493.	
PT	Chimeric and humanised IL-4 monoclonal antibodies (mAbs), deriv	
PT	from high affinity mAbs - useful in treatment of IL-4-mediated	
PT	and IgE-mediated allergic conditions	
PS	Disclosure; Fig.4; 97pp; English.	
CC	A humanized antibody heavy chain variable region and signal	
CC	sequence is given in R70192. The signal sequence is also	
CC	provided in R70193. The CDR sequences of the construct are	

CC	identical to the native CDRs of mouse anti-human IL-4 Mab
CC	3B9 (R70198-200).
S0	Sequence 141 AA;

Query Match 79.3%; Score 807; DB 13; Length 141;  
Best Local Similarity 81.3%; Pred. No. 1.85e-54;  
Matches 109; Conservative 12; Mismatches 11; Indels 2; Gaps 1;

```

Db 10 sllllwisgay--gvtlresgalvkptqtltlctctfsgfslstsgmgvswirppgkgl 67
    ||||| | || :|||:||||:|:||||:||||:||||:||||:||||:||||:||||:
Qv 7 SLLLLIIPAVVLQVWTLKESGPGILOPQVTLSLTCSFSGFSLTSGMGVSWIROPSCKGL 66

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```

Db      68 ewlahiywdddkrynpsslksrltiakdtsrnqvwltmtmndpvdttatyyccarretvfyy 127
        |||||
Ov      67 ewlahiywdddkrynpsslksrltiakdtsrnqvwltmtmndpvdttatyyccarretvfyy 126
        |||||

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Db      128 fdvwgrgtptvss 141
        ||||| || |||||
Qv      127 FDVWGAGTIVVSS 140

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## RESULT

ID	R88107	standard; Protein; 139 AA.
AC	R88107;	
DT	25-JUL-1996	(first entry)
DE	Murine anti-Protein C MAb HPC-4 VH gamma protein.	
KW	Epitope; activation; heavy chain; protein C; vitamin K; plasma protein;	
KW	zymogen; cleavage; mouse; humanised antibody; variable region;	
KW	light chain; inhibition; anticoagulant; coagulation; tumour.	
OS	Mus musculus.	
FS	Key	Location/Qualifiers
FT	Peptide	1..19
FT	/note= "signal peptide"	
FT	Peptide	20..139
FT	/note= "mature peptide"	
PN	W09534652-A1.	
PD	21-DEC-1995.	
PD	09-JUN-1995; U07372.	
PR	10-JUN-1994; US-259321.	
PA	(OKLA-) OKLAHOMA MED RES FOUNDR.	
PI	Esmon CT, Rezaie A;	
DR	WPI; 96-049681/05.	
DR	N-PSDB; T09299.	
PT	Calcium-binding monoclonal antibody immunoreactive with Protein C -	
PT	inhibits Protein C anticoagulant activation by	
PT	thrombin-thrombomodulin, e.g. for treating tumours	
PS	Claim 2; Page 29; 41pp; English.	
PS	This is the amino acid sequence of the heavy chain variable region from	
CC	the murine anti-protein C monoclonal antibody HPC-4 which recognises C	
CC	the activation peptide region (R88106) of the heavy chain of protein C,	
CC	a vitamin K-dependent plasma protein zymogen. Protein C is converted to	
CC	activated protein C (APC) by cleavage between the Arg-Ieu amino acid	
CC	contained within the activation peptide sequence. HPC-4 prevents prote	
CC	C activation to APC by binding to this region. The DNA sequences encodi	
CC	the variable regions of the heavy and light chains of the antibody	
CC	(T09299-302) were used to construct humanised antibodies using the PCR	
CC	primers T09303-9. The humanised antibodies are useful as inhibitors of	
CC	coagulation and can be used for the treatment of tumours by inhibiting	
CC	the anticoagulant activity of APC by preventing conversion of protein C	
CC	to APC.	
SQ	Sequence	139 AA;

Query Match 78.8%; Score 802; DB 17; Length 139;  
Best Local Similarity 81.4%; Pred. No. 4.69e-54;



Query Match 78.5%; Score 799; DB 13; Length 139;  
Best Local Similarity 82.1%; Pred. No. 8.21e-54;  
Matches 115; Conservative 10; Mismatches 14; Indels 1; Gaps 1;

	Query Match	73.8%; Score 751; DB 7; Length 141;
	Best Local Similarity	78.0%; Pred. No. 6.2/e-50;
	Matches	110; Conservative 11; Mismatches 19; Indels 1; Gaps 1;
D <b>b</b>	1 mdrtsflllmvpayvlscqlksgpgilqpsqtלטלctsfsgslstygmcvwirq	60
Q <b>y</b>	1 MNRUTSSLLLLLVPAYVLSOVTKESGCGILQPSTLTLCFSFGSGLTSGMGVSWIRQ	60
D <b>b</b>	61 ssqkglewlanywsdskaynpelknrtiskdtsmmqafkitnmdtadtaiyycagrg	120
Q <b>y</b>	61 PSGRGLEWLAHYMDKKRNPSTKSRLLTSKDTSSNQVFLEKITSVDTAUTATYYCARR-	119
D <b>b</b>	121 ategivsfdywghgmvtvss	141
O <b>v</b>	120 ETVFYFYFDWGAGTTVTSS	140

RESULT	8
ID	R53339 standard; Protein; 141 AA.
AC	R53339;

DT 18-NOV-1994 (first entry)  
DE KW50 cell-derived Ig H chain variable region.  
KW Monoclonal antibody; Ab; ganglioside GM2; chimera;  
KW chimeric antibody; expression vector; heavy; light; chain;  
KW hypervariable region; CDR; constant region; hybridoma;  
KW Ig; immunoglobulin; promoter; enhancer.  
OS Rat rattus.  
FH Key Location/Qualifiers  
FT Peptide 1..19  
FT /label= sig\_peptide  
PN AU9346181-A.  
PD 17-MAR-1994.  
PF 07-SEP-1993; 046181.  
PR 07-SEP-1992; JP-238452.  
PA (KYOW ) KYOWA HAKKO KOCYO KK.  
PI Hanai N, Hasegawa M, Koike M, Kuwana Y, Nakamura K;  
PI Shitara K;  
DR WPI; 94-126857/16.  
DR N-PSDB; Q45437.  
PT Humanised antibody specific for ganglioside GM2 - used for  
PT producing a cytotoxic effect on cancers such as melanoma,  
PT neuroblastoma and glioma.  
PS Reference example 1; Page 114-115; 191pp; English.  
CC Example 1 describes the construction of the vector pChiIgAL  
CC for chimeric human antibody L chain expression.  
CC Ig H chain promoter and enhancer genes were isolated from KW50  
CC cells (anti-human serum albumin).  
SQ Sequence 141 AA;

Query Match 73.8%; Score 751; DB 10; Length 141;  
Best Local Similarity 78.0%; Pred. No. 6.27e-50;  
Matches 110; Conservative 11; Mismatches 19; Indels 1; Gaps 1;

Db 1 mdrtsesflllmpayvlsqvtlkesgpgilqpsqtltscsfsgslstymcgvwlrq 60  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Qy 1 MNRFTSSULLLIPAYVLSQVTLKESGPGILQPSQTLSTCSFSGSLSTSGMGVSWIRQ 60

Db 61 segkglewlanvwadakympalnrltisktdmnnqfiktmdtadtaiycagrg 120  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Qy 61 PSGKGLWLAHIYWDKRNPNPSIKSLRTISKDTSSNQVFLKITSVDATATYYCARR- 119

Db 121 ategivsfydwghgymvtvas 141  
| || || | |||||  
Qy 120 ETVFYFVDFVWGAGTTFVTS 140

RESULT 9  
ID R92089 standard; Protein; 120 AA.  
AC R92089;  
DT 16-MAY-1996 (first entry)  
DE Anti-RSV F glycoprotein MAB 1129 VH.  
KW Humanised antibody; chimeric antibody; antibody engineering;  
KW monoclonal antibody; MAB 1129; respiratory syncytial virus; RSV;  
KW heavy chain; complementarity determining region; CDR.  
OS Mus musculus.  
FH Key Location/Qualifiers  
FT Region 31..36  
FT /label= CDR1  
FT Region 52..57  
FT /label= VDR2  
FT Region 100..109  
FT /label= CDR3  
PN W09605229-A1.  
PD 22-FEB-1996.

PF 09-AUG-1995; U10053.  
PR 15-AUG-1994; US-290592.  
PA (MEDI-) MEDIMUNE INC.  
PI Johnson LS;  
DR WPI; 96-139646/14.  
PT New chimeric antibodies against respiratory syncytial virus -  
PT comprise human antibodies with CDR's from the variable heavy and  
PT light chains of a murine antibody  
PS Example 7; Fig 7A-7B; 55pp; English.  
CC A human-mouse chimeric antibody heavy chain has a human Cos  
CC framework contg. complementarity determining region (CDRs) from the  
CC variable heavy (VH) chain of a murine monoclonal antibody (MAB 1129)  
CC against respiratory syncytial virus (RSV) glycoprotein F antigenic  
CC site C. CDRs from MAB 1129 VH (see R92089) were grafted into the  
CC human Cor VH region (R92086) or Cess VH region (R92087) to produce  
CC CDR-grafted MEDI-493 VH (R92088). A similar procedure was used to  
CC obtain CDR-grafted VL (R92091). The humanised antibody is used to  
CC treat RSV infection.  
SQ Sequence 120 AA;

Query Match 73.0%; Score 743; DB 16; Length 120;  
Best Local Similarity 86.8%; Pred. No. 2.78e-49;  
Matches 105; Conservative 4; Mismatches 11; Indels 1; Gaps 1;

Db 1 qvelsespgilqpsqtltscsfsgslstymcgvwlrqpsgglewladwddkdd 60  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Qy 20 QVTLKESGPGILQPSQTLSTCSFSGSLSTSGMGVSWIRQPSGKGLWLAHIYWDKDR 79

Db 61 ynpksrltisktdsenqvfiktgdtdatkyccare-mitnwfdwvgagttvtvs 119  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Qy 80 YNPSLKSLRTISKDTSSNQVFLKITSVDATATYYCARRTFYFVDFVWGAGTTFVTS 139

Db 120 s 120  
Qy 140 s 140

RESULT 10  
ID R58612 standard; Protein; 246 AA.  
AC R58612;  
DT 28-APR-1995 (first entry)  
DE IL-6 binding inhibitor.  
KW Human interleukin-6 binding inhibitor; IL-6; rheumatoid arthritis;  
KW septic shock; multiple myeloma; ss.  
OS Homo sapiens.  
PN EP-617126-A.  
PD 28-SEP-1994.  
PF 16-FEB-1994; 102346.  
PR 17-FEB-1993; JP-028173.  
PA (AJIN ) AJINOMOTO KK.  
PI Hamuro J, Nakazawa H, Shimamura T;  
DR WPI; 94-295777/37.  
DR N-PSDB; Q70612.  
PT Polypeptide inhibiting binding of human interleukin-6 (IL-6) to  
PT its receptor - useful for treating autoimmune disease induced  
PT or aggravated by IL-6  
PS Claim 5; Page 18; 26pp; English.  
CC Q70612 codes for human interleukin-6 binding inhibitor, the  
CC polypeptide described in R58612. This polypeptide inhibits the  
CC binding of human IL-6 to its receptor, and can therefore be  
CC useful in the treatment of a variety of autoimmune diseases;  
CC specifically in the treatment of rheumatoid arthritis, septic  
CC shock due to bacterial infection and multiple myeloma.  
SQ Sequence 246 AA;

	Query Match	72.6%;	Score 739;	DB 11;	Length 246;
	Best Local Similarity	84.9%;	Pred. No. 5,84e-49;		
	Matches	107;	Conservative	8;	Mismatches 6;
				Indels 5;	Gaps 4;
Db	122	tqvkleeegqgilqpstlsltcfsagfelstgmgvswirgpsdkglewlahihywdkdk	181		
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Qy	19	SQVTLKESGFIQLQPSTLITCSFSGFLSTGMSVIRGPSCKGLELAHLYWDDDK	78		
	:				
Db	182	hynpslkeritiskdstnqvflkitsvdtadtatycarr-slygnwgdyamdywgggt	240		
	:	:           :           :           :			
Qy	79	RYNPSLKSRUTISKDTSSNQVFLKITSVDTADTATYCARRETFV-YM--Y-FDWVGAGT	134		
	:	:           :           :           :			
Db	241	svtvas	246		
	:				
Qy	135	TVTVS	140		
	:				

RESULT	11
--------	----

ID	R54101 standard; Protein; 122 AA.
AC	R54101;
DT	08-FEB-1995 (first entry)
DE	Humanised MAb H-chain.
KW	Human; mouse; murine; heavy; light; chain; monoclonal; antibody;
KW	complementarity determining region; CDR; IgG; kappa; IIIB; IIIMN.
OS	Chimeric - Mus musculus.
FS	Chimeric - Homo sapiens.
OH	Key
FT	Region
FT	Location/Qualifiers
FT	31..37
FT	Region
FT	52..67
FT	Region
FT	100..111
FT	Region
FT	106141885-A.
PN	24-MAY-1994.
PD	05-NOV-1992; 322476.
PF	05-NOV-1992; JP-322476.
PR	(KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
PA	WPI; 94-205040/25.
DR	N-PSDB; Q68709.
DR	Recombinant anti-HIV monoclonal antibody - capable of
PT	neutralising strains which can not be neutralised by anti-IIIB
PT	and IIIMN antibodies
PT	Disclosure; Page 13; 23pp; Japanese.
PS	The sequences given in R54101-02 represent the heavy and light chains
PS	respectively of the humanised monoclonal antibody (MAb) of the
CC	invention. The antibody has the ability to neutralise human
CC	immunodeficiency virus. The antibody is classified as IgG kappa and
CC	has the sequence RIGPCR or RVGPCR in the principal neutralising
CC	domain. The antibody may be used to neutralise the clinically
CC	separate strains which cannot be neutralised by the neutralising
CC	antibodies against IIIB and IIIMN strains.
SQ	Sequence 122 AA;

Query Match 70.9%; Score 722; DB 11; Length 122;  
Best Local Similarity 86.3%; Pred. No. 1.38e-47;  
Matches 107; Conservative 5; Mismatches 7; Indels 5; Gaps 3;

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1  qvtlkespggilpsqtslsltcsfsgfsletfgmgvswirqpsgkvlewlahiywdddkh 60
   |||||
20  QVTLKESPGGIILOPQSTLSLTCFSFGFSLSSTSGMGVSWIRQPSGKGLEWLAHIYWDDDR 79

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61 vnpslksrltisedtsnnqvfllkittvtdadtatvvcarr--vfvqmsdfmdhwaqatsv 118

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QY      80 YNPSKSLTISKDTSSNQVFLXITSVOTADATYYCARRETFY--W-YEDVWGAGTTV 136
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Db      119 tvss 122
          |||||
Qv      137 TVSS 140
          |||||
```

RESULT 12

ID	R92088	standard; Protein; 120 AA.
AC	R92088;	
DT	16-MAY-1996	(first entry)
DE	CDR-grafted anti-RSV F glycoprotein MEDI-493 VH.	
KW	Humanised antibody; chimeric antibody; antibody engineering;	
KW	monoclonal antibody; MAb 1129; respiratory syncytial virus; RSV;	
KW	heavy chain; complementarity determining region; CDR.	
OS	Chimeric Homo sapiens;	
OS	Chimeric Mus musculus.	
FH	Key	Location/Qualifiers
FT	Region	31..36
FT	/label= CDR1	
FT	Region	52..67
FT	/label= VDR2	
FT	Region	100..109
FT	/label= CDR3	
FT	WO9605229-A1.	
PD	22-FEB-1996.	
PF	09-AUG-1995; UI0053.	
PF	15-AUG-1994; US-290592.	
PA	(MEDI-) MEDIMMUNE INC.	
PI	Johnson LS;	
DR	WPI; 96-139646/14.	
PT	New chimeric antibodies against respiratory syncytial virus -	
PT	comprise human antibodies with CDR's from the variable heavy and	
PT	light chains of a murine antibody	
PS	Example 7; Fig 7A-7B; 55pp; English.	
CC	A human-mouse chimeric antibody heavy chain has a human CDR	
CC	framework contg. complementarity determining region (CDR) from the	
CC	variable heavy (VH) chain of a murine monoclonal antibody (MAb 1129)	
CC	against respiratory syncytial virus (RSV) glycoprotein F antigenic	
CC	site C. CDRs from MAb 1129 VH (see R92089) were grafted into the	
CC	human CDR VH region (R92086) or Cess VH region (R92087) to produce	
CC	CDR-grafted MEDI-493 VH (R92088). A similar procedure was used to	
CC	obtain CDR-grafted VL (R92091). The humanised antibody is used to	
CC	treat RSV infection.	
SQ	Sequence	120 AA;

Query Match 68.4%; Score 696; DB 16; Length 120;  
Best Local Similarity 77.7%; Pred. No. 1.72e-45;  
Matches 94; Conservative 15; Mismatches 11; Indels 1; Gaps 1;

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Db 1 qvtlresgpalkvptqtltltctfsgfslstsgmsvgwirqpqgkalewladiwwddkdd 60
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Qv 20 QVTLKESGFGILQPSQVTLSTLTCFSFGFSLSTSGMGVSWIRQPSGKGLWLAHIYWDKKR 79

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Db 61 ynpalksrltiakdtsnqvvlkvtndmpadtatyycars-mitnwfyfdwaggtttvs 119  
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 Qv 80 YNPISKSLTISKDTSNOVFKITFSVDPADTATYYCARRETYYFWYFVWAGAGTTTVS 139  
 |||||

Db	120	s	120
Qy	140	s	140

## RESULT 13

ID R88109 standard; peptide; 120 AA.  
AC R88109;  
DT 25-JUL-1996 (first entry)  
DE Murine anti-Protein C MAb HPC-4 VH gamma mature peptide.  
KW Epitope; activation; heavy chain; protein C; vitamin K; plasma protein;  
KW zymogen; cleavage; mouse; humanised antibody; variable region;  
KW light chain; inhibition; anticoagulant; coagulation; tumour.  
OS Mus musculus.  
PN W09534652-A1.  
PD 21-DEC-1995.  
PF 09-JUN-1995; U07372.  
PR 10-JUN-1994; US-259321.  
PA (OKLA-) OKLAHOMA MED RES FOUND.  
PI Esmon CT, Rezaie A;  
DR WPI; 96-049681/05.  
DR N-PSDB; T09300.  
PT Calcium-binding monoclonal antibody immunoreactive with Protein C -  
PT inhibits Protein C anticoagulant activation by  
PT thrombin-thrombomodulin, e.g. for treating tumours  
PS Claim 2; Page 29; 41pp; English.  
CC This is the amino acid sequence of the mature peptide from the murine  
CC anti-protein C monoclonal antibody HPC-4 heavy chain variable region.  
CC HPC-4 recognises the activation peptide region (R88106) of the heavy  
CC chain of protein C, a vitamin K-dependent plasma protein zymogen.  
CC Protein C is converted to activated protein C (APC) by cleavage between  
CC the Arg-Leu amino acid contained within the activation peptide sequence.  
CC HPC-4 prevents protein C activation to APC by binding to this region.  
CC The DNA sequences encoding the variable regions of the heavy and light  
CC chains of the antibody (T09299-302) were used to construct humanised  
CC antibodies using the PCR primers T09303-9. The humanised antibodies are  
CC useful as inhibitors of coagulation and can be used for the treatment of  
CC tumours by inhibiting the anticoagulant activity of APC by preventing  
CC conversion of protein C to APC.  
SQ Sequence 120 AA;

Query Match 67.7%; Score 689; DB 17; Length 120;

Best Local Similarity 81.8%; Pred. No. 6.31e-45;  
Matches 99; Conservative 6; Mismatches 15; Indels 1; Gaps 1;

Db 1 qvtlkesgpilqpsqtlitlctslgfsalrtsgmgvgtwqpsgkglewlahiwdddkr 60

Qy 20 QVTLKESGPIQLQPSQTLSLTCFSFSLSTSGMGVSWIRQPSRGLEWLAHIYWDKKR 79

Db 61 ynpvlkerliibktsrkqvfkiasvdtadtatyycvrmdd-ydandygggtvts 119

Qy 80 YNPSLKSLRTISKDTSSNQVFLKITSVDTADTATYTCARRETVFYWFDVWGAGTTVTS 139

Db 120 s 120

Qy 140 s 140

## RESULT 14

ID R66299 standard; Protein; 119 AA.

AC R66299;

DT 07-AUG-1995 (first entry)

DE Human immunoglobulin variable heavy chain #5.

KW Primer; PCR; amplify; human; immunoglobulin; variable; heavy chain;

KW cosmid; placenta; vector; pJB81; E.coli; mammalian.

OS Homo sapiens.

PN W09476895-A.

PD 24-NOV-1994.

PF 10-MAY-1993; J00603.

PR 10-MAY-1993; W0-J00603.

PA (NISR) JAPAN TOBACCO INC.

PI Honjo T, Matsuda F;

DR WPI; 95-006791/01.

DR N-PSDB; Q78943.

PT DNA fragment comprising human immunoglobulin Vh genes - for the

PT production of human immunoglobulin in mammalian hosts

PS Disclosure; Page 36-37; 130pp; Japanese.

CC Protein sequences (R66295-51) are novel human immunoglobulin heavy chain

CC sequences encoded by novel isolated genes. The genes (Q78939-79002) were

CC isolated and cloned from a series of cosmid constructs: Y202; Y103; Y21;

CC Y6; Y24; 3-31; M84; M118 and M131, by PCR amplification using primers

CC Q78917-38. The genes are subdivided into 5 families of Vh genes. The

CC fragments cover a region of 800 kb. The DNA fragments were isolated from

CC high molecular weight DNA from human placenta. The DNA was partially

CC digested with TaqI restriction enzyme. The fragments were separated by

CC gel electrophoresis and 35-45 kb fractions were collected. The fragments

CC were ligated with ClaI-digested cosmid vector pJB81. The ligation

CC products were in vitro packed and infected into E.coli 490A. The

CC fragments were then subcloned by colony hybridisation. The Vh genes and

CC the DNA fragments encoding them are useful in producing human

CC immunoglobulin in mammalian hosts.

SQ Sequence 119 AA;

Query Match 65.8%; Score 670; DB 12; Length 119;

Best Local Similarity 72.3%; Pred. No. 2.14e-43;

Matches 86; Conservative 21; Mismatches 12; Indels 0; Gaps 0;

Db 1 mdtlostllllipwlsqitlkesgtlivtqtltctctsfsgfslstsgmgvswirq 60

Qy 1 MNRUTSSLLLLIVPAYLSQVTLKESGPIQLQPSQTLSLTCFSFSLSTSGMGVSWIRQ 60

Db 61 ppqkalewlllywmddkryspelskrltitktdeknqvlmtmndpvdttatycahr 119

Qy 61 PSRGLEWLAHIYWDKKRYPNPSLKSLRTISKDTSSNQVFLKITSVDTADTATYTCARR 119

## RESULT 15

ID R38315 standard; Protein; 139 AA.

AC R38315;

DT 04-DEC-1993 (first entry)

DE Sequence of the Vh of antibody B17X2

KW Variable heavy antibody chain; human subgroup 4 germline.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Region 50..56

FT /Label= CDR1

FT Region 71..86

FT /Label= CDR2

FT Region 119..126

FT /Label= CDR3

PN W09312231-A.

PD 24-JUN-1993.

PF 13-DEC-1991; AU0583.

PR 13-DEC-1991; W0-AU0583.

PA (DOMC) DOW CHEM AUSTRALIA LTD.

PI Johnson KS, Mezes PS, Richard RA;

DR WPI; 93-214173/26.

DR N-PSDB; Q45597.

PT New composite antibody binding to tumour associated TAG-72

PT antigen - includes light chain variable region from human

PT subgroup 4 germline gene, useful, opt. as conjugate, for

PT diagnosis or treatment of cancer

PS Disclosure; Figure 4; 150pp; English.

Search completed: Tue Mar 18 10:05:00 1997  
Job time : 51 secs.

(TM)

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Tabular output not generated.

Comp: TACCACAAGTCTGGGTCCA.....GGGGTCAATGGCACTCGAGT

Gap 6

Searched: 630489 seqs. 220513910 bases x 2

Listing first 45 summaries

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125:EST125 126:EST126 127:EST127 128:EST128 129:STS1

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	65	15.4	228	14	H24604	y140b06.r1 Homo sapie	6.17e-88
2	58	13.7	390	14	H26580	y113f10.r1 Homo sapie	2.61e-73
3	50	11.8	364	108	T27579	EST100049 Homo sapien	5.13e-57
4	43	10.2	125	11	H15753	y127D009.r1 Homo sapie	3.05e-43
5	32	7.6	331	108	T27715	EST13381 Homo sapiens	6.06e-23
6	30	7.1	180	108	T27730	EST13989 Homo sapiens	1.68e-19
7	30	7.1	299	108	T27727	EST13874 Homo sapiens	1.68e-19
8	28	6.6	325	109	T29716	EST91759 Homo sapiens	3.68e-16
9	27	6.4	418	118	T61697	y986f08.r1 Homo sapie	1.56e-14
10	26	6.1	410	15	H30111	yo59b04.r1 Homo sapie	6.17e-13
11	26	6.1	485	87	R4774	yj75f04.r1 Homo sapie	6.17e-13
12	25	5.9	169	85	R48619	yj68a01.r1 Homo sapie	2.25e-11
13	24	5.7	346	154	HSU53085	Human clone 7/24 mRNA	7.58e-10
14	24	5.7	346	163	HS530851	Human clone 7/24 mRNA	7.58e-10
15	23	5.4	318	43	HSC2NH041	H. sapiens partial cd	2.33e-08
16	23	5.4	478	19	H43753	yp21g01.r1 Homo sapie	2.33e-08
17	22	5.2	234	109	T28164	EST30734 Homo sapiens	6.47e-07
18	22	5.2	297	108	T27868	EST18962 Homo sapiens	6.47e-07
19	22	5.2	330	103	SSC1D10	S.-scrofa mRNA; expres	6.47e-07
20	22	5.2	428	119	T65452	yc73a07.r1 Homo sapie	6.47e-07
21	22	5.2	672	11	H15870	ym22b10.r1 Homo sapie	6.47e-07
22	21	5.0	287	108	T27609	EST101034 Homo sapien	1.62e-05
23	21	5.0	334	5	CELK087CYR	C.elegans cDNA clone	1.62e-05
24	21	5.0	340	6	CELK117E2R	C.elegans cDNA clone	1.62e-05
25	21	5.0	360	5	CELK102H1F	C.elegans cDNA clone	1.62e-05
26	21	5.0	360	5	CELK087GYF	C.elegans cDNA clone	1.62e-05
27	21	5.0	490	56	N31150	yx52g08.r1 Homo sapie	1.62e-05
28	20	4.7	106	130	G03791	human STS WI-91.	3.60e-04
29	20	4.7	245	110	T33317	EST57414 Homo sapiens	3.60e-04
30	20	4.7	377	43	HSC31A071	H. sapiens partial cd	3.60e-04
31	20	4.7	409	102	R1CS1A850A	Rice cDNA, partial se	3.60e-04
32	20	4.7	419	142	N82396	TgESTzy52g06.r1 Toxop	3.60e-04
33	20	4.7	419	29	T73816	ys11b01.r1 Homo sapie	3.60e-04
34	20	4.7	419	172	TG3964	TgESTzy52g06.r1 Toxop	3.60e-04
35	20	4.7	437	154	HSU53086	Human clone 8/24 mRNA	3.60e-04
36	20	4.7	437	163	HS530861	Human clone 8/24 mRNA	3.60e-04
37	20	4.7	484	21	H48330	yq77g02.r1 Homo sapie	3.60e-04
38	19	4.5	313	100	R97700	yq61b08.s1 Homo sapie	7.04e-03
39	19	4.5	360	6	CELK119C5F	C.elegans cDNA clone	7.04e-03
40	19	4.5	405	70	N71176	yv42b06.r1 Homo sapie	7.04e-03
41	19	4.5	405	159	N5176311	yv42b06.r1 Homo sapie	7.04e-03
42	19	4.5	405	141	HS716311	yv42b06.r1 Homo sapie	7.04e-03







Qy 298 GTTGTCTGACCATGACTAACTGACCGGTGACACCGCTACCTACTACTCGCTCG 356

RESULT 5  
LOCUS T27715 331 bp mRNA EST 06-SEP-1995  
DEFINITION EST13381 Homo sapiens cDNA 5' end similar to immunoglobulin gamma heavy chain V region (GB:M97921) (HT:3789).  
ACCESSION T27715  
NID 9609813  
KEYWORDS EST.  
SOURCE human primer=M13 Reverse library=Human Testis.  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 331)

REFERENCE 1 (bases 1 to 331)  
AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult,C.J., Lee,N., Kirkness,E.F., Weinstock,K.G., Cocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Chiu,M.-W., Clayton,R.A., Cline,R.T., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., FitzHugh,W.M., Fritchman,J.L., Geohagen,N.S.M., Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle Jr,P.S., Kelley,J.M., Klinek,K.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palancas,R.F., McDonald,L.A., Nguyen,D.T., Pellegrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.-J., Dimke,D., Feng,P., Ferrie,A., Fischer,C., Hastings,G.A., He,W.-W., Hu,J.-S., Greene,J.M., Gruber,J., Hudson,P., Kim,A., Kozak,D.L., Kunsch,C., Ji,H., Li,H., Meisener,P.S., Olsen,H., Raymond,L., Wei,Y.-F., Wing,J., Xu,C., Yu,G.-L., Ruben,S.M., Dillon,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.  
TITLE Initial Assessment of Human Gene Diversity and Expression Patterns Based Upon 52 Million Basepairs of cDNA Sequence  
JOURNAL Unpublished (1995)  
COMMENT Contact: Venter, JC  
The Institute for Genomic Research  
932 Clopper Rd, Gaithersburg, MD 20878  
Tel: 3018699056  
Fax: 3018699423  
Email: tdbinfo@db.tigr.org  
For clone availability, additional sequence and expression information related to this EST, please contact the TIGR Database (tdbinfo@db.tigr.org).

FEATURES  
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/note="human"  
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Best Local Similarity 60.9%; Pred. No. 6.06e-23;  
Matches 84; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

Db 89 ctgcagaggtcggccagcagctggtgaagccttcggagacccttcctcactgcact 148

Qy 70 CTGCGTGAATCCGGTCCGACCTAGTAAACCGACCCGCTGACGTTAACTCCACC 129

Db 149 gtctctggtgtntccgtctacagtgcacattttnaactggggtgggtccgcagggccca 208

Qy 130 TTCTCCGGTTTCTCCCTGTCGACCTCGCGGTATGGGTGTTTCTGATCGTCGAGCGCG 189

Db 209 ggaaggggctggagtg 226  
Qy 190 GGTAAAGCTCTAGATCG 207  
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LOCUS T27730 180 bp mRNA EST 06-SEP-1995  
DEFINITION EST13989 Homo sapiens cDNA 5' end similar to immunoglobulin heavy chain, V region (GB:212364) (HT:3115).  
ACCESSION T27730  
NID 9609828  
KEYWORDS EST.  
SOURCE human primer=M13 Reverse library=Human Testis.  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 180)

REFERENCE 1 (bases 1 to 180)  
AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult,C.J., Lee,N., Kirkness,E.F., Weinstock,K.G., Cocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Chiu,M.-W., Clayton,R.A., Cline,R.T., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., FitzHugh,W.M., Fritchman,J.L., Geohagen,N.S.M., Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle Jr,P.S., Kelley,J.M., Klinek,K.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palancas,R.F., McDonald,L.A., Nguyen,D.T., Pellegrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.-J., Dimke,D., Feng,P., Ferrie,A., Fischer,C., Hastings,G.A., He,W.-W., Hu,J.-S., Greene,J.M., Gruber,J., Hudson,P., Kim,A., Kozak,D.L., Kunsch,C., Ji,H., Li,H., Meisener,P.S., Olsen,H., Raymond,L., Wei,Y.-F., Wing,J., Xu,C., Yu,G.-L., Ruben,S.M., Dillon,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.  
TITLE Initial Assessment of Human Gene Diversity and Expression Patterns Based Upon 52 Million Basepairs of cDNA Sequence  
JOURNAL Unpublished (1995)  
COMMENT Contact: Venter, JC  
The Institute for Genomic Research  
932 Clopper Rd, Gaithersburg, MD 20878  
Tel: 3018699056  
Fax: 3018699423  
Email: tdbinfo@db.tigr.org  
For clone availability, additional sequence and expression information related to this EST, please contact the TIGR Database (tdbinfo@db.tigr.org).

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/note="human"  
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BASE COUNT 33 a 49 c 54 g 39 t 5 others  
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Query Match 7.1%; Score 30; DB 108; Length 180;  
Best Local Similarity 60.9%; Pred. No. 1.68e-19;  
Matches 78; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

Db 6 ctgcaggagtcaggactggtgaagccttcacagacctccctccactgcgncct 65  
 ||||| || ||||| || ||||| || || ||||| || ||||| || ||||| || ||||| ||  
 Qy 70 CTGCGTGAATCCGGTCGGCAGCTAGTTAAACCGACCGACCGCTGACCTGACCC 129  
 ||||| || ||||| || ||||| || || ||||| || ||||| || ||||| || ||||| ||  
 Db 66 gtctctgggtccatccatccagcagtggtggtactcctcctgagcgtggtccgagccaccca 125  
 ||||| || ||||| || || || ||||| || ||||| || ||||| || ||||| || ||||| ||  
 Qy 130 TTCTCCGGTTCTCCCTGTGTCGACCTCCGGTATGGGTGTTTCTCGATCCGTGAGCGCGC 189  
 ||||| || ||||| || || || ||||| || ||||| || ||||| || ||||| || ||||| ||  
 Db 126 gggaaaggg 133  
 || || ||  
 Qy 190 GGTAAAGG 197

RESULT 7  
 LOCUS T77727 299 bp mRNA EST 06-SEP-1995  
 DEFINITION EST13874 Homo sapiens cDNA 5' end similar to immunoglobulin mu  
 (gamma) heavy chain, V(IV)DJC regions (HT:3057).  
 ACCESSION T77727  
 NID g609825  
 KEYWORDS EST.  
 SOURCE human primer=M13 Reverse library=Human Testis.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata;  
 Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;  
 Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;  
 Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 299)  
 AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,  
 Bult,C.J., Lee,N., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,  
 White,O., Sutton,G., Blake,J.A., Brandon,R.C., Chiu,M.-W.,  
 Clayton,R.A., Cline,R.T., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,  
 FitzGerald,L.M., FitzHugh,W.M., Fritchman,J.L., Geoghagen,N.S.M.,  
 Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle Jr,P.S.,  
 Kelley,J.M., Klinek,K.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M.,  
 Merrick,J.M., Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T.,  
 Pellegrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L.,  
 Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R.,  
 Weidman,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A.,  
 Coleman,T.A., Collins,E.-J., Dimke,D., Feng,P., Ferrie,A.,  
 Fischer,C., Hastings,G.A., He,W.-W., Hu,J.-S., Greene,J.M.,  
 Gruber,J., Hudson,P., Kim,A., Kozak,D.L., Kunsch,C., Ji,H., Li,H.,  
 Meisner,P.S., Olsen,H., Raymond,L., Wei,Y.-F., Wing,J., Xu,C.,  
 Yu,G.-L., Ruben,S.M., Dillon,P.J., Fannon,M.R., Rosen,C.A.,  
 Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.  
 Initial Assessment of Human Gene Diversity and Expression Patterns  
 Based Upon 52 Million Basepairs of cDNA Sequence  
 Unpublished (1995)

CONTACT: Venter, JC  
 The Institute for Genomic Research  
 932 Clopper Rd, Gaithersburg, MD 20878  
 Tel: 3018699056  
 Fax: 3018699423  
 Email: tdbinfo@db.tigr.org  
 For clone availability, additional sequence and expression  
 information related to this EST, please contact the TIGR Database  
 (tdbinfo@db.tigr.org).

FEATURES  
 source  
 Location/Qualifiers  
 1..299  
 /organism="Homo sapiens"  
 /note="human"  
 mRNA  
 <1..>299  
 BASE COUNT 61 a 84 c 82 g 68 t 4 others  
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Query Match 7.1%; Score 30; DB 108; Length 299;  
 Best Local Similarity 67.9%; Pred. No. 1.68e-19;  
 Matches 57; Conservative 0; Mismatches 27; Indels 0; Gaps 0;  
 Db 79 cagctgcagctgcagagtcggggccagagactggtgaagccttcgagacccctgtccctc 138  
 ||||| ||||| || ||||| || ||||| || || ||||| || ||||| || ||||| || ||||| ||  
 Qy 61 CAGGTTACCTCGCTGAATCCGGTCGGCAGCTAGTTAAACCGACCGACCGCTGACGTTA 120  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||  
 Db 139 acctgcactgtctctggtggctcc 162  
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 Qy 121 ACCTGCACCTCTCCGCTTCTCC 144

RESULT 8  
 LOCUS T29716 325 bp mRNA EST 06-SEP-1995  
 DEFINITION EST91759 Homo sapiens cDNA 5' end similar to immunoglobulin heavy  
 chain V,D,J regions (GB:M34029) (HT:3782).  
 ACCESSION T29716  
 NID g611814  
 KEYWORDS EST.  
 SOURCE human primer=M13 Reverse library=Human Synovial membrane.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata;  
 Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;  
 Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;  
 Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 325)  
 AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,  
 Bult,C.J., Lee,N., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,  
 White,O., Sutton,G., Blake,J.A., Brandon,R.C., Chiu,M.-W.,  
 Clayton,R.A., Cline,R.T., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,  
 FitzGerald,L.M., FitzHugh,W.M., Fritchman,J.L., Geoghagen,N.S.M.,  
 Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle Jr,P.S.,  
 Kelley,J.M., Klinek,K.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M.,  
 Merrick,J.M., Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T.,  
 Pellegrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L.,  
 Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R.,  
 Weidman,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A.,  
 Coleman,T.A., Collins,E.-J., Dimke,D., Feng,P., Ferrie,A.,  
 Fischer,C., Hastings,G.A., He,W.-W., Hu,J.-S., Greene,J.M.,  
 Gruber,J., Hudson,P., Kim,A., Kozak,D.L., Kunsch,C., Ji,H., Li,H.,  
 Meisner,P.S., Olsen,H., Raymond,L., Wei,Y.-F., Wing,J., Xu,C.,  
 Yu,G.-L., Ruben,S.M., Dillon,P.J., Fannon,M.R., Rosen,C.A.,  
 Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.  
 Initial Assessment of Human Gene Diversity and Expression Patterns  
 Based Upon 52 Million Basepairs of cDNA Sequence  
 Unpublished (1995)

CONTACT: Venter, JC  
 The Institute for Genomic Research  
 932 Clopper Rd, Gaithersburg, MD 20878  
 Tel: 3018699056  
 Fax: 3018699423  
 Email: tdbinfo@db.tigr.org  
 For clone availability, additional sequence and expression  
 information related to this EST, please contact the TIGR Database  
 (tdbinfo@db.tigr.org).

FEATURES  
 source  
 Location/Qualifiers  
 1..325  
 /organism="Homo sapiens"  
 /note="human"  
 mRNA  
 <1..>325  
 BASE COUNT 72 a 92 c 81 g 80 t







Mar 19 07:59

US-08-612-929-11.rst

17

Devignes,M.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B.,  
Lorenzo,F., Mitchell,H., Mariage-Samson,R., Pietu,G., Pouliot,Y.,  
Sebastiani-Kabakchis,C. and Tessier,A.  
IMAGE: molecular integration of the analysis of the human genome  
and its expression

TITLE

JOURNAL

MEDLINE

COMMENT

C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)

95277534

Cloning method: total mRNA was oligo-(dT) primed and directionally  
cloned 5' -> 3' into the HindIII -> NotI sites of the lafmid BA  
vector;

Sequencing method: single read, full automatic;

Primer: M13\_reverse

cDNA sequence colinear to mRNA

Stretch removed: nothing

Normalization method: Bento Soares, P.N.A.S. 91:9228-9232 (1994);

Genexpress\_library\_id: C;

Genexpress\_sequence\_id: ylc-2nh04.

FEATURES

source

1..318

/organism="Homo sapiens"

/isolate="muscular atrophy patient"

/clone\_lib="normalized infant brain cDNA from B.Souares,

Psychiatry Dept. Columbia University USA"

/sex="female"

/tissue\_type="total brain"

/dev\_stage="3 months old"

BASE COUNT 58 a 104 c 84 g 68 t 4 others

ORIGIN

Query Match 5.4%; Score 23; DB 43; Length 318;

Best Local Similarity 74.5%; Pred. No. 2.33e-08;

Matches 35; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Db 54 ggtacttcgatctctggggccgtggcaccctggtcactgtctctca 100

||||| | | | | | | | | | | | | | | | | | | | |

Qy 377 GGTACTTCGACGTTGGCGTCGTGGTACCCACGTTACCGTGAGCTCA 423

Search completed: Wed Mar 19 08:01:27 1997

Job time : 283 secs.

\*\*\*\*\*

WATERMAN

(TM)

\*\*\*\*\*

Release 2.1D John F. Collins, Biocomputing Research Unit.  
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MPsrch\_nm n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed Mar 19 07:55:10 1997; MaePar time 41.64 Seconds  
Tabular output not generated. 885.965 Million cell updates/sec

Title: >US-08-612-929-11

Description: (1-423) from US08612929.seq

Perfect Score: 423

N.A. Sequence: 1 ATGGTGTTCAGACCCAGGT.....CCCGAGTACGGTGAGCTCA 423

Comp: TACCACACGTCGTGGGTCCA.....GGGTCATGGCAGCTCGACT

Scoring table: TABLE default

Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 113505 seqs, 43611913 bases x 2

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: n-geneseq25

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13  
14:part14 15:part15 16:part16 17:part17 18:part18  
19:part19 20:part20 21:part21 22:part22

Statistics: Mean 8.172; Variance 4.663; scale 1.753

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	DB	ID	Description	Pred. No.
1	421	99.5	423	14	Q83493 Humanized antibody 3B	8.96e-288
2	259	61.2	6285	22	T34109 Anti-IL-5 humanised a	2.88e-167
3	215	50.8	423	14	Q83492 Chimeric antibody 3B9	7.54e-135
4	199	47.0	357	22	T34093 Humanised 2B6 antibod	4.08e-123
5	153	36.2	483	14	Q83491 Mouse MAB 3B9 heavy c	1.29e-89
6	127	30.0	613	13	Q78943 Human immunoglobulin	6.72e-71
7	124	29.3	546	13	Q78964 Human immunoglobulin	9.40e-69
8	121	28.6	423	7	Q45597 Sequence encoding the	1.30e-66

9	120	28.4	120	14	Q83499 Heavy chain variable	6.75e-66
10	117	27.7	117	14	Q83498 Heavy chain variable	9.26e-64
11	115	27.2	360	19	T09300 Murine anti-Protein C	2.45e-62
12	115	27.2	417	19	T09299 Murine anti-Protein C	2.45e-62
13	114	27.0	418	13	Q75917 Anti-human IL-6 chima	1.26e-61
14	114	27.0	418	13	Q75916 Anti-human IL-6 chima	1.26e-61
15	112	26.5	738	12	Q70612 IL-6 binding inhibito	3.32e-60
16	111	26.2	366	11	Q68709 Humanised MAB H-chain	1.30e-59
17	107	25.3	429	11	Q64166 Sequence of mouse VH	1.16e-56
18	107	25.3	630	13	Q78948 Human immunoglobulin	1.16e-56
19	103	24.3	120	14	Q83500 Heavy chain variable	7.77e-54
20	103	24.3	418	13	Q75889 Mouse heavy chain var	7.77e-54
21	96	22.7	812	6	Q37056 Rat immunoglobulin H	6.51e-49
22	94	22.2	812	11	Q45437 RMS0 cell-derived Ig	1.64e-47
23	68	16.1	84	14	Q83518 Signal sequence 3' pr	1.40e-29
24	63	14.9	83	14	Q83517 Signal sequence 5' pr	3.28e-26
25	60	14.2	60	22	T34108 Signal peptide coding	3.31e-24
26	60	14.2	60	14	Q83494 Human antibody signal	3.31e-24
27	60	14.2	400	1	N80499 Encodes V region of L	3.31e-24
28	60	14.2	407	4	Q26047 V-region of L-chain o	3.31e-24
29	60	14.2	5703	22	T34110 Anti-IL-5 humanised a	3.31e-24
30	58	13.7	1047	2	Q10572 Human Natriuretic Pep	7.05e-23
31	57	13.5	57	10	Q44851 Signal sequence for p	3.23e-22
32	54	12.8	3314	10	Q58896 Humanised anti-CEA sF	3.05e-20
33	52	12.3	619	1	N80498 Encodes V region of L	6.18e-19
34	52	12.3	1088	10	Q56735 Sequence of HumAVL ge	6.18e-19
35	52	12.3	1097	7	Q45602 Sequence of the Humd	6.18e-19
36	52	12.3	1373	1	N80941 Encodes Vchi region o	6.18e-19
37	49	11.6	351	1	Q06214 VH domain of antibody	5.43e-17
38	49	11.6	354	4	Q26757 431/26 VH hum.	5.43e-17
39	49	11.6	357	6	Q38670 MAB GAH variable regi	5.43e-17
40	49	11.6	799	13	Q78977 Human immunoglobulin	5.43e-17
41	49	11.6	1288	17	T04181 Plasmid pfv-pp fragme	5.43e-17
42	48	11.3	1047	2	Q10572 Human Natriuretic Pep	2.39e-16
43	47	11.1	923	17	T04171 Plasmid pSW1VHD1.3VKD	1.05e-15
44	47	11.1	1615	12	Q70667 ScFv-DNaseI fusion DN	1.05e-15
45	47	11.1	1952	15	Q91987 Fv restriction fragme	1.05e-15

## ALIGNMENTS

RESULT 1  
ID Q83493 standard; cDNA; 423 BP.  
AC Q83493;  
DT 20-SEP-1995 (first entry)  
DE Humanized antibody 3B9 heavy chain.  
KW Humanized antibody; antibody engineering; monoclonal antibody;  
KW MAb; interleukin-4; IL-4; allergy; da.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT CDS 1..423  
FT /tag= a  
FT sig\_peptide 1..57  
FT /tag= b  
FT mat\_peptide 58..423  
FT /tag= c  
PN WO9507301-A.  
PD 16-MAR-1995.  
PF 07-SEP-1994; U10308.  
PR 07-SEP-1993; US-117366.  
PR 14-OCT-1993; US-136783.  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
PA (SMIK ) SMITHKLINE BEECHAM PLC.  
PI Gross MS, Holmes SD, Sylvester DR;

DR MP1; 95-123387/16.  
DR P-PSDB; R70192.  
PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived  
PT from high affinity mAbs - useful in treatment of IL-4-mediated  
PT and IgE-mediated allergic conditions  
PS Disclosure; Fig.4; 97pp; English.  
CC A humanized antibody heavy chain variable region and signal  
CC sequence is given in R70192. The signal sequence is also  
CC provided in R70193. The CDR sequences of the construct are  
CC identical to the native CDRs of mouse anti-human IL-4 mAb  
CC 389 (R70198-200).  
SQ Sequence 423 BP; 84 A; 131 C; 102 G; 106 T;

Query Match 99.5%; Score 421; DB 14; Length 423;  
Best Local Similarity 99.8%; Pred. No. 8,96e-288;  
Matches 422; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 atggtgttcagaccaggtcttcattctctgttctctggatctctggctacggg 60  
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Qy 1 ATGGTGTTCAGACCCAGGCTTCATTCTCTGTCTGTGATCTCTGGTGCCTACGGG 60  
|||||  
Db 61 caggttacctcgtgaatccggtccggcgaactagttaaaccgaccagacctgacgtta 120  
|||||  
Qy 61 CAGGTTACCTCGCTGAATCCGGTCCGGCACTAGTTAAACCGACGACCTGACGTTA 120  
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Db 121 acctgcacctctcoggtttctccctgtgcacctccggtatgggtgttctcgtacgt 180  
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Qy 121 ACCTGCACCTTCTCGGTTTCTCCCTGTGACCTCGGATGGGTGTTCTCGATCGGT 180  
|||||

Db 181 cagccgcgggttaaggtctagaatggctgtcactatctactgggacgacgacaaact 240  
|||||  
Qy 181 CAGCGCGCGGGTAAAGGTCTAGAAATGGCTGGCTGCATCTACTGGGACGACGAAAGCT 240  
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Db 241 tacaaccgagcgtgaatccgctgaccatatacaagacacacctccgtaccaggtt 300  
|||||  
Qy 241 TACAACCGGAGCCTGAATCCCGCTCTGACGATATCCAAAGACACCTCCCGTACCAGGTT 300  
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Db 301 gttctgaccatgaactaacatggaccggttgacaccgctactactactcgtcgcagc 360  
|||||  
Qy 301 GTTCTGACCATGACTTAACATGGACCGGTTGACACCGCTACCTACTACTGCGCTCAGCG 360  
|||||

Db 361 gaaaccgttttctactggtactcgcagcttgggtogtggtaaccaccagttaccgtgagc 420  
|||||  
Qy 361 GAACCGTTTTTCTACTGGTACTTTCGACGTTTGGGTCCTGCTACCCAGTTACCGTGAGC 420  
|||||

Db 421 tca 423  
|||  
Qy 421 TCA 423  
|||

RESULT 2  
AC T34109 standard; DNA; 6285 BP.  
AC T34109;  
DE Anti-IL-5 humanised antibody heavy chain plasmid pCDIL5HZHC1.0.  
KW Antibody engineering; humanised antibody; chimeric antibody; Fab;  
KW interleukin-5; IL-5; eosinophil; asthma; allergic rhinitis;  
KW atopic dermatitis; therapy; diagnosis; heavy chain; VH;  
KW monoclonal antibody; mAb; plasmid pCDIL5HZHC1.0; ds; cyclic.  
OS Synthetic.  
PN W09621000-A2.  
PD 11-JUL-1996.  
PF 22-DEC-1995; U17082.  
PR 23-DEC-1994; US-363131.

PR 06-JUN-1995; US-470110.  
PR 06-JUN-1995; US-467420.  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
PA (SMIK ) SMITHKLINE BEECHAM PIC.  
PI Ames RS, Appelbaum ER, Chaiken IM, Cook RM, Gross MS;  
PI Holmes SD, McMillan LJ, Theisen TW;  
DR MP1; 96-333976/33.  
PT New monoclonal antibody to human interleukin-5 - used to produce  
PT products for the treatment and diagnosis of conditions associated  
PT with excess eosinophil prodn., e.g asthma etc.  
PS Example 4; Page 70-75; 120pp; English.  
CC pCDIL5HZHC1.0 (T34109) is a pUC19-based plasmid that incorporates  
CC a DNA sequence (see also T34093) coding for a humanised heavy chain  
CC (R98488) of murine anti-human interleukin-5 (IL-5) monoclonal  
CC antibody 2B6 as well as a beta-lactamase gene, an SV40 replication  
CC origin, a cytomegalovirus promoter, a signal sequence (see also  
CC T34108), a polyA signal from bovine growth hormone (BGH), a  
CC beta-globin promoter, a dihydrofolate-reductase gene and another  
CC BGH polyA signal. pCDIL5HZHC1.0 and pCNIL5HZLC1.0 (T34110) coding  
CC for the humanised light chain were co-transfected into COS cells  
CC for prodn. of humanised 2B6 antibody. This can be used for the  
CC diagnosis and treatment of IL-5-mediated conditions, e.g. asthma,  
CC allergic rhinitis and atopic dermatitis.  
SQ Sequence 6285 BP; 1544 A; 1637 C; 1611 G; 1493 T;

Query Match 61.2%; Score 259; DB 22; Length 6285;  
Best Local Similarity 84.2%; Pred. No. 2.88e-167;  
Matches 356; Conservative 0; Mismatches 61; Indels 6; Gaps 2;

Db 1010 atggtgttcagaccaggtcttcattctctgttctctggatctctgggtacggg 1069  
|||||  
Qy 1 ATGGTGTTCAGACCCAGGCTTCATTCTCTGTGCTCTGGATCTCTGGTGCCTACGGG 60  
|||||

Db 1070 caggttacctcgtgaatccggtccgcaactagttaaaccgaccagacctgacgtta 1129  
|||||  
Qy 61 CAGGTTACCTCGCTGAATCCGGTCCGGCACTAGTTAAACCGACGACCTGACGTTA 120  
|||||

Db 1130 acctgcacctcctcoggtttctccctgacgagcta---ta---gtgtacactgggtccgt 1183  
|||||  
Qy 121 ACCTGCACCTTCTCCGTTTCTCCCTGTGACCTCCGGTATGGGTGTTCTCGATCCGT 180  
|||||

Db 1184 cagccgcgggttaaggtctagaatggctgggtgtaatatgggttagtgaggacacagat 1243  
|||||  
Qy 181 CAGCGCGCGGGTAAAGGTCTAGAAATGGCTGGCTGCATCTACTGGGACGACGAAAGCT 240  
|||||

Db 1244 tataattcgggtctctatgtccgtctgtcgatatccaaagacacctccgtacacaggtt 1303  
|||||  
Qy 241 TACAACCGGAGCCTGAATCCCGCTCTGACGATATCCAAAGACACACCTCCGCTACCAGGTT 300  
|||||

Db 1304 gttctgaccatgaactaacatggaccggttgacaccgctactactactcgtcgtcgagat 1363  
|||||  
Qy 301 GTTCTGACCATGACTTAACATGGACCGCGGTTGACACCGCTACCTACTACTGCGCTCAGCGC 360  
|||||

Db 1364 cccctcttcttactaaggctgactactcgtgggtcgtgtgtacccagttaccgtgagc 1423  
|||||  
Qy 361 GAACCGGTTTTTCTACTGGTACTTTCGACGTTTGGGTCGTGGTACCCCACTTACCCGTGAGC 420  
|||||

Db 1424 tca 1426  
|||  
Qy 421 TCA 423  
|||

RESULT 3  
ID Q83492 standard; cDNA; 423 BP.





Mar 19:07:54

US-08-612-929-11.rmg

7

Db 61 acctgacacgtctccgtttctccctgacagcta---ta---gtgtacacgtggtcgt 114  
|||||  
Qy 121 ACCTGACACGTTCTCCGTTTCTCCCTCTCGACCTCCGGTATGGGTGTTCTCGATCCGT 180  
Db 115 cagccgcgggttaaggtctagaatggctgggtgtaatatgggtcagtggagacagat 174  
|||||  
Qy 181 CAGCCGCCGGTAAAGGCTAGAAATGGCTGGCTCACATCTACTGGGACGACGACAAAGCT 240  
Db 175 tataatcgctctcatgctcccgctgtcgatctccaaagacacccctcccgtaaccaggtt 234  
|||||  
Qy 241 TACAAACCCGAGCGCTGAATCCCGCTCTGACGATATCCAAAGACACACCTCCCGTACACAGGTT 300  
Db 235 gtctgaccatgactaacatgacccggttgacaccgctactactactactcgtcgtcgat 294  
|||||  
Qy 301 GTTCTGACCATGACTAATGACGCCGGTTGACACCGCTACCTACTACTGCGGTGACGCC 360  
Db 295 ccccttctctactacggttgactactgggtcgtggtgacccagttaccctaccgtgagc 354  
|||||  
Qy 361 GAAACCGTTTCTACTGCTACTCTGACGTTTGGGTCGTGCTACCCAGTTACCGTGAGC 420  
Db 355 tca 357  
|||  
Qy 421 TCA 423

RESULT 5

ID Q83491 standard; cDNA; 483 BP.  
AC Q83491;  
DT 20-SEP-1995 (first entry)  
DE Mouse MAb 3B9 heavy chain.  
KW Chimeric antibody; humanized antibody; antibody engineering;  
KW monoclonal antibody; MAb; interleukin-4; IL-4; allergy; ds.  
OS Mus sp.  
FH Key Location/Qualifiers  
FT CDS 64..483  
FT /\*tag= a 64..120  
FT sig\_peptide /\*tag= b 121..483  
FT mat\_peptide /\*tag= c  
PN W09507301-A.  
PD 16-MAR-1995.  
PF 07-SEP-1994; U10308.  
PR 07-SEP-1993; US-117366.  
PR 14-OCT-1993; US-136783.  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
PA (SMIK ) SMITHKLINE BEECHAM PLC.  
PI Gross MS, Holmes SD, Sylvester DR;  
DR WPI: 95-123387/16.  
DR P-PSDB; R70190.  
PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived from high affinity mAbs - useful in treatment of IL-4-mediated and IgE-mediated allergic conditions  
PS Disclosure; Fig.2; 97pp; English.  
CC Spleen cells from mice immunized with human IL-4 were used to prepare hybridomas, which were screened for anti-IL-4 MAb secretion. Only clone 3B9 was positive. cDNA clones of the 3B9 light and heavy chains were cloned into pCEM7f+ and transformed into E. coli DH5-alpha. The clones were sequenced (Q83490-91), and used for antibody engineering.  
SQ Sequence 483 BP; 108 A; 130 C; 124 G; 121 T;

Query Match 36.2%; Score 153; DB 14; Length 483;  
Best Local Similarity 71.1%; Pred. No. 1.29e-89;

Mar 19:07:54

US-08-612-929-11.rmg

8

Matches 258; Conservative 0; Mismatches 105; Indels 0; Gaps 0;  
Db 121 caggttaactctgaaagagctgcccctggggatattgagccctcccagaccctcagtcgtg 180  
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Qy 61 CAGGTTACCGTCCGTGAATCCGGTCCGGCTAGTAAACCGACCCAGACCTGACGTTA 120  
Db 181 acttggtttctctcgtggttttcaactgagcactctggtatgggtgagctggattcgt 240  
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Qy 121 ACCTGACACCTTCTCCGTTTCTCCCTCTCGACCTCCGGTATGGGTGTTCTCGATCCGT 180  
Db 241 cagccttcaggaaaggctctggagtggctgggcacacatttactgggatgatgacaagcgc 300  
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Qy 181 CAGCCGCCGGGTAAAGGCTCTAGAAATGGCTGGCTCACATCTACTGGGACGACGACAAAGCT 240  
Db 301 tataacccatccctgaagagcggcgtcacatctccaaggtacacctccagcaaccagcta 360  
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Qy 241 TACAAACCCGAGCGCTGAATCCCGCTCTGACGATATCCAAAGACACACCTCCCGTAAACAGGTT 300  
Db 361 ttctcgaagatcacagctgtggacacatgcagatactgcccatactactgctcgaaga 420  
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Qy 301 GTTCTGACCATGACTAATGACGCCGGTTGACACCGCTACCTACTACTGCTGCTGACGC 360  
Db 421 gagactgttctactggtactcgtcgtggtggcgaggagaccaggtcacctgtctcc 480  
|||||  
Qy 361 GAAACCGTTTCTACTGCTACTCTGACGTTTGGGTCGTGCTACCCAGTTACCGTGAGC 420  
Db 481 tca 483  
|||  
Qy 421 TCA 423

RESULT 6

ID Q78943 standard; DNA; 613 BP.  
AC Q78943;  
DT 07-AUG-1995 (first entry)  
DE Human immunoglobulin variable heavy chain #5.  
KW Primer; PCR; amplify; human; immunoglobulin; variable; heavy chain;  
KW cosmid; placenta; vector; pJB81; E.coli; mammalian; ds.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT CDS 71..513  
FT /\*tag= a  
FT /product= human immunoglobulin variable heavy chain  
FT intron 117..202  
FT /\*tag= b  
FT misc\_signal 514..516  
FT /\*tag= c  
FT /note= "miscellaneous signal, does not conform to  
FT terminator or splice site sequence"  
PN W09426895-A.  
PD 24-NOV-1994.  
PF 10-MAY-1993; J00603.  
PR 10-MAY-1993; WO-J00603.  
PA (NIBS ) JAPAN TOBACCO INC.  
PA Honjo T, Matsuda F;  
DR WPI: 95-006791/01.  
DR P-PSDB; R66299.  
PT DNA fragment comprising human immunoglobulin Vh genes - for the production of human immunoglobulin in mammalian hosts  
PS Disclosure; Page 36-37; 130pp; Japanese.  
CC A series of genes (Q78939-79002) encoding human immunoglobulin variable heavy chains. The genes were isolated and cloned from a series of cosmid constructs: Y202; Y103; Y21; Y6; Y24; 3-31; M84; M18 and M131, by PCR amplification using primers Q78917-38. The genes are subdivided into 5







Db	287	agaaccagggtgctcgtccatgaacacacgtgggtcccgagggaacacagccacacataattac	346
Qy	290	GTAACCAAGGTTGTTCTGACCATGCTAAACATGCACCGCGTTGACACCGCTACCTACTACT	349
Db	347	gtgc 350	
Qy	350	gcgc 353	
RESULT 14			
ID	Q75916 standard; DNA; 418 BP.		
AC	Q75916;		
DT	23-AUG-1995 (first entry)		
DE	Anti-human IL-6 chimaeric Ab H chain V region in HEL-RVH-SK2a.		
KW	Primer; PCR; amplify; kappa; light chain; variable region; mouse; human;		
KW	interleukin; antibody; hybridoma; CDR; framework; constant region;		
KW	heavy chain; disorder; antigenicity; ds.		

FT	/*tag= b	
FT	mat peptide	58..417
FT	/*tag= c	
PN	W09428159-A.	
PD	08-DEC-1994.	
PF	30-MAY-1994;	J00859.
PR	31-MAY-1993;	JP-129787.
PA	(CHUS ) CHUGAI SEIYAKU KK.	
PA	(CHUS ) CHUGAI PHARM CO LTD.	
PI	Hirata Y, Sato K, Tsuchiya M;	
DR	WPI; 95-022828/03.	
DR	P-PSDB; R67658.	
PT	Antibody against IL-6 - useful for the therapy and treatment of	
PT	IL-6 related disorders.	
PS	Claim 21; Page 60-61; 82pp; Japanese.	

CC (R77201-3) inserted into several framework regions (FR) (R77204-7) and  
CC (ii) a human light chain constant region and (b) a heavy chain with (i)  
CC variable region containing 3 CDR (R77212-4) inserted into an FR  
CC (R77215-8) and (ii) a human light chain constant region. The FR of the  
CC light chain may be mouse derived (Q75888) or from the human antibody REI  
CC The heavy chain FR may also be mouse derived (Q75889) or from the human  
CC antibody DAM. The antibodies can be used in the treatment of IL-6  
CC related disorders. The antibodies are useful as they have low  
CC antigenicity due to the use of human derived sequences and low  
CC antigenicity mouse derived sequences.  
SQ Sequence 418 BP; 94 A; 116 C; 110 G; 98 T;

CC light chain may be mouse derived (Q75888) or from the human antibody REB1

CC The heavy chain FR may also be mouse derived (Q75898) or from the human antibody REB1

CC antibody DW4. The antibodies can be used in the treatment of IL-6 related disorders. The antibodies are useful as they have low antigenicity due to the use of human derived sequences and low antigenicity mouse derived sequences.

CC Sequence 418 BP; 94 A; 116 C; 110 G; 98 T;

SQ

CC antigenicity due to the use of human derived sequences and low  
CC antigenicity mouse derived sequences.  
SQ Sequence 418 BP; 94 A; 116 C; 110 G; 98 T;

Query Match 27.0%; Score 114; DB 13; Length 418;  
Best Local Similarity 68.8%; Pred. No. 1.26e-61;  
Matches 209; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

Db 47 gtgctcactccccagtgactctgaggaggtctggacctgccttgdagacctacacaga 106  
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Qy 50 GTGCTTACGGCAGGTTCCTCGCTCAATCCGGTCCGGCACTACTTAACGCCACCAGA 109

Qy 50 GTGCTACGGGCAGGTTACCCCTGGCTGAATCCGGTCCGGCACTAGTTAAACCGACCCAGA 109

Db	546	ctataaccatccctgaagagccggtccacaatctccaagataactccaccaaacagggt	605
Qy	240	TTACACCCGAGCCTGAATCCCGCTCTGACGATATCCAAAGACACCTCCGCTAACCAGGT	299
Db	606	attctccaagatcaccagctggagactgcagatactgcacatactctgtgctcga	663
Qy	300	TGTTCTGACCATGACTAACATGACCGGCTTGACACCGGTACTCTACTACCTGCGGCTCGA	357

Qy	230	ACGACAAACGGTTACAAACCGAGCGCTGAAATCCCGTCTGACGATATCCAAAGACACCTCCC	289
Db	287	agaaccagggtgtcctgtccatgaacacgctgggtcccgagggaacacggccacattact	346
Qy	290	GTAACCAAGGTTCTTGTGACCATGCTAATCATGGACCGCGGTGACACGCGTACCTACT	349
Db	347	gtgc 350	
Qy	350	gcgc 353	

Query Match 26.5%; Score 112; DB 12; Length 738;  
Best Local Similarity 68.8%; Pred. No. 3.32e-60;  
Matches 205; Conservative 0; Mismatches 93; Indels

[illegible]

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WATERMAN

(TM)

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MPsrch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed Mar 19 07:48:09 1997; MaePar time 286.77 Seconds  
1214.896 Million cell updates/sec

Tabular output not generated.

Title: >US-08-612-929-11

Description: (1-423) from US08612929.seq

Perfect Score: 423

N.A. Sequence: 1 ATGGCTTTCAGACCCAGGT.....CCCGAGTTACGTCAGCTCA 423

Comp: TACCACACGCTTGGGTCCA.....GGGTCATGGCAGCTGAGT

Scoring table: TABLE default

Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 279077 seqs, 411808665 bases x 2

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: embl-new5

1:BCT 2:FUN 3:INV1 4:INV2 5:ORG 6:MAM 7:VRT 8:PLN 9:PRI  
10:PRO1 11:PRO2 12:ROD 13:SYN 14:UNC 15:VIR

Database: genbank94

16:BCT1 17:BCT2 18:BCT3 19:BCT4 20:BCT5 21:BCT6 22:BCT7  
23:BCT8 24:BCT9 25:INV1 26:INV2 27:INV3 28:INV4 29:INV5  
30:INV6 31:INV7 32:MAM1 33:MAM2 34:MAM3 35:VRT1 36:VRT2  
37:VRT3 38:PAT1 39:PAT2 40:PAT3 41:PHG 42:PLN1 43:PLN2  
44:PLN3 45:PLN4 46:PLN5 47:PLN6 48:PLN7 49:PLN8 50:PRI1  
51:PRI2 52:PRI3 53:PRI4 54:PRI5 55:PRI6 56:PRI7 57:PRI8  
58:PRI9 59:PRI10 60:PRI11 61:PRI12 62:PRI13 63:ROD1  
64:ROD2 65:ROD3 66:ROD4 67:ROD5 68:ROD6 69:ROD7 70:ROD8  
71:STR 72:SYN 73:UNA 74:VRL1 75:VRL2 76:VRL3 77:VRL4  
78:VRL5 79:VRL6 80:VRL7 81:VRL8

Database: genbank-new5

82:BCT 83:INV1 84:INV2 85:MAM 86:VRT 87:PAT 88:PHG  
89:PLN 90:PRI 91:ROD 92:STR 93:SYN 94:UNA 95:VRL

Database: u-embl46\_94

96:part1

Statistics: Mean 10.141; Variance 4.217; scale 2.405

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description	Pred. No.
1	139	32.9	389	59	HUMIGHCXH	Human fetal Ig heavy	5.05e-104
2	135	31.9	363	62	U00575	Human immunoglobulin	3.84e-100
3	132	31.2	460	59	HUMIGHV2H	Human Ig germline hea	3.09e-97
4	131	31.0	417	56	HSVHRA10	H.sapiens mRNA for im	2.87e-96
5	131	31.0	461	59	HUMIGHV2J	Human Ig germline hea	2.87e-96
6	130	30.7	297	54	HSIGVHLI1	H.sapiens variable re	2.66e-95
7	130	30.7	432	56	HSVHIF3	H.sapiens mRNA for im	2.66e-95
8	130	30.7	445	59	HUMIGHV2F	Human Ig germline hea	2.66e-95
9	129	30.5	363	56	HSVHP46	H.sapiens mRNA P46 fo	2.46e-94
10	129	30.5	366	62	S73953	Ig VH-immunoglobulin	2.46e-94
11	129	30.5	460	59	HUMIGHV2K	Human Ig germline hea	2.46e-94
12	128	30.3	288	54	HSIGDP27	H.sapiens germline Ig	2.27e-93
13	128	30.3	406	59	HUMIGAMKB	Human Ig rearranged a	2.27e-93
14	128	30.3	433	54	HSIGVHC2B	H.sapiens germline im	2.27e-93
15	128	30.3	461	59	HUMIGHV2D	Human Ig germline hea	2.27e-93
16	127	30.0	296	62	S69331	IgVH2/JH6-anti-pyruva	2.09e-92
17	127	30.0	366	62	U00552	Human clone Anu43-3 Ig	2.09e-92
18	127	30.0	369	62	U00555	Human clone Anu43-2 I	2.09e-92
19	127	30.0	415	54	HSIGHC2B	H.sapiens Ig rearrang	2.09e-92
20	127	30.0	442	59	HUMIGHV2E	Human Ig germline hea	2.09e-92
21	127	30.0	448	59	HUMIGHV2I	Human Ig germline hea	2.09e-92
22	127	30.0	460	59	HUMIGHV2C	Human Ig germline hea	2.09e-92
23	127	30.0	580	59	HUMIGHV2X	Human immunoglobulin	2.09e-92
24	127	30.0	613	56	HSVII5	H.sapiens VII-5 gene	2.09e-92
25	126	29.8	288	54	HSIGDP28	H.sapiens germline Ig	1.93e-91
26	126	29.8	433	54	HSIGVHC2A	H.sapiens germline im	1.93e-91
27	126	29.8	433	54	HSIGVH2	H.sapiens germline im	1.93e-91
28	126	29.8	433	54	HSIGVHC2E	H.sapiens germline im	1.93e-91
29	126	29.8	433	54	HSIGVHC2	H.sapiens germline im	1.93e-91
30	126	29.8	433	54	HSIGVH1A	H.sapiens germline im	1.93e-91
31	126	29.8	438	56	HSWAD3VR	H.sapiens heavy chain	1.93e-91
32	125	29.6	356	55	HSU00507	Human immunoglobulin	1.77e-90
33	124	29.3	366	64	MMIGMSMJ	Mouse mRNA for variab	1.63e-89
34	124	29.3	433	54	HSIGVHC1	H.sapiens germline im	1.63e-89
35	124	29.3	433	54	HSIGVH1B	H.sapiens germline im	1.63e-89
36	124	29.3	433	54	HSIGVHC2D	H.sapiens germline im	1.63e-89
37	124	29.3	440	59	HUMIGHV2B	Human Ig germline hea	1.63e-89
38	124	29.3	444	59	HUMIGHV2G	Human Ig germline hea	1.63e-89
39	124	29.3	546	59	HUMIGH226X	Human immunoglobulin	1.63e-89
40	123	29.1	360	63	MMHCVR3	M.musculus (A.SW) mRN	1.49e-88
41	123	29.1	441	62	S67984	Ig VH1 JH5-anti-HIV	1.49e-88
42	122	28.8	440	59	HUMIGHV2A	Human Ig germline hea	1.37e-87
43	121	28.6	360	65	MMU22979	Mus musculus CB17 SCI	1.25e-86
44	121	28.6	399	59	HUMIGHVAA	Human Ig rearranged h	1.25e-86
45	121	28.6	469	52	HSACVRA	H.sapiens DNA for mon	1.25e-86

## ALIGNMENTS

RESULT 1  
LOCUS HUMIGHCXH 389 bp mRNA PRI 11-JUL-1995  
DEFINITION Human fetal Ig heavy chain variable region (clone M60) mRNA,  
partial cds.  
ACCESSION M34027  
NID g185270  
KEYWORDS D-region; J-region; V-region; immunoglobulin heavy chain;  
processed gene.  
SOURCE Homo sapiens (individual\_isolate\_H8409) (clone: M60) 104 day foetus









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Db 121 cagccccagaaagccctggagtgcttgacactcattattggatgatgaagcgc 180
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Qy 181 CAGCCGCGGGTAAAGTGCTAGAAATGGCTGGCTACATCTACTGGGACGACGACAAAGT 240

Db 181 tacagccattctctgaagagcaggctcaccatcaccagaagacacacctccaaaaaccagggtg 240
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Qy 241 TACAACCGGAGCGCTGAATCCGGCTGTGACGATATCCAAAGACACCTCCCGTAACCAAGTT 300

Db 241 gtccttacaatgaccaacatggaccctgtggacacgccacatatattctgtgcacg 296
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Qy 301 GTTCTGACCATGACTACATGACCGCGGTGACACCGGTACTACTACTGCGGCTCG 356

RESULT 7
LOCUS HSVHF3 432 bp RNA PRI 15-FEB-1996
DEFINITION H.sapiens mRNA for immunoglobulin heavy chain V-region (clone
CDN3IF3).
ACCESSION 247235
NID g1197326
KEYWORDS immunoglobulin; immunoglobulin heavy chain; variable region.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Eukaryotes; Mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 113)
AUTHORS Demaison,C., David,D., Letourneur,F., Zouali,M., Saragosti,S. and
Theze,J.
TITLE A cDNA/anchor-PCR approach to analyse the human VH gene repertoire
expressed by peripheral CD19+ B cells reveals a strong bias usage
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 432)
AUTHORS Demaison,C.
TITLE Direct Submission
JOURNAL Submitted (16-DEC-1994) Christophe Demaison, Immunologie, Unite
d'Immunogenetique Cellulaire-Institut Pasteur, 25, rue du Docteur
Roux, Paris, 75015, FRANCE
REFERENCE 3 (bases 1 to 432)
AUTHORS Demaison,C., David,D., Letourneur,F., Theze,J., Saragosti,S. and
Zouali,M.
TITLE Analysis of human VH gene repertoire expression in peripheral CD19+
B cells
JOURNAL Immunogenetics 42 (5), 342-352 (1995)
MEDLINE 9606568
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source Location/Qualifiers
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/organism="Homo sapiens"
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Matches 213; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

Db 58 cagatcaccttgaaagagctgtgctcctacgtgtgaaacccacacagacctcacgctg 117
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Db 178 cagccccagaaagccctggagtgcttgacactcattattggatgatgaagcgc 237
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Qy 181 CAGCCGCGGGTAAAGTGCTAGAAATGGCTGGCTCAGATCTACTTGGGACGACGACAAAGT 240

Db 238 tacagccattctctgaagagcaggctcaccatcaccagaagacacacctccaaaaaccagggtg 297
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Qy 241 TACAACCGGAGCGCTGAATCCGGCTGTGACGATATCCAAAGACACACCTCCCGTAACCAAGTT 300

Db 298 gtccttacaatgaccaacatggaccctgtggacacgccacatatattctgtgcacg 353
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Qy 301 GTTCTGACCATGACTACATGACCGCGGTGACACCGGTACTACTACTGCGGCTCG 356

RESULT 8
LOCUS HUMIGHV2F 445 bp DNA PRI 16-MAR-1994
DEFINITION Human Ig germline heavy-chain mRNA, subgroup VH2, V-region, 5' end.
ACCESSION L21967
NID g405211
KEYWORDS immunoglobulin heavy chain; variable region subgroup VH2.
SOURCE Homo sapiens DNA.
ORGANISM Homo sapiens
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Primates; Haplorhini; Catarrhini; Hominidae.
REFERENCE 1 (bases 1 to 445)
AUTHORS Andris,J.S., Brodeur,B.R. and Capra,J.D.
TITLE Molecular characterization of human antibodies to bacterial
antigens: utilization of the less frequently expressed VH2 and VH6
heavy chain variable region gene families
JOURNAL Mol. Immunol. 30 (17), 1601-1616 (1993)
MEDLINE 94067179
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source Location/Qualifiers
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/germline
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sig_peptide join(1..46,133..143)
intron 47..137
V_region 144..440
misc_signal /product="immunoglobulin heavy chain"
441..445
/notes="immunoglobulin heptamer/nonamer recombination
signal; putative"
BASE COUNT 100 a 128 c 104 g 113 t
ORIGIN
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Best Local Similarity 72.1%; Pred. No. 2.66e-95;
Matches 212; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

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Qy 63 GGTACCCCTCGCTGAATCCGGTCCGGCACTAGTTAAACCCGACCCCTGACGTTAAC 122

Db 206 ctgacaccttctctgggttctcactcagcactagtggaatgtgtgagctggatccgtca 265
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Qy 123 CTGCACCTTCTCCGCTTCTCCCTGTGCACTCCGCTATGGGTGTTTCTTGGATCCGTCA 182
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11

Db 266 gcccccaggagccttgagtgcttcacgcttgattgattgattgataataacta 325  
Qy 183 ccccccgggttaagctgtagaatggctggctcacatctcagacgacgacaaacgtta 242

Db 326 cagcaatctctgaagaccaggtccaccatctccaagacacactccaaaacacaggtggt 385  
Qy 243 caaccccgagctgaattcccgctgcagatatccaaagacacactcccgtaaccaggtgt 302

Db 386 ccttaaatgaccaaactgagacccttgagacagccagccagctattactgtgcacg 439  
Qy 303 tctgaccatgactaaatggacccggctgacacggctacctaactgactgacctcg 356

RESULT 9  
LOCUS HSRVP46 363 bp RNA PRI 01-JUN-1993  
DEFINITION H.sapiens mRNA P46 for IG heavy chain variable region.  
ACCESSION X64147  
NID g37827  
KEYWORDS Ig heavy chain; immunoglobulin;  
immunoglobulin heavy chain variable region; VH region.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Eukaryotes; Mitochondrial eukaryotes; Metazoa/Eumycota group;  
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;  
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata;  
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;  
Catarrhini; Hominiidae; Homo.

REFERENCE 1 (bases 1 to 363)  
AUTHORS Ebeling, S.B., Schutte, M.E., Akkermans-Koolhaas, K.E., Bloem, A.C.,  
Gnelli-Meyling, F.H. and Logtenberg, T.

TITLE Expression of members of the Immunoglobulin VH3 gene families is  
not restricted at the level of individual genes in human chronic  
lymphocytic leukemia

JOURNAL Int. Immunol. 4 (3), 313-320 (1992)

MEDLINE 92232604

REFERENCE 2 (bases 1 to 363)

AUTHORS Ebeling, S.

TITLE Direct Submission

JOURNAL Submitted (23-DEC-1991) to the EMBL/GenBank/DBJ databases. S.

COMMENT Ebeling, Dept. Clinical Immunology, University Hospital Utrecht,  
Heidelberglaan, 3584 CX Utrecht, THE NETHERLANDS  
See also X64234-43 & X64147.

FEATURES Location/Qualifiers

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/organism="Homo sapiens"

/dev\_stage="adult"

/tissue\_type="peripheral blood"

/cell\_type="B lymphocyte"

/cell\_line="peripheral blood from CLL patient P46"

/isolate="P46"

/chromosome="14"

misc\_feature 1..300

/note="VH2 gene"

misc\_feature 301..327

/note="D segment"

misc\_feature 328..363

/note="JH4 gene"

BASE COUNT 87 a 109 c 95 g 72 t

ORIGIN

Query Match 30.5%; Score 129; DB 56; Length 363;

Best Local Similarity 67.8%; Pred. No. 2,466-94;

Matches 246; Conservative 0; Mismatches 117; Indels 0; Gaps 0;

Mar 19:07:53

US-08-612-929-1.lrg

12

Db 1 cagatcacctgaagagctcgtcctacgctgggtgaacccacacagccctcacgtg 60  
Qy 61 CAGGTTACCTCGCTGATCCGGTCCGGCACTAGTTAAACCCGACCCCTGAGGTTA 120

Db 61 acctgcaacctctcgtgggtctcactcagcactagtggagtgggtgggtggatccgt 120  
Qy 121 ACCTGCACCTTCTCCGGTTTCTCCCTCTCGACCTCCGGTATGGGTGTTCTCTGGATCGGT 180

Db 121 cagccccaggaagccctcgagtggctgacctcattatttggatgatgaagcgc 180  
Qy 181 CAGCGCCGGGTTAAAGTCTAGAAATGGCTGGCTCACAATCTACTGGGACGACCAAAAGT 240

Db 181 tacagccatctctgaagagcaggctcacatccacaaaggacacactccaaaacacaggtg 240  
Qy 241 TACAACCCGAGCCTGAAATCCCGTCTGAGATATCCAAAGACACCTCCCGTAACCAAGTT 300

Db 241 gtcctacaatgaccaacatggaccctgtggacacagccacacacattactgtgcacacagg 300  
Qy 301 GTTGTGACCATGACTAACATGGACCGGTTGACACCGCTACCTACTACTGCGGTGCAGGC 360

Db 301 tatagtggctacgagggcgtaggcgactactggggccagggaaacctgggtcacccgtccc 360  
Qy 361 GAAACCGTTTTCTACTGCTTTCGACGTTTGGGTCGTGGTACCCAGTTACCGTGAGC 420

Db 361 tea 363  
Qy 421 TCA 423

RESULT 10  
LOCUS S73953 366 bp mRNA PRI 28-APR-1995  
DEFINITION Ig VH-immunoglobulin heavy chain VDJ region [human, chronic  
lymphocytic leukemia patient ARN, mRNA Partial, 366 nt].

ACCESSION S73953

NID g786355

KEYWORDS human chronic lymphocytic leukemia patient ARN.

SOURCE Homo sapiens

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 366)

AUTHORS Korganow, A.S., Martin, T., Weber, J.C., Lioure, B., Lutz, P.,

Knapp, A.M. and Pasquali, J.L.

TITLE Molecular analysis of rearranged VH genes during B cell chronic  
lymphocytic leukemia: intraclonal stability is frequent but not

constant

JOURNAL Leuk. Lymphoma 14 (1-2), 55-69 (1994)

MEDLINE 95004012

REMARK GenBank staff at the National Library of Medicine created this  
entry [NCBI gibbsq 157305] from the original journal article.

This sequence comes from Fig. 2.

FEATURES Location/Qualifiers

source 1..366

/organism="Homo sapiens"

/note="human"

Join(1..296,324..366)

/partial

/gene="Ig VH"

/note="Method: conceptual translation supplied by author.  
This sequence comes from Fig. 2."

/codon\_start=1

/product="immunoglobulin heavy chain VDJ region"

/db\_xref="PID:g786355"

/translation="QITAKESGPTLVKPTQITLTCTFCGSLSTSGVGWIRQPPG  
KALEMALIYWDKDRYSFSLKSLRTITKDTSKNQVLITWMDPDTATYYCAHHY

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BASE COUNT      90 a 106 c      95 g      75 t
ORIGIN
Query Match      30.5%; Score 129; DB 62; Length 366;
Best Local Similarity 72.0%; Pred. No. 2,46e-94;
Matches 211; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

Db      1  cagatcacctgaagagctgtgctcctcaagctggtgaacccacacagaccctcacgctg 60
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy      61  CAGGTTACCTGCGGTGAATCCGGTCGGGCACTAGTTAAACCGACCCAGACCCCTGACGTTA 120
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      61  acctgcaacctctctgggtctcactcagcactagtgagggtgggtgtgggtggtacgtg 120
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy      121  ACCTGCACTCTTCGGGTTTCCCTGTCGACCTCGGATAGGCTGTTTCCCTGGATCCGT 180
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      121  cagccccaggaaagccctggagtggttgacctatttattgggatgataagcgc 180
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy      181  CAGCCCGCGGGTAAAGGCTAGATGGCTGGCTCACATCTACTGGGACGACGACAACGTT 240
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      181  tacagccatctctgaagagcagctcacatcaccagacacacctccaaaaccagggtg 240
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Qy      241  TACAACCGCGCCTGAATCCCGTCTCAGCATATCCAAAGACACCTCCCGTAACCAAGTT 300
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      241  gtccttaaatgacaaactggacctgtggacacagccacacattattactgtgc 293
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy      301  GTTCTGACCATGACTACATGACCGCGGTGACACCGCTACCTACTACTGCGC 353
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 11
LOCUS      HUM1GVH2K      460 bp      DNA      PRI      16-MAR-1994
DEFINITION Human Ig germline heavy-chain mRNA, subgroup VH2, V-region, 5' end.
ACCESSION      L21972
NID      9405216
KEYWORDS      immunoglobulin heavy chain; variable region subgroup VH2.
SOURCE      Homo sapiens DNA.
ORGANISM      Homo sapiens
               Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
               Eutheria; Primates; Haplorhini; Catarrhini; Hominiidae.
REFERENCE      1 (bases 1 to 460)
AUTHORS      Andris,J.S., Brodeur,B.R. and Capra,J.D.
TITLE      Molecular characterization of human antibodies to bacterial
               antigens: utilization of the less frequently expressed VH2 and VH6
               heavy chain variable region gene families
JOURNAL      Mol. Immunol. 30 (17), 1601-1616 (1993)
MEDLINE      94067179
FEATURES
    source          Location/Qualifiers
    1..460
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    /germline
    /sequenced_mol="DNA"
    47..132
    intron
    144..440
    V_region        /product="immunoglobulin heavy chain"
    441..460
    misc_signal      /note="immunoglobulin heptamer/nonamer recombination
    signal; putative"
BASE COUNT      108 a 136 c      105 g      111 t
ORIGIN
Query Match      30.5%; Score 129; DB 59; Length 460;
Best Local Similarity 72.0%; Pred. No. 2,46e-94;
Matches 211; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

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```

Db      144  caggtcacctgaagagctgtggtcctcagctggtgaacccacacagaccctcacgctg 203
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Qy      61  CAGGTTACCTGCGGTGAATCCGGTCGGGCACTAGTTAAACCGACCCAGACCCCTGACGTTA 120
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Db      204  acctgcaacctctctgggtctcactcagcactagtgagggtgggtgtgggtggtacgtg 263
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Qy      121  ACCTGCACTCTTCGGGTTTCCCTGTCGACCTCGGATAGGCTGTTTCCCTGGATCCGT 180
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      264  cagccccaggaaagccctggagtggttgacctatttattgggatgataagcgc 323
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Db      324  tacgagccatctctgaagagcaggtgtcacatcaccagacacacctccaaaaccagggtg 383
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy      241  TACAACCGCGCCTGAATCCCGTCTCAGCATATCCAAAGACACCTCCCGTAACCAAGTT 300
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      384  gtccttaaatgacaaactggacctgtggacacagccacacattattactgtgc 436
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Qy      301  GTTCTGACCATGACTACATGACCGCGGTGACACCGCTACCTACTACTGCGC 353
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 12
LOCUS      HSIGDP27      288 bp      DNA      PRI      11-DEC-1992
DEFINITION H.sapiens germline Ig H-chain V-region (DP-27).
ACCESSION      Z12329
NID      932875
KEYWORDS      immunoglobulin; immunoglobulin heavy chain; variable region.
SOURCE      human.
ORGANISM      Homo sapiens
               Eukaryota; Mitochondrial eukaryotes; Metazoa/Eumycota group;
               Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
               Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
               Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;
               Catarrhini; Hominiidae; Homo.
REFERENCE      1 (bases 1 to 288)
AUTHORS      Tomlinson,M.
TITLE      Direct Submission
JOURNAL      Submitted (04-JUN-1992) to the EMBL/GenBank/DBJ databases. Ian
               Tomlinson, MRC Centre for Protein Engineering, Hills Road,
               Cambridge, CB2 2QH, U.K
REFERENCE      2 (bases 1 to 288)
AUTHORS      Tomlinson,I.M., Walter,G., Marks,J.D., Llewelyn,M.B. and Winter,G.
TITLE      The repertoire of human germline VH sequences reveals about fifty
               groups of VH segments with different hypervariable loops
JOURNAL      J. Mol. Biol. 227 (3), 776-798 (1992)
MEDLINE      93021117
FEATURES
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    /dev_stage="adult"
    /tissue_type="blood"
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    /clone="DP-27"
    /isolate="DP"
    /sex="Male"
    <1..>288
    /codon_start=1
    /product="Ig H-chain V-region (DP-27)"
    /db_xref="PID:932876"
    /translation="QVTLRESGPAIVKPTQTLITLCTFSGLSTSGMYSWIRQPPG
    KALDWLALIDWDHDDKYISTSLKTLTISKDTSKNQVLTMTNMDPVDATYY"
BASE COUNT      72 a      86 c      69 g      61 t

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## ORIGIN

Query Match	30.3%;	Score 128;	DB 59;	Length 406;
Best Local Similarity	71.6%;	Pred. No. 2,27e-93;		
Matches	212;	Conservative	0;	Mismatches 84; Indels 0; Gaps 0;

Db	32	caggtcaccttgagggagtctggtcctcgctggtgaacaccacacagccctcacactg	91
Qy	61	CAGGTACCCCTGCGTGAATCCGGTCGGGACTATTAAACGACCACGACCCCTGACGTTA	120
Db	92	aactgcaccttctctgggtctctcaetcagacactagtggaaatctctgtgagctggatccgt	151
Qy	121	ACCTGCACCTTCTCGGGTTCTCCCTGTGCGACTCCGGTATGGGTGTTTCTCGTAGCCTG	180
Db	152	cagccccagggagggccctggagtggctgactcgttgactgggatgatataaat	211
Qy	181	CAGCCGCCGGGTAAAGTCTTAGAATGGCTGCTCACATCTACTGGGACACGACCAACAGCT	240
Db	212	tacagcacattctctgaagaagagactcaccatctccaggacacactcccacacccgggtg	271
Qy	241	TACAACCGAGCCTGAAATCCCGTCTGACGATATCCAAGAAGACACTCCCGTAACCAAGTT	300
Db	272	gtccttaacaatgaccaatggacctgtggacacagccaogtactcttgtgcagc	327
Qy	301	GTTCTGACATGACTAACATGGACCGGTTGACACCGCTTACTTACTACTCGCGTCG	356

RESULT	14
LOCUS	HSGVHC2B 433 bp DNA PRI 30-OCT-1995
DEFINITION	H.sapiens germline immunoglobulin heavy chain, variable region, (VH2-MC2b).
ACCESSION	X92243
NID	g1045171
KEYWORDS	germ line; immunoglobulin.
SOURCE	human.
ORGANISM	Homo sapiens
AUTHORS	Eukaryotae; mitochondrion eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae;
TITLE	Use of family specific leader region primers for PCR amplification of the human heavy chain variable region gene repertoire
JOURNAL	Mol. Immunol. 29 (2), 193-203 (1992)
MEDLINE	92178228
FEATURES	Location/Qualifiers 1..433 /organism="Homo sapiens" BASE COUNT     95 a 123 c 102 g 113 t ORIGIN
Query Match	30.3%; Score 128; DB 54; Length 433;
Best Local Similarity	72.1%; Pred. No. 2.27e-03;
Matches	209; Conservative 0; Mismatches 81; Indels 0; Gaps 0;
Dbb	144 caggtcaaccttaggaagtctggcttcgcctggtagaacccacacagaccctcacactg 203 
Qy	61 CAGGTTTACCCTTCGGTGTAATCCGTCCGCCACTAGTTAAACCGACCCAGACCCCTGCAGTTA 120
Dbb	204 acctgcacctctcctgggttctcatcactcagcactagtggatgtgtgagctgatccgt 263 
Qy	121 ACCTGCACCTTCTCCGGTTTCTCCCTGTCACACCCGGGTATGGGTTCTTCCTGGATCCGT 180
Dbb	264 cagcccccgaggaaagccctggagtggtctgcactcattgattgggagtgatgataaatac 323

		/organism="Homo sapiens"			
BASE COUNT	95 a	123 c	102 g	113 t	
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	Best Local Similarity	72.1%;	Pred. No. 2,27e-93;		
Matches	209; Conservative	0;	Mismatches 81;	Indels 0; Gaps 0;	
Db	144	caggtcaccttgaggagctcgttgcgctcggtgaaccacacagacctcacactg	203		
Qy	61	CAGGTTACCCCTCGTGAATCCGGTCGGCACTAGTTAAACGCCACCACGCCCTGCAGTTA	120		
Db	204	acctgcacctctctgggtttctcaactcagccactagtggaaatgtgtgagctggatcagctg	263		
Qy	121	ACCTGCACCTTCGGGTTCCTCCTCGACTCCGGTATGGGTGTTTCCTGGATCCGCT	180		
Db	264	cagcccccggggaagcccctggagtggttgtcactcatgatattggatgatgataaat ac	323		

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Qy 241 TAGAACCGCCCTGAAATCCCGTCTCAGCATATCCAAAGACACTCCCCTGAACCAAGTT 300
Db 384 gtcttaaatgaaccaatagaccctgtggacacagccagtattactgtcacg 439
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Qy 301 GTTCTGACCATGACTAACAATGGACCGCGGTTCACACCGCTACTCCTACTACTGCCTCG 356
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Search completed: Wed Mar 19 07:54:50 1997  
Job time : 401 secs.

Search completed: Wed Mar 19 07:54:50 1997  
Job time : 401 secs.



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WVPSRLH (TM)

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MParch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Mar 18 10:05:17 1997; MaePar time 4.30 Seconds  
608.232 Million cell updates/sec

Tabular output not generated.

Title: >US-08-612-929-12  
Description: (1-141) from US08612929.pep  
Perfect Score: 1068  
Sequence: 1 MWLQTVFISLLWISGAYG.....TVFYVFDWGRGPTVSS 141

Scoring table: PAM 150  
Gap 11

Searched: 52205 seqs, 18531385 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: swiss-prot33  
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10

Statistics: Mean 43.081; Variance 80.072; scale 0.538

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	655	61.3	120	4	HV2B_HUMAN IG HEAVY CHAIN V-II R	7.85e-114
2	652	61.0	121	4	HV2E_HUMAN IG HEAVY CHAIN V-II R	3.56e-113
3	640	59.9	125	4	HV2D_HUMAN IG HEAVY CHAIN V-II R	1.50e-110
4	607	56.8	126	4	HV2A_HUMAN IG HEAVY CHAIN V-II R	2.40e-103
5	605	56.6	147	4	HV2H_HUMAN IG HEAVY CHAIN PRECUR	6.54e-103
6	563	52.7	119	4	HV2C_HUMAN IG HEAVY CHAIN V-II R	8.68e-94
7	479	44.9	144	4	HV43_MOUSE IG HEAVY CHAIN PRECUR	1.04e-75
8	456	42.7	137	4	HV46_MOUSE IG HEAVY CHAIN PRECUR	8.28e-71
9	447	41.9	115	4	HV44_MOUSE IG HEAVY CHAIN PRECUR	6.76e-69
10	431	40.4	135	4	HV02_XENLA IG HEAVY CHAIN PRECUR	1.66e-65
11	418	39.1	122	4	HV3G_HUMAN IG HEAVY CHAIN V-III	9.18e-63
12	416	39.0	116	4	HV51_MOUSE IG HEAVY CHAIN PRECUR	2.42e-62
13	412	38.6	116	4	HV61_MOUSE IG HEAVY CHAIN PRECUR	1.68e-61

14	407	38.1	116	4	HV60_MOUSE IG HEAVY CHAIN PRECUR	1.90e-60
15	403	37.7	119	4	HV38_MOUSE IG HEAVY CHAIN V REGI	1.31e-59
16	402	37.6	117	4	HV62_MOUSE IG HEAVY CHAIN PRECUR	2.13e-59
17	402	37.6	119	4	HV3I_HUMAN IG HEAVY CHAIN V-III	2.13e-59
18	397	37.2	129	4	HV2F_HUMAN IG HEAVY CHAIN V-II R	2.38e-58
19	394	36.9	136	4	HV01_XENLA IG HEAVY CHAIN PRECUR	1.01e-57
20	392	36.7	136	4	HV16_MOUSE IG HEAVY CHAIN PRECUR	2.65e-57
21	386	36.1	123	4	HV24_MOUSE IG HEAVY CHAIN V REGI	4.75e-56
22	384	36.0	122	4	HV21_MOUSE IG HEAVY CHAIN V REGI	1.24e-55
23	383	35.9	117	4	HV2G_HUMAN IG HEAVY CHAIN V-II R	2.01e-55
24	383	35.9	123	4	HV18_MOUSE IG HEAVY CHAIN V REGI	2.01e-55
25	382	35.8	121	4	HV3J_HUMAN IG HEAVY CHAIN V-III	3.25e-55
26	382	35.8	123	4	HV19_MOUSE IG HEAVY CHAIN V-III	3.25e-55
27	381	35.7	117	4	HV30_HUMAN IG HEAVY CHAIN V-III	5.25e-55
28	381	35.7	146	4	HV2I_HUMAN IG HEAVY CHAIN PRECUR	5.25e-55
29	377	35.3	123	4	HV22_MOUSE IG HEAVY CHAIN V REGI	3.58e-54
30	377	35.3	123	4	HV23_MOUSE IG HEAVY CHAIN V REGI	3.58e-54
31	373	34.9	119	4	HV40_MOUSE IG HEAVY CHAIN V REGI	2.43e-53
32	372	34.8	122	4	HV3H_HUMAN IG HEAVY CHAIN V-III	3.93e-53
33	369	34.6	116	4	HV1A_RABBIT IG HEAVY CHAIN V-A1 R	1.65e-52
34	369	34.6	119	4	HV37_MOUSE IG HEAVY CHAIN V REGI	1.65e-52
35	370	34.6	122	4	HV20_MOUSE IG HEAVY CHAIN V REGI	1.02e-52
36	368	34.5	119	4	HV3N_HUMAN IG HEAVY CHAIN V-III	2.66e-52
37	366	34.3	115	4	HV3F_HUMAN IG HEAVY CHAIN V-III	6.93e-52
38	364	34.1	126	4	HV3K_HUMAN IG HEAVY CHAIN V-III	1.80e-51
39	363	34.0	119	4	HV3M_HUMAN IG HEAVY CHAIN V-III	2.90e-51
40	361	33.8	115	4	HV3S_HUMAN IG HEAVY CHAIN V-III	7.53e-51
41	358	33.5	117	4	HV13_MOUSE IG HEAVY CHAIN V REGI	3.15e-50
42	358	33.5	117	4	HV2B_RABBIT IG HEAVY CHAIN V-A2 R	3.15e-50
43	358	33.5	136	4	HV2C_RABBIT IG HEAVY CHAIN PRECUR	3.15e-50
44	357	33.4	117	4	HV03_CAICR IG HEAVY CHAIN PRECUR	5.07e-50
45	357	33.4	123	4	HV25_MOUSE IG HEAVY CHAIN V REGI	5.07e-50

## ALIGNMENTS

RESULT 1  
ID HV2B\_HUMAN STANDARD; PRT; 120 AA.  
AC P01815;  
DT 21-JUL-1986 (REL. 01, CREATED)  
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
DT 21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)  
DE IG HEAVY CHAIN V-II REGION (COR).  
OS HOMO SAPIENS (HUMAN).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; PRIMATES.  
RN [1]  
RP SEQUENCE.  
RX MEDLINE; 70258837.  
RA PRESS E.M., HOGG N.M.;  
RL BIOCHEM. J. 117:641-660(1970).  
CC -!- THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA PROTEIN.  
DR PIR; A02089; GIHUCO.  
DR HSP; P01789; 2FGW.  
KW IMMUNOGLOBULIN V REGION; GLYCOPROTEIN.  
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT DISULFID 22 94  
FT CARBOHYD 62 62  
FT NON TER 120 120  
SQ SEQUENCE 120 AA; D690F656 CRC32;

Query Match 61.3%; Score 655; DB 4; Length 120;  
Best Local Similarity 81.3%; Pred. No. 7.85e-114;  
Matches 100; Conservative 6; Mismatches 12; Indels 5; Gaps 3;

Mar 18 10:03

US-08-612-920-12.rsp

3

Db 1 qvtlresgpalvkptqtlitctfsgfslstgmcvgwvqirppgkalewlaridwdddky 60  
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Qy 21 QVTLRESGALVKPTQTLITCTFSGFSLSTGMCVSWIRQPPCKGLEWLAHIYWDGDKR 80  
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Db 61 yntelettriskdtsnqvltm---dpvdtatycarivitvpsapagymdwgrgtptv 117  
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Qy 81 YNPSIKSLRITISKOTSRNQVLTMTNNDPVDATYYCARRETTFY-W-YFDVWGRGTPTV 138  
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Db 118 vas 120  
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Qy 139 VSS 141  
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RESULT 2  
ID HV2D HUMAN STANDARD; PRT; 121 AA.  
AC P01817;  
DT 21-JUL-1986 (REL. 01, CREATED)  
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
DT 21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)  
DE IG HEAVY CHAIN V-II REGION (HE).  
OS HOMO SAPIENS (HUMAN).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; PRIMATES.  
RN [1]  
RP SEQUENCE.  
RX MEDLINE; 70114712.  
RA CUNNINGHAM B.A., PFLUM M.N., RUTISHAUSER U., EDELMAN G.M.;  
RL PROC. NATL. ACAD. SCI. U.S.A. 64:997-1003 (1969).  
CC -/- THIS GAMMA-1 CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.  
DR PIR; A02093; GIHUE.  
DR HSSP; P01772; IFGV.  
KW IMMUNOGLOBULIN V REGION.  
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT NON\_TER 121 121  
SQ SEQUENCE 121 AA; 13483 MW; B91154F1 CRC32;

Query Match 61.08; Score 652; DB 4; Length 121;  
Best Local Similarity 71.3%; Pred. No. 3.56e-113;  
Matches 87; Conservative 22; Mismatches 11; Indels 2; Gaps 2;

Db 1 qvtlresgpalvkptqtlitctfsgfslstgmcvgwvqirppgkalewlaridwdddk 60  
|||||  
Qy 21 QVTLRESGALVKPTQTLITCTFSGFSLSTGMCVSWIRQPPCKGLEWLAHIYWDGDKR 79  
|||||  
Db 61 rfsepelkerltvtrtdkngvltmndpvdtdatycvhrhrptl-afdwgqgtkvav 119  
|||||  
Qy 80 RYNPSIKSLRITISKOTSRNQVLTMTNNDPVDATYYCARRETTFYWFYFDVWGRGTPTV 139  
|||||  
Db 120 ss 121  
|||  
Qy 140 SS 141  
|||

RESULT 3  
ID HV2D HUMAN STANDARD; PRT; 125 AA.  
AC P01817;  
DT 21-JUL-1986 (REL. 01, CREATED)  
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
DT 21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)  
DE IG HEAVY CHAIN V-II REGION (MCE).  
OS HOMO SAPIENS (HUMAN).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; PRIMATES.

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RN [1]  
RP SEQUENCE.  
RX MEDLINE; 81118242.  
RA GERBER-JENSON B., KAZIN A., KEHOE J.M., SCHEFFEL C., ERICKSON B.W.,  
RA LITMAN G.W.;  
RL J. IMMUNOL. 126:1212-1216 (1981).  
CC -/- THIS CHAIN WAS DERIVED FROM A MONOCLONAL IGM CRYOIMMUNOGLOBULIN.  
DR PIR; A02092; MHRUMC.  
DR HSSP; P01772; IFGV.  
KW IMMUNOGLOBULIN V REGION.  
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT NON\_TER 125 125  
SQ SEQUENCE 125 AA; 13783 MW; 7F897793 CRC32;  
Query Match 59.9%; Score 640; DB 4; Length 125;  
Best Local Similarity 73.6%; Pred. No. 1.50e-110;  
Matches 92; Conservative 17; Mismatches 12; Indels 4; Gaps 3;

Db 1 qitlkesgptlvkptetltctfsgfslstgmcvgwvqirppgkalewlaridwdddkr 60  
|||||  
Qy 21 QVTLRESGALVKPTQTLITCTFSGFSLSTGMCVSWIRQPPCKGLEWLAHIYWDGDKR 80  
|||||  
Db 61 yepelrlerltgktdsrnqvltmndpvdsgtyfcahrppwrftgnlggfdxwqgtl 120  
|||||  
Qy 81 YNPSIKSLRITISKOTSRNQVLTMTNNDPVDATYYCARRET-TFY-WY-FDVMGRGTP 136  
|||||  
Db 121 vtvas 125  
|||||  
Qy 137 VTSS 141  
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RESULT 4

ID HV2A HUMAN STANDARD; PRT; 126 AA.  
AC P01814;  
DT 21-JUL-1986 (REL. 01, CREATED)  
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
DT 21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)  
DE IG HEAVY CHAIN V-II REGION (OU).  
OS HOMO SAPIENS (HUMAN).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; PRIMATES.  
RN [1]  
RP SEQUENCE.  
RX MEDLINE; 74005511.  
RA PUTNAM F.W., FLORENT G., PAUL C., SHINODA T., SHIMIZU A.;  
RL SCIENCE 182:287-291 (1973).  
CC -/- THIS MU CHAIN WAS ISOLATED FROM A WALDENSTROM'S MACROGLOBULIN.  
DR PIR; A02088; MHRUOU.  
DR HSSP; P01607; IFGV.  
KW IMMUNOGLOBULIN V REGION.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT DISULFID 22 97  
FT NON\_TER 126 126  
SQ SEQUENCE 126 AA; 14276 MW; 459E1429 CRC32;

Query Match 56.8%; Score 607; DB 4; Length 126;  
Best Local Similarity 69.3%; Pred. No. 2.40e-103;  
Matches 88; Conservative 18; Mismatches 14; Indels 7; Gaps 5;

Db 1 qvtltesgpalvkpqlitctfsgfslstgmrsvswirppgkalewlarib-bbdkf 59  
|||||  
Qy 21 QVTLRESGALVKPTQTLITCTFSGFSLSTGMCVSWIRQPPCKGLEWLAHIYWDGDKR 80  
|||||  
Db 60 ywsteltriskndeknqvlinimvpydtatycarvsvmagyfyymvdywqkg 119  
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	Query Match	56.6%;	Score 605;	DB 4;	Length 147;
	Best Local Similarity	75.0%;	Pred. No. 6.54e-103;		
	Matches	84;	Conservative	14;	Mismatches 13;
				Indels	1;
				Gaps	1;
Db	9	llltvpsvlgcnvlnresgpalvkhathlclctfsglsvntgrmsvswirppqkalew	68		
		:  :			
Qy	11	LLLWI-SGAYGQVTLRESGPALVXPQTLLTCTFSGFSLSGMSGVSWIRPPQKLEW	69		
Db	69	laridwdddkyygtstetrltstskdtsknqvylkvtnmdpadtatyycaarmq	120		
Qy	70	LHIYVDDKRYNP SLKSLRLTISDTSRNQVLTWINDPVTATYYCARRE	121		

[illegible]

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DR  PIR; A02091; G1HDDH.
DR  HSSP; P01607; IFGV.
KW  IMMUNOGLOBULIN V REGION.
FT  MOD_RES      1      1      PYRROLIDONE CARBOXYLIC ACID.
FT  NON_TER      119    119
SQ  SEQUENCE     119 AA; 13045 MW;  0613C2B6 CRC32;

Query Match      52.7%; Score 563; DB 4; Length 119;
Best Local Similarity 68.6%; Pred. No. 8.68e-94;
Matches 83; Conservative 12; Mismatches 24; Indels 2; Gaps 2;

Db 1 qvtresgalvrptqltlctcfsgfslagetmcvawirqpgealewlawdlinddky 60
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 21 QVTLRESGPALVRPTQTLTLCTCFSGFSLSTSGVSWIRQPGKGLWLAHYWDDDKR 80
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 61 ygasletrlavsktdsknqvlsmntvpgdstatyycaars-cqsg-yfdywgqgllvtvs 118
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 81 YNFSLSKRLTSKDSRQNVLTNTNMDPDTATYYCARRETVFYFDVWGEGIPTVTS 140
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 119 a 119
Qy 141 S 141

RESULT 7
ID HV43 MOUSE STANDARD; PRT; 144 AA.
AC P01819;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN PRECURSOR V REGION (MOPC 141).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC FURTHIERA; RODENTIA.

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RN	[1]	SEQUENCE FROM N.A.	
RP		MEDLINE; 81012133.	
RX			
RA		SARANO H., MAKI R., KUROSAWA Y., ROEDER W., TONEGAWA S.;	
RL		NATURE 286:676-683 (1980).	
RC	-!	THE SEQUENCE SHOWN IS TRANSLATED FROM A DIFFERENTIATED GENE	
CC		ISOLATED FROM A MYELOMA THAT SECRETES IGG2B.	
DR	PIR; A02094; G2MS14.		
DR	HSP; P01772; IFDL.		
KW	IMMUNOGLOBULIN V REGION; SIGNAL.		
FT	SIGNAL	1 19	
FT	CHAIN	20 144	IG HEAVY CHAIN V REGION (MOPC 141).
FT	NON TER	144 144	
SO	SEQUENCE	144 AA;	15759 MW: 10E3A531 CRC32;
SO			

Query Match	44.9%;	Score 479;	DB 4;	Length 144;
Best Local Similarity	57.4%;	Pred. No. 1.04e-75;		
Matches	74;	Conservative	23;	Mismatches 22; Indels 10; Gaps 7;
Dbl	19	sqqvkessgplvapqsksitctvsgfsl-t-gygvnvrppqkglewltci-wngngs	75	
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Qy	20	GQVTLRESGPALUKPTQLTLCFSCFSLSGMSVMIRPPCKGLELAHIYWDKDK	79	
Dbl	76	tdynstlkerlitikdsksqvfklmnsldtddtaryycasviyyvgrsdkyftldywq	135	
	:	: :       :	:	:
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Qy	80	R-YNPISLRSLITSKDTSNQOVLMTNMDPVDIATTCARRETVEY-H---YF--DWNG	132	
Dbl	136	qgtsevtvs	144	
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Qy	133	RGTPVTVS	141	

RESULT 8  
 ID HV46 MOUSE STANDARD; PRT; 137 AA.  
 AC P01872;  
 DT 21-JUL-1986 (REL. 01, CREATED)  
 DT 01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)  
 DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)  
 DE IG HEAVY CHAIN PRECURSOR V REGION (MOPC 315).  
 OS MUS MUSCULUS (MOUSE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; RODENTIA.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 89238351.  
 RA RINFRET A., HORNE C., DORRINGTON K.J., KLEIN M.;  
 RL MOL. IMMUNOL. 26:431-434 (1989).  
 RN [2]  
 RP SEQUENCE OF 1-31.  
 RX MEDLINE; 78094475.  
 RA JIJKA R.L., PESTKA S.;  
 RL PROC. NATL. ACAD. SCI. U.S.A. 74:5692-5696 (1977).  
 RN [3]  
 RP SEQUENCE OF 1-21.  
 RX MEDLINE; 79148758.  
 RA SCHECHTER I., WOLF O., ZEMMEL R., BURSTEIN Y.;  
 RL FED. PROC. 38:1839-1845 (1979).  
 RN [4]  
 RP SEQUENCE OF 19-136.  
 RX MEDLINE; 74170779.  
 RA FRANCIS S.H., LESLIE R.G.O., HOOD L., EISEN H.N.;  
 RL PROC. NATL. ACAD. SCI. U.S.A. 71:1123-1127 (1974).  
 RN [5]  
 RP REVISION TO 53.  
 RX MEDLINE; 77244979.  
 RA HOOD L., MARGOLIES M.N., GIVOL D., ZAKUT R.;  
 RL UNPUBLISHED RESULTS, CITED BY:  
 RL PADLAN E.A., DAVIES D.R., PECHT I., GIVOL D., WRIGHT C.;  
 RL COLD SPRING HARB. SYMP. QUANT. BIOL. 41:627-637 (1977).  
 CC -1- THIS ALPHA CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT HAS  
 CC ANTI-DINITROPHENYL ACTIVITY.  
 DR ENBL; M27638; G602707; -.  
 DR ENBL; X07880; G295908; -.  
 DR PIR; P10102; AVMS35.  
 DR HSP; P01789; 2FGW.  
 KW IMMUNOGLOBULIN V REGION; SIGNAL.  
 FT SIGNAL 1 18  
 FT CHAIN 19 137 IG HEAVY CHAIN V REGION (MOPC 315).  
 FT DOMAIN 19 48 FRAMEWORK 1.  
 FT DOMAIN 49 54 COMPLEMENTARITY-DETERMINING 1.  
 FT DOMAIN 55 68 FRAMEWORK 2.  
 FT DOMAIN 69 84 COMPLEMENTARITY-DETERMINING 2.  
 FT DOMAIN 85 116 FRAMEWORK 3.  
 FT DOMAIN 117 126 COMPLEMENTARITY-DETERMINING 3.  
 FT DOMAIN 127 137 FRAMEWORK 4.  
 FT DISULFID 40 114 BY SIMILARITY.  
 FT CONFLICT 15 15 G -> GG (IN G295908).  
 FT CONFLICT 15 15 G -> H (IN REF. 2).  
 FT CONFLICT 77 78 GY -> YG (IN REF. 4).  
 FT CONFLICT 102 102 N -> D (IN REF. 4).  
 FT CONFLICT 123 123 MISSING (IN REF. 4).  
 FT NON TER 137 137  
 SQ SEQUENCE 137 AA; 15399 MW; 155A5E8D CRC32;

Query Match 42.7%; Score 456; DB 4; Length 137;  
 Best Local Similarity 53.4%; Pred. No. 8.28e-71;  
 Matches 70; Conservative 28; Mismatches 31; Indels 2; Gaps 2;  
 Db 9 lltalpgimsdvqlqespgqlvlpesqalsltcvtqysi-taqyfwirqfpgnklewl 67  
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 Qy 11 LLLMISGAYGVTLRESGPAVKPTQTLLTCTFSGFSLSSTSGMGVSWIRQPPGKLEWL 70  
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 Db 68 gfikydsngynpslknrvaitrdtsenqffliknsvttdetatyccagndhly-yfdy 126  
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 Qy 71 AH1YDDDKRYNPSIKSLTISKDTSRNQVLTMTNMDPVDYATYTCARRETVFYWFYDV 130  
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 Db 127 wggqgttltses 137  
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 Qy 131 WGRGTPVTYSS 141  
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 RESULT 9  
 ID HV44 MOUSE STANDARD; PRT; 115 AA.  
 AC P01820;  
 DT 21-JUL-1986 (REL. 01, CREATED)  
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DT 01-AUG-1992 (REL. 23, LAST ANNOTATION UPDATE)  
 DE IG HEAVY CHAIN PRECURSOR V REGION (PJ14).  
 OS MUS MUSCULUS (MOUSE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; RODENTIA.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 81012133.  
 RA SAKANO H., MAKI R., KUROSAWA Y., ROEDER W., TONEGAWA S.;  
 RL NATURE 286:676-683 (1980).  
 DR PIR; A02095; HVMS14.  
 DR HSP; P01772; 1FDL.  
 KW IMMUNOGLOBULIN V REGION; SIGNAL.  
 FT SIGNAL 1 19  
 FT CHAIN 20 115 IG HEAVY CHAIN V REGION (PJ14).  
 FT NON TER 115 115  
 SQ SEQUENCE 115 AA; 12447 MW; 6E782F62 CRC32;  
 Query Match 41.9%; Score 447; DB 4; Length 115;  
 Best Local Similarity 55.5%; Pred. No. 6.76e-69;  
 Matches 66; Conservative 22; Mismatches 26; Indels 5; Gaps 5;  
 Db 1 mavlallf-clvtfpccilqsvqlkespglvpasqelsitctvgfsl-t-gygvnvr 57  
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
 Qy 1 MVLATQVFISLLLTISGAYGVTLRESGPAVKPTQTLLTCTFSGFSLSSTSGMGVSWIR 60  
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
 Db 58 qppkgkglewlgmi-wgdsdynealkerlsiskdnksqvlkmslqtdtdtaryca 115  
 || || :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||  
 Qy 61 QPPCKGLEWLAHYWDDDKR-YNPSIKSLTISKDTSRNQVLTMTNMDPVDYATYCA 118  
 || || :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||  
 RESULT 10  
 ID HV02 XENLA STANDARD; PRT; 135 AA.  
 AC P20857;  
 DT 01-FEB-1991 (REL. 17, CREATED)  
 DT 01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)  
 DT 01-FEB-1991 (REL. 17, LAST ANNOTATION UPDATE)  
 DE IG HEAVY CHAIN PRECURSOR V REGION (XIG14) (FRAGMENT).  
 OS XENOPUS LAEVIS (AFRICAN CLAWED FROG).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AMPHIBIA; ANURA.  
 RN [1]  
 RP SEQUENCE FROM N.A.



FT CHAIN 19 116 IG HEAVY CHAIN V REGION (1B43).  
FT DOMAIN 19 48 FRAMEWORK 1.  
FT DOMAIN 49 53 COMPLEMENTARITY-DETERMINING 1.  
FT DOMAIN 54 67 FRAMEWORK 2.  
FT DOMAIN 68 84 COMPLEMENTARITY-DETERMINING 2.  
FT DOMAIN 85 116 FRAMEWORK 3.  
FT DISULFID 40 114 BY SIMILARITY.  
FT NON\_TER 116 116  
SQ SEQUENCE 116 AA; 13158 MW; 10EAE67 CRC32;

Query Match 38.6%; Score 412; DB 4; Length 116;  
Best Local Similarity 48.7%; Pred. No. 1.68e-61;  
Matches 57; Conservative 30; Mismatches 29; Indels 1; Gaps 1;  
Db 1 mrvlllclftafgiledvqlqesgplvkpsqslctctvtgysl-tsqywhwlrqf 59  
Qy 3 lqtqvflsllwlgaygqvlturesgpalvkptqltltctsfsgslstsgmvgvswirqp 62  
Db 60 pnnklewmyihygsntsympalksrirtdsknqfllqlnsvttedtatyycar 116  
Qy 63 pckglemlahiywddkrrnpslksrltiskotsrnqovlwtmndpvdvtatyycar 119

RESULT 14  
ID RV60 MOUSE STANDARD; PRT; 116 AA.  
AC P18331;  
DT 01-NOV-1990 (REL. 16, CREATED)  
DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)  
DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)  
DE IG HEAVY CHAIN PRECURSOR V REGION (M315).  
OS MUS MUSCULUS (MOUSE).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; RODENTIA.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/CJ;  
RX MEDLINE; 89279149.  
RA LEVY N.S., MALPIERO U.V., LEBECQUE S.G., GEARHART P.J.;  
RL J. EXP. MED. 169:2007-2019 (1989).  
DR PIR; JT0509; HVMS31.  
DR HSP; P01825; IBAF.  
KW IMMUNOGLOBULIN V REGION; SIGNAL.  
FT SIGNAL 1 18  
FT CHAIN 19 116 IG HEAVY CHAIN V REGION (M315).  
FT DOMAIN 19 48 FRAMEWORK 1.  
FT DOMAIN 49 53 COMPLEMENTARITY-DETERMINING 1.  
FT DOMAIN 54 67 FRAMEWORK 2.  
FT DOMAIN 68 84 COMPLEMENTARITY-DETERMINING 2.  
FT DOMAIN 85 116 FRAMEWORK 3.  
FT DISULFID 40 114 BY SIMILARITY.  
FT NON\_TER 116 116  
SQ SEQUENCE 116 AA; 13095 MW; 810F397 CRC32;

Query Match 38.1%; Score 407; DB 4; Length 116;  
Best Local Similarity 53.2%; Pred. No. 1.90e-60;  
Matches 58; Conservative 26; Mismatches 24; Indels 1; Gaps 1;

Db 9 lltaipgiledvqlqesgplvkpsqslctctvtgysl-tsqywmwlrqfpgnklewm 67  
Qy 11 lllltsgayqvlturesgpalvkptqltltctsfsgslstsgmvgvswirqpckglewl 70  
Db 68 gyisdydgennpslknriidtrtdsknqfllklnsvttedtatyycar 116  
Qy 71 ahlywddkrrnpslksrltiskotsrnqovlwtmndpvdvtatyycar 119

RESULT 15  
ID HV38 MOUSE STANDARD; PRT; 119 AA.  
AC P01808;  
DT 21-JUL-1986 (REL. 01, CREATED)  
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
DT 21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)  
DE IG HEAVY CHAIN V REGION (T601).  
OS MUS MUSCULUS (MOUSE).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; RODENTIA.  
RN [1]  
RP SEQUENCE.  
RX MEDLINE; 79223895.  
RA RAO D.N., RUDIKOFF S., KRUTZSCH H., POTTER M.;  
RL PROC. NAVL. ACAD. SCI. U.S.A. 76:2890-2894 (1979).  
CC -!- THIS CHAIN WAS ISOLATED FROM AN IGA MYELOMA PROTEIN THAT BINDS  
CC GALACTAN.  
DR PIR; A02078; AVMST6.  
DR HSP; P01810; IFVM.  
KW IMMUNOGLOBULIN V REGION.  
FT NON\_TER 119 119  
SQ SEQUENCE 119 AA; 13169 MW; EEE850E1 CRC32;

Query Match 37.7%; Score 403; DB 4; Length 119;  
Best Local Similarity 50.8%; Pred. No. 1.31e-59;  
Matches 62; Conservative 21; Mismatches 34; Indels 5; Gaps 3;  
Db 1 evkllesgglvpggslklscaasgfdfrsym--swvrgpgkglewigeinpsdetsi 58  
Qy 21 qvlturesgpalvkptqltltctsfsgslstsgmvgvswirqpckglemlahiywddk- 79  
Db 59 nytpslkdkfiisrdnakntlylqmskvrseatalyycarl-yygyfdwaggtvtv 116  
Qy 80 rrvnslksrltiskotsrnqovlwtmndpvdvtatyycarretvfywfdwgcrgctptv 139  
Db 117 ss 118  
Qy 140 SS 141

Search completed: Tue Mar 18 10:05:26 1997  
Job time : 9 secs.







22-Apr-1995

```
ACCESSIONS      A36005
REFERENCE
#authors        Schroeder Jr., H.W.; Wang, J.Y.
#journal         Proc. Natl. Acad. Sci. U.S.A. (1990) 87:6146-6150
#title          Preferential utilization of conserved immunoglobulin heavy
                chain variable gene segments during human fetal life.
#cross-references MUID:90349571
#accession       A36005
#status          preliminary
#molecule_type  mRNA
#residues        1-121 ##label SCH
#cross-references GB:M34027
CLASSIFICATION  #superfamily immunoglobulin V region; immunoglobulin homology
SUMMARY          #length 121 #molecular-weight 13557 #checksum 6899

Query Match      64.0%; Score 683; DB 5; Length 121;
Best Local Similarity 82.6%; Pred. No. 3.16e-71;
Matches 100; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

Db 1 evtlresgpalvkptqltltctlygfelsatgmcvswirppqkalewialidwddky 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 21 QVTLRESGPAVKPTQTLTUTCTFSGLSTSGMGVSWIRQPPGKLEWIAHYWDDDKR 80
   |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 yetelkrltikdtknqvltmtndpvdtdatyyearinnwgegfdlwrgtltvts 120
   |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 81 YNPSIKSLRTISKDTSRNQVLTMTNMDPDVDTATYTCARRETVFYWYFDVWGRGTPVTS 140

Db 121 s 121
|
Qy 141 s 141

RESULT 6
ENTRY    PT0174      #type fragment
TITLE    Ig heavy chain precursor V region (IdB5.7) - mouse (fragment)
ORGANISM #formal name Mus musculus #common name house mouse
DATE     31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change
#cross-references MUID:91287738
#accession PT0174
#molecule_type mRNA
#residues 1-143 ##label PER
#experimental_source strain BALB/c
COMMENT   IdB5.7 is an antibody to anti-alpha (1-6) dextran.
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
SUMMARY     #length 143 #checksum 3660

Query Match      61.6%; Score 658; DB 5; Length 143;
Best Local Similarity 71.5%; Pred. No. 6.28e-68;
Matches 98; Conservative 19; Mismatches 15; Indels 5; Gaps 3;

Db 7 eflillivpaylsgvtlkeqppilqpsqqlaltcsfgfslstsgmvswwirppsgql 66
   |:||| | | :|||:|||||:|:|||||:|||||:|||||:|||||:|||||:
Qy 10 SLLWISGAY--QVTLRESGPAVKPTQTLTUTCTFSGLSTSGMGVSWIRQPPGKGL 67

Db 67 ewlahiewdddllynlpalkerltikdtsrnqvflkitedvtdatyyccarrerygny 126
```

```
||||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Qy 68 EWLIAHYWDDDKRYPNPSIKSLRTISKDTSRNQVLTMTNMDPDVDTATYTCARRETVF--Y 125

Db 127 lqpldywggtvttvss 143
   :|:|:|:|:|:|:|
Qy 126 WY-FDVWGRGTPVTVSS 141

RESULT 7
ENTRY    GIHUCO      #type complete
TITLE    Ig heavy chain V-II region (Cor) - human
ORGANISM #formal name Homo sapiens #common name man
DATE     #sequence_revision 23-Oct-1981 #text_change 16-Feb-1996
ACCESSIONS A02089
REFERENCE  A90250
#authors   Press, E.M.; Hogg, N.M.
#journal   Biochem. J. (1970) 117:641-660
#title     The amino acid sequences of the Fd fragments of two human
           gamma1 heavy chains.
#cross-references MUID:70258837
#accession A02089
#molecule_type protein
#residues 1-120 ##label PRE
COMMENT   This chain was isolated from an IgG1 myeloma protein.
GENETICS
#gene      GDB:IGHV8
#cross-references GDB:G00-128-528
#map position 14q32.33
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS      glycoprotein; pyroglutamic acid
FEATURE
15-96
1         #domain immunoglobulin homology #label IMM\
          #modified site pyrrolidone carboxylic acid (Gln) #status
          experimental\
22-94      #disulfide bonds #status experimental\
62         #binding site carbohydrate (Asn) (covalent) #status
          experimental
SUMMARY     #length 120 #molecular-weight 13226 #checksum 7076

Query Match      61.3%; Score 655; DB 2; Length 120;
Best Local Similarity 81.3%; Pred. No. 1.56e-67;
Matches 100; Conservative 6; Mismatches 12; Indels 5; Gaps 3;

Db 1 qvtlresgpalvkptqltltctfsgfslstsgmvswwirppqkalewialidwddky 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 21 QVTLRESGPAVKPTQTLTUTCTFSGLSTSGMGVSWIRQPPGKLEWIAHYWDDDKR 80

Db 61 yntletrltikdtsrnqvltm---dpvdtatyyccarltvipapagymdvwrgtqpt 117
   |||:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 81 YNPSIKSLRTISKDTSRNQVLTMTNMDPDVDTATYTCARRETVFY-W-YFDVWGRGTPVT 138

Db 118 vss 120
|||
Qy 139 VSS 141

RESULT 8
ENTRY    GIHUEH      #type complete
TITLE    Ig heavy chain V-II region (He) - human
ORGANISM #formal name Homo sapiens #common name man
DATE     #sequence_revision 07-May-1981 #text_change 16-Feb-1996
ACCESSIONS A02093
REFERENCE  A02093
#authors   Cunningham, B.A.; Pflumm, M.N.; Rutishauser, U.; Edelman,
```



```
#accession S26328
##status preliminary
##molecule_type mRNA
##residues 1-116 ##label STA
##cross-references EMBL:X59198
SUMMARY
    #length 116 #molecular-weight 12895 #checksum 8145

Query Match      58.0%; Score 619; DB 12; Length 116;
Best Local Similarity 71.6%; Pred. No. 8.49e-63;
Matches 83; Conservative 13; Mismatches 19; Indels 1; Gaps 1;

Db 2 eaggilqpsqtlsctsfsgslstsmgvgwirqpsgkglewllhllwndskypnal 61
    |||||:::|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 26 ESGPALVKPTQTTLTCTSGFSLTSGMGVSWIRQPPGKGLEWLAHIYWDKKRNP 85
    |||||:||||| |||:::| ||||| ||||| ||||| ||||| ||||| |||||

Db 62 krltikdtdymnqvfkianvtdatdyccarian-wdwyfdwsgagtvtves 116
    |||||:||||| |||:::| ||||| ||||| ||||| ||||| ||||| |||||
Qy 86 KSRUTISKOTSRNQVLTMTNMDPVDATYTCARRETVFWYFDWVGRTPTVSS 141
    |||||:||||| |||:::| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 12
ENTRY      S26924      #type fragment
TITLE      Ig heavy chain V region (DP-28) - human (fragment)
ORGANISM   #formal_name Homo sapiens #common_name man
DATE       22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
10-Nov-1995
ACCESSIONS S26924
REFERENCE   S26885
  authors   Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.;
            Winter, G.
  #journal   J. Mol. Biol. (1992) 227:776-798
  #title     The repertoire of human germline V(H) sequences reveals about
            fifty groups of V(H) segments with different hypervariable
            loops.
#accession S26924
##status preliminary
##molecule_type DNA
##residues 1-96 ##label TOM
##cross-references EMBL:212330
SUMMARY
    #length 96 #checksum 9197

Query Match      57.9%; Score 618; DB 11; Length 96;
Best Local Similarity 89.6%; Pred. No. 1.15e-62;
Matches 86; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Db 1 qvtlkesgpalvkptqtlctctfsgfslstsmgvswirqppgkalewlaridwddkf 60
    |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:|||||
Qy 21 QVTLRESGALVKPTQTTLTCTSGFSLTSGMGVSWIRQPPGKGLEWLAHIYWDKKR 80
    |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:|||||

Db 61 yetelkrltikdtsknqvltmtndpvdtdtaty 96
    |:|||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:
Qy 81 YNPSIAKSLRTISKOTSRNQVLTMTNMDPVDATYTY 116
    |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:

RESULT 13
ENTRY      S26923      #type fragment
TITLE      Ig heavy chain V region (DP-27) - human (fragment)
ORGANISM   #formal_name Homo sapiens #common_name man
DATE       22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
10-Nov-1995
ACCESSIONS S26923
REFERENCE   S26885
  authors   Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.;
            Winter, G.
  #journal   J. Mol. Biol. (1992) 227:776-798
  #title     The repertoire of human germline V(H) sequences reveals about
            fifty groups of V(H) segments with different hypervariable
            loops.
#accession S26923
##status preliminary
##molecule_type DNA
##residues 1-96 ##label TOM
##cross-references EMBL:212329
SUMMARY
    #length 96 #checksum 8452

Query Match      57.6%; Score 615; DB 11; Length 96;
Best Local Similarity 90.8%; Pred. No. 2.84e-62;
Matches 87; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Db 1 qvtlresgpalvkptqtlctctfsgfslstsmgvswirqppgkalewlaridwddk 60
    |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:|||||
Qy 21 QVTLRESGALVKPTQTTLTCTSGFSLTSGMGVSWIRQPPGKGLEWLAHIYWDKKR 80
    |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:|||||

Db 61 yetelkrltikdtsknqvltmtndpvdtdtaty 96
    |:|||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:
Qy 81 YNPSIAKSLRTISKOTSRNQVLTMTNMDPVDATYTY 116
    |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:

RESULT 14
ENTRY      MHU00U      #type complete
TITLE      Ig heavy chain V-II region (Ou) - human
ORGANISM   #formal_name Homo sapiens #common_name man
DATE       #sequence_revision 13-Jul-1981 #text_change 16-Feb-1996
ACCESSIONS A02088
REFERENCE   A02088
  authors   Putnam, F.W.; Florent, G.; Paul, C.; Shinoda, T.; Shimizu, A.
  #journal   Science (1973) 182:287-291
  #title     Complete amino acid sequence of the mu heavy chain of a human
            IgM immunoglobulin.
#cross-references MUID:74005511
#accession A02088
##molecule_type protein
##residues 1-126 ##label PUT
COMMENT     This mu chain was isolated from a Waldenström's macroglobulin.
GENETICS
  #gene      GDB:IGHV8
  ##cross-references GDB:G00-128-528
  #map_position 14q32.33
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS       pyroglutamic acid
FEATURE
  1           #modified_site pyrrolidone carboxylic acid (Gln) #status
            experimental
22-97         #disulfide bonds #status experimental
SUMMARY
    #length 126 #molecular-weight 14276 #checksum 4310

Query Match      56.8%; Score 607; DB 2; Length 126;
Best Local Similarity 69.3%; Pred. No. 3.19e-61;
Matches 88; Conservative 18; Mismatches 14; Indels 7; Gaps 5;

Db 1 qvtltesgpalvkpqtltctctfsgfslstsmrsvwirppgkalewlarib-bbdkf 59
    |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:|||||
Qy 21 QVTLRESGALVKPTQTTLTCTSGFSLTSGMGVSWIRQPPGKGLEWLAHIYWDKKR 80
    |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:|||||

Db 60 ywstelrtrlskndsknqvlinmnpvdtdtatyccarvsvmaggymvymdvwkg 119
    |:|||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:
Qy 81 Y-NPSIAKSLRTISKOTSRNQVLTMTNMDPVDATYTCARR-ETV---FYWYF-DWVG 134
    |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:

```

```
#journal      J. Mol. Biol. (1992) 227:776-798
#title        The repertoire of human germline V(H) sequences reveals about
            fifty groups of V(H) segments with different hypervariable
            loops.
#accession    S26923
##status      preliminary
##molecule_type DNA
##residues    1-96 ##label TOM
##cross-references EMBL:212329
SUMMARY
    #length 96 #checksum 8452

Query Match      57.6%; Score 615; DB 11; Length 96;
Best Local Similarity 90.8%; Pred. No. 2.84e-62;
Matches 87; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Db 1 qvtlresgpalvkptqtlctctfsgfslstsmgvswirqppgkalewlaridwddk 60
    |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:|||||
Qy 21 QVTLRESGALVKPTQTTLTCTSGFSLTSGMGVSWIRQPPGKGLEWLAHIYWDKKR 80
    |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:|||||

Db 61 yetelkrltikdtsknqvltmtndpvdtdtaty 96
    |:|||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:
Qy 81 YNPSIAKSLRTISKOTSRNQVLTMTNMDPVDATYTY 116
    |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:

RESULT 14
ENTRY      MHU00U      #type complete
TITLE      Ig heavy chain V-II region (Ou) - human
ORGANISM   #formal_name Homo sapiens #common_name man
DATE       #sequence_revision 13-Jul-1981 #text_change 16-Feb-1996
ACCESSIONS A02088
REFERENCE   A02088
  authors   Putnam, F.W.; Florent, G.; Paul, C.; Shinoda, T.; Shimizu, A.
  #journal   Science (1973) 182:287-291
  #title     Complete amino acid sequence of the mu heavy chain of a human
            IgM immunoglobulin.
#cross-references MUID:74005511
#accession A02088
##molecule_type protein
##residues 1-126 ##label PUT
COMMENT     This mu chain was isolated from a Waldenström's macroglobulin.
GENETICS
  #gene      GDB:IGHV8
  ##cross-references GDB:G00-128-528
  #map_position 14q32.33
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS       pyroglutamic acid
FEATURE
  1           #modified_site pyrrolidone carboxylic acid (Gln) #status
            experimental
22-97         #disulfide bonds #status experimental
SUMMARY
    #length 126 #molecular-weight 14276 #checksum 4310

Query Match      56.8%; Score 607; DB 2; Length 126;
Best Local Similarity 69.3%; Pred. No. 3.19e-61;
Matches 88; Conservative 18; Mismatches 14; Indels 7; Gaps 5;

Db 1 qvtltesgpalvkpqtltctctfsgfslstsmrsvwirppgkalewlarib-bbdkf 59
    |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:|||||
Qy 21 QVTLRESGALVKPTQTTLTCTSGFSLTSGMGVSWIRQPPGKGLEWLAHIYWDKKR 80
    |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:|||||

Db 60 ywstelrtrlskndsknqvlinmnpvdtdtatyccarvsvmaggymvymdvwkg 119
    |:|||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:
Qy 81 Y-NPSIAKSLRTISKOTSRNQVLTMTNMDPVDATYTCARR-ETV---FYWYF-DWVG 134
    |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:

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Mar 18 10:04

US-08-612-929-12.rpr

11

Db 120 ttvtvs 126

| | | | |

Qy 135 TPTVTSS 141

RESULT 15

ENTRY GZHUCS #type complete  
TITLE Ig heavy chain precursor V-II region (Cess) - human  
ORGANISM #formal\_name Homo sapiens #common\_name nan  
DATE 17-Mar-1987 #sequence\_revision 17-Mar-1987 #text\_change 16-Feb-1996

ACCESSIONS A02090

REFERENCE A02090

fauthors Takahashi, N.; Noma, T.; Honjo, T.  
#journal Proc. Natl. Acad. Sci. U.S.A. (1984) 81:5194-5198  
#title Rearranged immunoglobulin heavy chain variable region (V-H) pseudogene that deletes the second complementarity-determining region.

#cross-references MUID:84298107

#accession A02090

##molecule\_type mRNA

##residues 1-147 ##label TAK

##note the sequence was determined from the differentiated gene  
##note the authors translated the codon GCG for residue 16 as Trp, TGG for residue 142 as Met, TCA for residue 143 as Val, CCG for residue 144 as Thr, TCT for residue 145 as Val, CTT for residue 146 as Ser, and CAG for residue 147 as Ser

GENETICS

#gene GDB:ICHV8

##cross-references GDB:G00-128-528

#map\_position 14q32.33

#introns 15/3

CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology  
KEYWORDS immunoglobulin

FEATURE

1-19

20-147

#domain signal sequence #status predicted #label SIG\  
#product Ig heavy chain V-II region (Cess) #status predicted #label MAT\  
#domain V segment #status predicted #label VAR\  
#domain D segment #status predicted #label DIV\  
#domain J segment #status predicted #label JOI  
#length 147 #molecular-weight 16323 #checksum 3237

Query Match

56.6%; Score 605; DB 2; Length 147;

Best Local Similarity 75.0%; Pred. No. 5.8e-61;

Matches 84; Conservative 14; Mismatches 13; Indels 1; Gaps 1;

Db 9 llltvsqvlsgvlnresgaivkathtltctfsglsvntrgmavswirppgkalew 68

||| : || :||| ||||| :||| ||||| :||| :||| ||||| :|||

Qy 11 LLLMI-SGAYCQVTLRESGALVKEQTLLTCTSGESLSTSGVSWIRQPPCKGLEW 69

Db 69 lardwdddkygtetlektksngvklvtnmdpadtatyyccarmq 120

||| : ||||| || : ||||| ||||| : ||||| : ||||| : ||||| :

Qy 70 LAHIYDDDKRYNPLKSLRLTISKDTSRQNVLTWNTMDPVDATYYCARRE 121

Search completed: Tue Mar 18 10:06:26 1997  
Job time : 42 secs.



Mar 18 10:05

US-08-612-929-12.fag

3

PI Gross MS, Holmes SD, Sylvester DR;  
DR WPI; 95-123387/16.  
DR N-PSDB; Q83493.  
PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived  
from high affinity mAbs - useful in treatment of IL-4-mediated  
PT and IgE-mediated allergic conditions  
PS Disclosure; Fig.4; 97pp; English.  
CC A humanized antibody heavy chain variable region and signal  
sequence is given in R70192. The signal sequence is also  
CC provided in R70193. The CDR sequences of the construct are  
CC identical to the native CDRs of mouse anti-human IL-4 MAb  
CC 389 (R70198-200).  
SQ Sequence 141 AA;

Query Match 100.0%; Score 1068; DB 13; Length 141;  
Best Local Similarity 100.0%; Pred. No. 2.02e-79;  
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 mvltqtqvfiillllwisagayqvtlresgpalkvptqtlitctcfagfslstsgmgsuir 60  
|||||  
Qy 1 MVLTQTVFISLLLTISGAYQVTLRESGPALKVPTQTLITCTCFGSLSLSTSGMGSWIR 60  
|||||

Db 61 qpqgkglewlahiywdddkrynpkslkerltiskdtsrnqvltmtndpvdttatycarr 120  
|||||  
Qy 61 QPPCKGLEWLAHIYWDKRYNPSSLSKSLTISKDTSRNQVVLTMNDPVDVTATYYCARR 120  
|||||

Db 121 etvfywyfdwgrgtpvtss 141  
|||||  
Qy 121 ETVFYWFYFDWGRGTPVTSS 141  
|||||

RESULT 2

ID R70191 standard; Protein; 141 AA.  
AC R70191;  
DT 20-SEP-1995 (first entry)  
DE Chimeric antibody 389 heavy chain.  
KW Chimeric antibody; antibody engineering; monoclonal antibody;  
MAB; interleukin-4; IL-4; allergy.  
OS Homo sapiens; Mus sp.  
FH Key Location/Qualifiers  
FT Peptide 1..19  
FT /label= Sig\_peptide  
FT Region 51..57  
FT /label= CDR  
FT /note= "complementarity determining region"  
FT Region 72..87  
FT /label= CDR  
FT /note= "complementarity determining region"  
FT Peptide 120..130  
FT /label= CDR  
FT /note= "complementarity determining region"  
PN WO9507301-A.  
PD 16-MAR-1995.  
PE 07-SEP-1994; U10308.  
PR 07-SEP-1993; US-117366.  
PR 14-OCT-1993; US-136783.  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
PA (SMIK ) SMITHKLINE BEECHAM PLC.  
PI Gross MS, Holmes SD, Sylvester DR;  
DR WPI; 95-123387/16.  
DR N-PSDB; Q83492.  
PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived  
from high affinity mAbs - useful in treatment of IL-4-mediated  
PT and IgE-mediated allergic conditions

Mar 18 10:05

US-08-612-929-12.fag

4

PS Disclosure; Fig.3; 97pp; English.  
CC A human/mouse chimeric antibody heavy chain variable region was  
CC constructed (given in R70191) that contained the mouse anti-human  
CC IL-4 MAb 389 variable region including 3 CDRs (R70198-200) and a  
CC human antibody signal peptide (R70193). The construct was used  
CC for humanized antibody production.  
SQ Sequence 141 AA;

Query Match 88.3%; Score 943; DB 13; Length 141;  
Best Local Similarity 86.5%; Pred. No. 9.59e-69;  
Matches 122; Conservative 11; Mismatches 8; Indels 0; Gaps 0;

Db 1 mvltqtqvfiillllwisagayqvtlresgpalkvptqtlitctcfagfslstsgmgsuir 60  
|||||  
Qy 1 MVLTQTVFISLLLTISGAYQVTLRESGPALKVPTQTLITCTCFGSLSLSTSGMGSWIR 60  
|||||

Db 61 qpqgkglewlahiywdddkrynpkslkerltiskdtsrnqvltkitedtadtatycarr 120  
|||||  
Qy 61 QPPCKGLEWLAHIYWDKRYNPSSLSKSLTISKDTSRNQVVLTMNDPVDVTATYYCARR 120  
|||||

Db 121 etvfywyfdwgrgtpvtss 141  
|||||  
Qy 121 ETVFYWFYFDWGRGTPVTSS 141  
|||||

RESULT 3

ID R70190 standard; Protein; 140 AA.  
AC R70190;  
DT 20-SEP-1995 (first entry)  
DE Mouse MAB 389 heavy chain.  
KW Chimeric antibody; humanized antibody; antibody engineering;  
monoclonal antibody; MAB; interleukin-4; IL-4; allergy.  
OS Mus sp.  
FH Key Location/Qualifiers  
FT Peptide 1..19  
FT /label= Sig\_peptide  
FT Region 50..56  
FT /label= CDR  
FT /note= "complementarity determining region"  
FT Region 71..86  
FT /label= CDR  
FT /note= "complementarity determining region"  
FT Region 119..129  
FT /label= CDR  
FT /note= "complementarity determining region"  
PN WO9507301-A.  
PD 16-MAR-1995.  
PE 07-SEP-1994; U10308.  
PR 07-SEP-1993; US-117366.  
PR 14-OCT-1993; US-136783.  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
PA (SMIK ) SMITHKLINE BEECHAM PLC.  
PI Gross MS, Holmes SD, Sylvester DR;  
DR WPI; 95-123387/16.  
DR N-PSDB; Q83491.  
PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived  
from high affinity mAbs - useful in treatment of IL-4-mediated  
PT and IgE-mediated allergic conditions  
PS Disclosure; Fig.2; 97pp; English.  
CC Spleen cells from mice immunized with human IL-4 were used to prepare  
CC hybridomas, which were screened for anti-IL-4 MAb secretion. Only  
CC clone 389 was positive. cDNA clones of the 389 light and heavy  
CC chains were cloned into pGEM7f+ and transformed into E. coli  
CC DH5-alpha. The clones were sequenced (Q83490-91), and used for

CC antibody engineering.  
SQ Sequence 140 AA;

Query Match 75.6%; Score 807; DB 13; Length 140;  
Best Local Similarity 81.3%; Pred. No. 3.57e-57;  
Matches 109; Conservative 12; Mismatches 11; Indels 2; Gaps 1;  
  
Db 7 allilivpavleqvtkesgqilqpksqtlslctsfsgfslstsgmvgvswirqpqskgl 66  
||||| | | :|||:||||::: |:|||:||||:|||||:|||||:|||||:|||||:|||||  
Qy 10 SLLLWISGAY--GQVTLRESGPAVKPTQLTLCTFSGFSLSSTGMCVSWIRQPPGKGL 67  
  
Db 67 exlahiywdddkrynpelkeritiektsenqvflikitevdadtatyyccarretvfyy 126  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Qy 68 ENLAHYWDDKRYNPSIKSRLTISKDTSRNQVLTMTNMDPVDYATTCARRETVFYWY 127  
  
Db 127 fdwvsgattvtvss 140  
||||| || |||||  
Qy 128 FDWVGRCPTVTVSS 141

## RESULT 4

ID R92088 standard; Protein; 120 AA.  
AC R92088;  
DT 16-MAY-1996 (first entry)  
DE CDR-grafted anti-RSV F glycoprotein MEDI-493 VH.  
KW Humanised antibody; chimeric antibody; antibody engineering;  
KW monoclonal antibody; MAb 1129; respiratory syncytial virus; RSV;  
KW heavy chain; complementarity determining region; CDR.  
OS Chimeric Homo sapiens;  
OS Chimeric Mus musculus.  
FH Key Location/Qualifiers  
FT Region 31..36  
FT /Label= CDR1  
FT Region 52..67  
FT /Label= VDR2  
FT Region 100..109  
FT /Label= CDR3  
PN W09605229-A1.  
PD 22-FEB-1996.  
PF 09-AUG-1995; U10053.  
PR 15-AUG-1994; US-290592.  
PA (MEDI-) WEDIMMUNE INC.  
PI Johnson LS;  
DR WP1; 96-139646/14.  
PT New chimeric antibodies against respiratory syncytial virus -  
PT comprise human antibodies with CDR's from the variable heavy and  
PT light chains of a murine antibody  
PS Example 7; Fig 7A-7B; 55pp; English.  
CC A human-mouse chimeric antibody heavy chain has a human CDR  
CC framework contg. complementarity determining region (CDRe) from the  
CC variable heavy (VH) chain of a murine monoclonal antibody (MAb 1129)  
CC against respiratory syncytial virus (RSV) glycoprotein F antigenic  
CC site C. CDRs from MAb 1129 VH (see R92089) were grafted into the  
CC human Cor VH region (R92086) or Cess VH region (R92087) to produce  
CC CDR-grafted MEDI-493 VH (R92088). A similar procedure was used to  
CC obtain CDR-grafted VL (R92091). The humanised antibody is used to  
CC treat RSV infection.  
SQ Sequence 120 AA;

Query Match 69.2%; Score 739; DB 16; Length 120;  
Best Local Similarity 84.3%; Pred. No. 2.07e-51;  
Matches 102; Conservative 5; Mismatches 13; Indels 1; Gaps 1;  
  
Db 1 qvtlresgalvkptqltlctfsgfslstsgmvgvswirqpqskalewladwddkdd 60

Qy 21 QVTLRESGPAVKPTQLTLCTFSGFSLSSTGMCVSWIRQPPKGLWLAHYWDDDKR 80  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 61 ynpelkeritiektsenqvflikitevdadtatyyccarretvfyyfdwvsgattvtvs 119  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Qy 81 YNPSIKSRLTISKDTSRNQVLTMTNMDPVDYATTCARRETVFYWFDWVGRCPTVTVS 140  
  
Db 120 s 120  
|  
Qy 141 s 141

## RESULT 5

ID R66299 standard; Protein; 119 AA.  
AC R66299;  
DT 07-AUG-1995 (first entry)  
DE Human immunoglobulin variable heavy chain #5.  
KW Primer; PCR; amplify; human; immunoglobulin; variable; heavy chain;  
KW cosmid; placenta; vector; pJB81; E.coli; mammalian.  
OS Homo sapiens.  
PN W09426895-A.  
PD 24-NOV-1994.  
PF 10-MAY-1993; J00603.  
PR 10-MAY-1993; W0-J00603.  
PA (N15B ) JAPAN TOBACCO INC.  
PI Honjo T, Matsuoka F;  
DR WP1; 95-006791/01.  
DR N-PSDB; Q78943.  
PT DNA fragment comprising human immunoglobulin Vh genes - for the  
PT production of human immunoglobulin in mammalian hosts  
PS Disclosure; Page 36-37; 130pp; Japanese.  
CC Protein sequences (R66295-51) are novel human immunoglobulin heavy chain  
CC sequences encoded by novel isolated genes. The genes (Q78939-79002) were  
CC isolated and cloned from a series of cosmid constructs: Y202; Y103; Y21;  
CC Y6; Y24; 3-31; M84; M118 and M131, by PCR amplification using primers  
CC Q78917-38. The genes are subdivided into 5 families of Vh genes. The  
CC fragments cover a region of 800 kb. The DNA fragments were isolated from  
CC high molecular weight DNA from human placenta. The DNA was partially  
CC digested with *TaqI* restriction enzyme. The fragments were separated by  
CC gel electrophoresis and 35-45 kb fractions were collected. The fragments  
CC were ligated with *ClaiI*-digested cosmid vector pJB81. The ligation  
CC products were in vitro packed and infected into *E.coli* 490A. The  
CC fragments were then subcloned by colony hybridisation. The Vh genes and  
CC the DNA fragments encoding them are useful in producing human  
CC immunoglobulin in mammalian hosts.  
SQ Sequence 119 AA;

Query Match 64.2%; Score 686; DB 12; Length 119;  
Best Local Similarity 82.9%; Pred. No. 6.22e-47;  
Matches 92; Conservative 14; Mismatches 4; Indels 1; Gaps 1;  
  
Db 9 llltipwslvsgitlkesgtylvpktqtlctfsgfslstsgmvgvswirqpqskalew 68  
||| |:: :|||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Qy 11 LLLWISG-AYGQVTLRESGPAVKPTQLTLCTFSGFSLSSTGMCVSWIRQPPKGLW 69  
  
Db 69 laliywdddkrynpelkeritiektsknqvflikitevdadtatyyccahr 119  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Qy 70 LAHYWDDKRYNPSIKSRLTISKDTSRNQVLTMTNMDPVDYATTCARR 120

## RESULT 6

ID R38315 standard; Protein; 139 AA.  
AC R38315;  
DT 04-DEC-1993 (first entry)

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[illegible]





CC the activation peptide region (R88106) of the heavy chain of protein C,

CC separate strains which cannot be neutralised by the neutralising antibodies against IIB and IIMN strains.

CC separate strains which cannot be re-



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US-08-612-929-12.rag

15

Db 61 ynpvkrliiskdskqvfkiasvtdadtatycvrrmdd-ydamdywgqtsvts 119  
||| ||||| |||||:| |:::| ||||| | | ||:|||||  
Qy 81 YNFKSRUTITSKOTSRNQVLTMTNMDPVDVTATTCARRETVFYWFDVWGRGTPVTS 140

Db 120 s 120  
Qy 141 s 141

# RESULT 15

ID R66318 standard; Protein; 119 AA.  
AC R66318;  
DT 03-AUG-1995 (first entry)  
DE Human immunoglobulin variable heavy chain #24.  
KW Primer; PCR; amplify; human; immunoglobulin; variable; heavy chain;  
KW cosmid; placenta; vector; pB81; E.coli; mammalian.  
OS Homo sapiens.  
PN W09426895-A.  
PD 24-NOV-1994.  
PF 10-MAY-1993; J00603.  
PR 10-MAY-1993; W0-J00603.  
PA (NLSB ) JAPAN TOBACCO INC.  
PI Honjo T, Matsuda F;  
DR NPI; 95-006791/01.  
DR N-PSDB; Q78964.  
PT DNA fragment comprising human immunoglobulin Vh genes - for the  
PT production of human immunoglobulin in mammalian hosts  
PS Claim 35; Page 64-65; 130pp; Japanese.  
CC Protein sequences (R66295-51) are novel human immunoglobulin heavy chain  
CC sequences encoded by novel isolated genes. The genes (Q78939-79002) were  
CC isolated and cloned from a series of cosmid constructs: Y202; Y103; Y21;  
CC Y6724; 3-31; M84; M118 and M131, by PCR amplification using primers  
CC Q78917-38. The genes are subdivided into 5 families of Vh genes. The  
CC fragments cover a region of 800 kb. The DNA fragments were isolated from  
CC high molecular weight DNA from human placenta. The DNA was partially  
CC digested with TagI restriction enzyme. The fragments were separated by  
CC gel electrophoresis and 35-45 kb fractions were collected. The fragments  
CC were ligated with ClaI-digested cosmid vector pB81. The ligation  
CC products were in vitro packed and infected into E.coli 490A. The  
CC fragments were then subcloned by colony hybridisation. The Vh genes and  
CC the DNA fragments encoding them are useful in producing human  
CC immunoglobulin in mammalian hosts.  
SQ Sequence 119 AA;

Query Match 58.4%; Score 624; DB 12; Length 119;  
Best Local Similarity 72.9%; Pred. No. 1.04e-41;  
Matches 86; Conservative 16; Mismatches 15; Indels 1; Gaps 1;

Db 1 mdtlcytlilllttspwlsqvtksqplvktptltlctctvsfslsnarmgvsirq 60  
::| : ||| : : ||||| |||||:||||| ||||| : |||||  
Qy 3 lqtqvflsllmISG-AYGQVTLRESGPAUVKPTQTTLCTFSGFSLSLSTSGMGVSWIRQ 61

Db 61 ppgkalewlahifendekysvtelkerltiskdskqvltatmdpvdtdatycar 118  
||||:|||||: :|:| : ||||| |||||:||||| ||||| |||||  
Qy 62 PPGKLEWLAHIYWDKRYNPSIKSRUTITSKOTSRNQVLTMTNMDPVDVTATTCAR 119

Search completed: Tue Mar 18 10:07:12 1997  
Job time : 29 secs.

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WATERMAN

(TM)

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MParch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed Mar 19 08:08:10 1997; MaePar time 208.67 Seconds  
830.598 Million cell updates/sec

Tabular output not generated.

Title: &gt;US-08-612-929-13

Description: (1-393) from US08612929.seq

Perfect Score: 393

N.A. Sequence: 1 ATGGGATGACCTCTATCAT.....CCAAAGTGGAGATCAACGCT 393

Comp: TACCTACTCGACATAGTA.....GGTTCACCTCTAGTTTGA

Scoring table: TABLE default

Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 630489 seqs, 220513910 bases x 2

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: EST-STS

1:EST1 2:EST2 3:EST3 4:EST4 5:EST5 6:EST6 7:EST7 8:EST8  
9:EST9 10:EST10 11:EST11 12:EST12 13:EST13 14:EST14  
15:EST15 16:EST16 17:EST17 18:EST18 19:EST19 20:EST20  
21:EST21 22:EST22 23:EST23 24:EST24 25:EST25 26:EST26  
27:EST27 28:EST28 29:EST29 30:EST30 31:EST31 32:EST32  
33:EST33 34:EST34 35:EST35 36:EST36 37:EST37 38:EST38  
39:EST39 40:EST40 41:EST41 42:EST42 43:EST43 44:EST44  
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51:EST51 52:EST52 53:EST53 54:EST54 55:EST55 56:EST56  
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69:EST69 70:EST70 71:EST71 72:EST72 73:EST73 74:EST74  
75:EST75 76:EST76 77:EST77 78:EST78 79:EST79 80:EST80  
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93:EST93 94:EST94 95:EST95 96:EST96 97:EST97 98:EST98  
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EST-STS-TWO  
100:EST100 101:EST101 102:EST102 103:EST103 104:EST104  
105:EST105 106:EST106 107:EST107 108:EST108 109:EST109  
110:EST110 111:EST111 112:EST112 113:EST113 114:EST114  
115:EST115 116:EST116 117:EST117 118:EST118 119:EST119  
120:EST120 121:EST121 122:EST122 123:EST123 124:EST124  
125:EST125 126:EST126 127:EST127 128:EST128 129:STS1

Database:

130:STS2 131:STS3 132:STS4 133:STS5 134:STS6 135:STS7  
136:STS8 137:STS9 138:STS10 139:STS11 140:STS12  
141:STS13 142:STS14 143:STS15 144:STS16 145:STS17  
146:STS18 147:STS19 148:STS20 149:STS21 150:STS22  
151:STS23 152:STS24 153:STS25 154:STS26 155:STS27  
156:STS28 157:STS29 158:STS30 159:STS31 160:STS32  
161:STS33 162:STS34 163:STS35 164:STS36 165:STS37  
166:STS38 167:STS39 168:STS40 169:STS41 170:STS42  
171:STS43 172:STS44 173:STS45 174:STS46

Statistics: Mean 9.913; Variance 1.988; scale 4.987

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	146	37.2	364	108	EST100049 Homo sapien	5.40e-234
2	114	29.0	210	91	y83c03.r1 Homo sapie	6.94e-170
3	112	28.5	393	108	EST100653 Homo sapien	6.33e-166
4	109	27.7	488	14	y148g05.r1 Homo sapie	5.33e-160
5	107	27.2	470	25	y40h01.r1 Homo sapie	4.69e-156
6	100	25.4	463	91	y82d09.r1 Homo sapie	2.58e-142
7	96	24.4	516	91	y142h11.r1 Homo sapie	1.65e-134
8	93	23.7	381	109	EST69430 Homo sapiens	1.12e-128
9	92	23.4	434	127	ye24e07.r1 Homo sapie	9.72e-127
10	92	23.4	503	79	yh57e08.r1 Homo sapie	9.72e-127
11	91	23.2	279	109	EST89211 Homo sapiens	8.40e-125
12	90	22.9	383	109	EST98711 Homo sapiens	7.21e-123
13	89	22.6	467	14	y165d05.r1 Homo sapie	6.16e-121
14	84	21.4	438	90	y122f09.r1 Homo sapie	2.54e-111
15	83	21.1	390	20	yp22b04.r1 Homo sapie	2.09e-109
16	79	20.1	397	85	yj55c03.r1 Homo sapie	8.84e-102
17	78	19.8	261	85	yj54h03.r1 Homo sapie	7.00e-100
18	78	19.8	383	108	EST19007 Homo sapiens	7.00e-100
19	76	19.3	387	92	yj81e03.r1 Homo sapie	4.28e-96
20	76	19.3	395	109	EST69384 Homo sapiens	4.28e-96
21	75	19.1	332	109	EST77181 Homo sapiens	3.31e-94
22	74	18.8	366	14	y165f06.r1 Homo sapie	2.54e-92
23	72	18.3	359	108	EST100475 Homo sapien	1.45e-88
24	72	18.3	408	96	yp12g07.r1 Homo sapie	1.45e-88
25	71	18.1	359	14	y161g07.r1 Homo sapie	1.08e-86
26	71	18.1	367	117	yc01b07.r1 Homo sapie	1.08e-86
27	70	17.8	132	118	yb98g11.r1 Homo sapie	7.98e-85
28	69	17.8	438	91	yj82d12.r1 Homo sapie	7.98e-85
29	69	17.6	570	92	yj81d08.r1 Homo sapie	5.83e-83
30	68	17.3	390	14	y113f10.r1 Homo sapie	4.22e-81
31	67	17.0	430	27	yr86f06.r1 Homo sapie	3.03e-79
32	65	16.5	405	85	yj65f10.r1 Homo sapie	1.50e-75
33	65	16.5	451	126	ye15d10.r1 Homo sapie	1.50e-75
34	65	16.5	464	118	yc16e03.r1 Homo sapie	1.50e-75
35	64	16.3	203	18	yo53d07.r1 Homo sapie	1.04e-73
36	63	16.0	213	14	y147d10.r1 Homo sapie	7.14e-72
37	62	15.8	357	109	EST69270 Homo sapiens	4.83e-70
38	62	15.8	445	85	yj66c09.r1 Homo sapie	4.83e-70
39	59	15.0	257	86	yj71a07.r1 Homo sapie	1.39e-64
40	59	15.0	288	108	EST100107 Homo sapien	1.39e-64
41	58	14.8	141	18	y167h12.r1 Homo sapie	8.91e-63
42	57	14.5	443	85	yj56g05.r1 Homo sapie	5.64e-61









Qy 389 AACG 392

RESULT 6 R69532 463 bp mRNA EST 01-JUN-1995  
LOCUS yj32d09.r1 Homo sapiens cDNA clone 155249 5' similar to gb:M63438  
DEFINITION IG KAPPA CHAIN PRECURSOR V-III REGION (HUMAN);.  
ACCESSION R69532  
NID g843049  
KEYWORDS EST.  
SOURCE human clone-155249 library=Soares breast 2NbHBst vector=pT7T3D  
(Pharmacia) with a modified polylinker host=DH10B (ampicillin  
resistant) primer=M13RP1 Reitel=Not I Reite2=Eco RI Adult female.  
1st strand cDNA was primed with a Not I - oligo(dT) primer [5'  
TGTTACCAATCTCAAGTGGAGCGCGCCCTTTTTTTTTTTTTTTT 3'],  
double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia),  
digested with Not I and cloned into the Not I and Eco RI sites of a  
modified pT7T3 vector (Pharmacia). Library went through one round  
of normalization to a Cot = 230. Library constructed by Bento  
Soares and M.Fatima Bonaldo.

ORGANISM Homo sapiens  
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;  
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;  
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;  
Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 463)

REFERENCE Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,  
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,  
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,  
Trevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and  
Wilson,R.  
TITLE The WashU-Merck EST Project  
JOURNAL Unpublished (1995)  
COMMENT

Contact: Wilson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
High quality sequence stops: 394  
Source: IMAGE Consortium, LLNL  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES  
source  
1..463  
/organism="Homo sapiens"  
/clone="155249"  
/notes="human"

BASE COUNT 103 a 125 c 115 g 114 t 6 others  
ORIGIN

Query Match 25.4%; Score 100; DB 91; Length 463;  
Best Local Similarity 78.3%; Pred. No. 2.58e-142;  
Matches 137; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

Db 171 ctggtaccagcaaacctggccaggtcccgagttctctatctatgtgtgcatccaccag 230  
|||||  
|||||

Qy 171 CTGGTATCAGCAGAAACCCGGGCGAGCTCTTAACTTGTCTATTTCGCTGCATCCCAATCT 230  
|||||

Db 231 ggcactggatcccgaggttcagtgccagtgccagtgccagtgccagtgccagtgccag 290  
|||||  
|||||

Qy 231 AGAATCTGGGGTACCTGACCGATTTCAGTGGCAGCCGGGCTGGGACAGATTTCTACTCTAC 290  
|||||  
|||||

Db 291 catcagcagctgcagctgaagatttgcagttattgtctattattgtcagcaataaat 345  
|||||  
|||||

Qy 291 CATCAGCAGCTGCAGCGCTGAAGATGTGGCGGTATACTACTGTCTCAGCAAGATTAAT 345  
|||||  
|||||

RESULT 7 R67559 516 bp mRNA EST 30-MAY-1995  
LOCUS y142h11.r1 Homo sapiens cDNA clone 141957 5' similar to  
DEFINITION gb:X00965\_cdel1 IG KAPPA CHAIN PRECURSOR V-I REGION (HUMAN);.  
ACCESSION R67559  
NID g840197  
KEYWORDS EST.  
SOURCE human clone-141957 library=Soares placenta Nb2HP vector=pT7T3D  
(Pharmacia) with a modified polylinker host=DH10B (ampicillin  
resistant) primer=M13RP1 Reitel=Not I Reite2=Eco RI Female placenta  
obtained at birth (full term). 1st strand cDNA was primed with a  
Not I - oligo(dT) primer [5'  
AACTGGAGAAATTCGCGCGCGCAGGAATTTTTTTTTTTTTTTT 3'], double-stranded  
cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not  
I and cloned into the Not I and Eco RI sites of the modified pT7T3  
vector. Library went through one round of normalization. Library  
constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM Homo sapiens  
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;  
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;  
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;  
Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 516)

REFERENCE Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,  
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,  
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,  
Trevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and  
Wilson,R.  
TITLE The WashU-Merck EST Project  
JOURNAL Unpublished (1995)  
COMMENT

Contact: Wilson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
High quality sequence stops: 313  
Source: IMAGE Consortium, LLNL  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES  
source  
1..516  
/organism="Homo sapiens"  
/clone="141957"  
/notes="human"

BASE COUNT 118 a 137 c 120 g 134 t 7 others  
ORIGIN

Query Match 24.4%; Score 96; DB 91; Length 516;  
Best Local Similarity 73.3%; Pred. No. 1.65e-134;  
Matches 173; Conservative 0; Mismatches 60; Indels 3; Gaps 2;

Db 170 acctatttaattggatcatcagcaaaaccagggaagccctaaactctatccagcgt 229  
|||||  
|||||

Qy 160 AGTTATATGAATGTGATCAGCAGAAACCCGGGCGAGCTCTTAACTTGTCTCATTTACGCT 219  
|||||  
|||||

Db 230 gcatcctatttgcgaatgggtccatcaaggttcacgttgagtgagtgatctggaacagat 289  
||||| || || ||||| || ||||| ||||| || ||||| ||||| ||||| ||||| |||||  
Qy 220 GCATCCAACTAGATCTGGGGTACTGACCCGATTCAGTGGCAGCGGTCTGGGACAGAT 279  
Db 290 ttcaactcaccatccacagctgcgaactgaagatttgcgaacttacttctctgtcaaca 349  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Qy 280 TTCACTCTCACCATCAGCAGCGCTGCAGGCTGCAAGATGTGGCATATAC-TGTCAGCA 338  
Db 350 gagttacactgccccttcatttttttgcggggangtaccgaaggtgatgatacaacg 405  
||| | || | || | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Qy 339 AAGTAATGAGGATCC--TCGAGGTTCCGGGAGGACCAAGGTGAGATCAACG 392

RESULT 8  
LOCUS T29114 381 bp mRNA EST 06-SEP-1995  
DEFINITION EST69430 Homo sapiens cDNA 5' end similar to immunoglobulin light chain V(III), J(V) regions (GB:227170) (HT:3121).

ACCESSION T29114  
NID 9611212  
KEYWORDS EST.  
SOURCE human primer=M13 Reverse library=Human Lymphoid tissue.  
ORGANISM Homo sapiens

Eukaryotes; Metazoa; Eumetazoa; Bilateria; Coelomata;  
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;  
Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;  
Euthera; Archonta; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 381)

ADAMS, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,  
Bult, C.J., Lee, N., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,  
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Chiu, M.-W.,  
Clayton, R.A., Cline, R.T., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,  
Fitzgerald, L.M., FitzHugh, W.M., Fritchman, J.L., Geoghagen, N.S.M.,  
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle Jr, P.S.,  
Kelley, J.M., Kline, K.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M.,  
Merrick, J.M., Moreno-Palancas, R.F., McDonald, L.A., Nguyen, D.T.,  
Pellegrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L.,  
Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R.,  
Weidman, J.F., Li, Y., Bedarik, D.P., Cao, L., Cepeda, M.A.,  
Coleman, T.A., Collins, E.-J., Dimke, D., Feng, P., Ferrie, A.,  
Fischer, C., Hastings, G.A., He, W.-W., Hu, J.-S., Greene, J.M.,  
Gruber, J., Hudson, P., Kim, A., Kozak, D.L., Kunsch, C., Ji, H., Li, H.,  
Meissner, P.S., Oleen, H., Raymond, L., Wei, Y.-F., Wing, J., Xu, C.,  
Yu, G.-L., Ruben, S.M., Dillon, P.J., Fannon, M.R., Rosen, C.A.,  
Haeletine, W.A., Fields, C., Fraser, C.M. and Venter, J.C.  
Initial Assessment of Human Gene Diversity and Expression Patterns  
Based Upon 52 Million Basepairs of cDNA Sequence  
Unpublished (1995)

CONTACT: Venter, J.C.  
The Institute for Genomic Research  
932 Clopper Rd, Gaithersburg, MD 20878  
Tel: 3018699056  
Fax: 3018699423  
Email: tdbinfo@db.tigr.org

For clone availability, additional sequence and expression  
information related to this EST, please contact the TIGR Database  
(tdbinfo@db.tigr.org).  
FEATURES  
source Location/Qualifiers  
1..381  
/organism="Homo sapiens"  
/note="human"  
mRNA <1..>381  
BASE COUNT 86 a 109 c 97 g 86 t 3 others  
ORIGIN

Query March 23.7%; Score 93; DB 109; Length 381;  
Best Local Similarity 78.7%; Pred. No. 1.12e-128;  
Matches 133; Conservative 0; Mismatches 35; Indels 1; Gaps 1;

Db 172 ctggtaccagcagaacactggccaggctccaggctcctcatctatgatgcacccaacg 231  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Qy 171 CTGCTATACGACGAAACCCGGGCGCTCTAAGTTGCTCATTTACGCTGCATCCAATCT 230

Db 232 ggcgcgtggcactccacagacaggttcaactggcagtggtgtgggacagacttcactctcac 291  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Qy 231 AGAATCTGGGGTACTGACCGATTTCAGTGGCAGCGGTCTGGGACAGATTTCACCTCTCAC 290

Db 292 catcagcagactggcgtgaagatttgcagtgatctatnctgtcagca 340  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Qy 291 CATCAGCAGCT-GCAGCTGAAGATGTGGCAGTATACTACTGTCTCAGCA 338

RESULT 9  
LOCUS T29178 434 bp mRNA EST 22-MAR-1995  
DEFINITION ye24e07.r1 Homo sapiens cDNA clone 118692 5' similar to gb:L33034  
IG KAPPA CHAIN V-I REGION (HUMAN);.

ACCESSION T29178  
NID g725091  
KEYWORDS EST.  
SOURCE human clone=118692 library=Stratagene lung (#937210)  
vector=pBluescript SK- host=SOBR cells (kanamycin resistant)  
primer=M13R1 Reite=EcoRI Reite2=XhoI Normal lung tissue from a 72  
year old male. Cloned unidirectionally. Primer: Oligo dT. Average  
insert size: 1.0 kb; Uni-ZAP XR Vector; 5' adaptor sequence:  
5'-GAATTCGGCAGCAG-3'; 3' adaptor sequence:  
5'-CTCAGAGTTTTTTTTTTTTTTT-3'.

ORGANISM Homo sapiens  
Eucaryotes; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;  
Euthera; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 434)  
Hillier, L., Clark, N., Duboue, T., Elliston, K., Hawkins, M.,  
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,  
Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevaskis, E.,  
Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.  
WashU-Merck EST Project  
Unpublished (1995)

CONTACT: Wilson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
High quality sequence stops: 265  
Source: IMAGE Consortium, LNL  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
FEATURES  
source Location/Qualifiers  
1..434  
/organism="Homo sapiens"  
/clone="118692"  
/note="human"

BASE COUNT 103 a 107 c 103 g 118 t 3 others  
ORIGIN  
Query Match 23.4%; Score 92; DB 127; Length 434;  
Best Local Similarity 72.2%; Pred. No. 9.72e-127;





## COMMENT

Contact: Wilson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.wustl.edu  
High quality sequence stops: 352  
Source: IMAGE Consortium, LNL  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.

## FEATURES

source  
1..467  
/organism="Homo sapiens"  
/clone="163113"  
/note="human"

BASE COUNT 96 a 122 c 122 g 123 t 4 others  
ORIGIN

Query Match 22.6%; Score 89; DB 14; Length 467;  
Best Local Similarity 68.2%; Pred. No. 6.16e-121;  
Matches 195; Conservative 0; Mismatches 88; Indels 3; Gaps 3;

Db 63 gatattgatgactcagtcacactctccagcccgctcaccctcgagagcgccctcc 122

Qy 58 CATATCGTATGACCCAGCTCCAGACTCGTAGTGTCTGCGGAGAGGCCACC 117

Db 123 atctctcgaagtctagtcagagcctctacatagtagatgacagttattgttgagg 182

Qy 118 ATCAACTGCAAGGCCCTCCAAAGTGTG-AT-TA-TGATGGTGATAGTATATGA 174

Db 183 tacctcgagaagccaggacagtcctccagctcctgatctattgttcttaagggccc 242

Qy 175 TATCAGCAGAAACCGGGAGGCTCTTAAGTCTCATTTACGCTGCATCCATCTAG 234

Db 243 tcggggtccctgacaggttcagtcagtcagtcagtcagtcagtcagtcagtcagtc 302

Qy 235 TCTGGGTACTGACCCGATTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAG 294

Db 303 agtagatggagctgagatgttgctttttattactgcagtcgacaa 348

Qy 295 AGCAGCTGCAGGCTGAAGATGTGGCAGTATACTACTCTCAGCAAA 340

RESULT 14  
LOCUS R64603 438 bp mRNA EST 26-MAY-1995  
DEFINITION Y122109.r1 Homo sapiens cDNA clone 140009 5' similar to gb:M63438  
IG KAPPA CHAIN PRECURSOR V-III REGION (HUMAN);.

ACCESSION R64603  
NID g936572  
KEYWORDS EST.  
SOURCE human clone=140009 library=Soares placenta Nb2HP vector=pT7T3D  
(Pharmacia) with a modified polylinker host=DH10B (ampicillin

resistant) primer=M13RP1 Rsite=Not I Rsite2=Eco RI Female placenta  
obtained at birth (full term). 1st strand cDNA was primed with a  
Not I - oligo(dT) primer [5']

ACTGGAGAAATTCGGCCGCGAGGAATTTTTTTTTTTTTTTTTTTT 3', double-stranded  
cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not  
I and cloned into the Not I and Eco RI sites of the modified pT7T3  
vector. Library went through one round of normalization. Library  
constructed by Bento Soares and M.Fatima Bonaldo.

## ORGANISM

Homo sapiens  
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;

Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;  
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;  
Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.  
REFERENCE 1 (bases 1 to 438)

## AUTHORS

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,  
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,  
Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and  
Wilson, R.

## TITLE

## JOURNAL

## COMMENT

The WashU-Merck EST Project

Unpublished (1995)

Contact: Wilson RK

WashU-Merck EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@wustl.wustl.edu

High quality sequence stops: 290

Source: IMAGE Consortium, LNL

This clone is available royalty-free through LNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

## FEATURES

source

1..438

/organism="Homo sapiens"

/clone="140009"

/note="human"

BASE COUNT 114 a 110 c 114 g 96 t 4 others

ORIGIN

Query Match 21.4%; Score 84; DB 90; Length 438;

Best Local Similarity 77.3%; Pred. No. 2.54e-111;

Matches 119; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

Db 24 ggatccagacaggttcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 83

Qy 239 GGGTACCTGACCGATTTCAGTGGCAGGGGCTCGGACAGATTTTCACTCTCACCATCAGCA 298

Db 84 gactggagcctgaagatttgcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 143

Qy 299 GCTTCGAGGCTGACAGATGTCGAGTATACTACTGTACGAAAGTAATGAGGATCTCTCCGA 358

Db 144 ctgttgccaggggacacagtcgagatcaaacg 177

Qy 359 GGTTCGGCGGAGGACCAAGGTGGAGATCAACG 392

RESULT 15

LOCUS H45841 390 bp mRNA EST 31-JUL-1995

DEFINITION yp22b04.r1 Homo sapiens cDNA clone 188143 5' similar to gb:M99603

IG KAPPA CHAIN V-I REGION (HUMAN);.

ACCESSION H45841

NID g921893

KEYWORDS EST.

SOURCE human clone=188143 library=Soares breast 3NbHBst vector=pT7T3D

(Pharmacia) with a modified polylinker host=DH10B (ampicillin

resistant) primer=M13RP1 Rsite=Not I Rsite2=Eco RI Adult human.

1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-

TGTTACCAATCTCAAGTGGAGCGGCCCTTTTTTTTTTTTTTTTTT 3'],

double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia),

digested with Not I and cloned into the Not I and Eco RI sites of a

modified pT7T3 vector (Pharmacia). Library went through one round

of normalization to a Cot = 20. Library constructed by Bento Soares

Search completed: Wed Mar 19 08:11:47 1997  
Job time : 217 secs.

\*\*\*\*\*

WATERMAN

(TM)

\*\*\*\*\*

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MPsrch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed Mar 19 08:06:58 1997; MsePar time 41.85 Seconds  
819.095 Million cell updates/sec

Tabular output not generated.

Title: &gt;US-08-612-929-13

Description: (1-393) from US08612929.seq

Perfect Score: 393

N.A. Sequence: 1 ATGGGATGACCTGCTATCAT.....CCAGGTGGAGATCAACCT 393  
Comp: TACCCTACCTGCACATGTA.....GGTTCACCTCTAGTTGCA

Scoring table: TABLE default

Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 113505 seqs, 43611913 bases x 2

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: n-geneseq25

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13  
14:part14 15:part15 16:part16 17:part17 18:part18  
19:part19 20:part20 21:part21 22:part22

Statistics: Mean 8.325; Variance 5.169; scale 1.611

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	389	99.0	393	14	Q83520 Humanized antibody 3B	7.09e-242
2	389	99.0	393	14	Q73986 Humanized antibody 3B	7.09e-242
3	223	56.7	339	10	Q44828 Humanised light chain	9.30e-129
4	221	56.2	339	10	Q44827 Humanised light chain	2.08e-127
5	218	55.5	5703	22	T34110 Anti-IL-5 humanised a	2.21e-125
6	215	54.7	396	14	Q83490 Mouse MAb 3B9 light c	2.33e-123
7	213	54.2	339	22	T34094 Humanised 2B6 antibod	5.20e-122
8	207	52.7	333	12	Q70372 Anti HIV antibody lig	5.75e-118

9	207	52.7	333	11	Q65554 Mouse anti-HIV mu5.5	5.75e-118
10	205	52.2	393	6	Q36609 Anti-CD4 antibody MT	1.28e-116
11	205	52.2	619	1	N80498 Encodes V region of L	1.28e-116
12	205	52.2	1088	10	Q56735 Sequence of Hum4VL ge	1.28e-116
13	205	52.2	1373	1	N80941 Encodes Vchi region o	1.28e-116
14	202	51.4	900	1	Q04039 Anti-Leu 3a light cha	1.34e-114
15	200	50.9	733	4	Q25658 Mouse 0.5beta anti-HI	2.96e-113
16	200	50.9	780	1	N90495 A V chi region gene.	2.96e-113
17	200	50.9	1028	7	Q45606 Sequence of pATDFLAG	2.96e-113
18	200	50.9	1330	7	Q45605 Sequence of Hum4 VL-C	2.96e-113
19	200	50.9	1359	7	Q45607 Sequence of pSC49FLAG	2.96e-113
20	198	50.4	334	1	N90492 Gene fragment of immu	6.54e-112
21	198	50.4	400	1	N80499 Encodes V region of L	6.54e-112
22	198	50.4	1361	10	Q56740 Sequence of plasmid p	6.54e-112
23	197	50.1	1097	7	Q45602 Sequence of the Hum4	3.08e-111
24	195	49.6	342	6	Q33032 MAB GAH variable regi	6.80e-110
25	194	49.4	7305	18	T15933 Anti-IgE VL expressio	3.19e-109
26	191	48.6	336	2	Q12684 Murine IB4 light chai	3.30e-107
27	191	48.6	360	12	Q17118 Monoclonal antibody L	3.30e-107
28	190	48.3	334	9	Q55002 Murine anti-CD18 Ab 6	1.55e-106
29	187	47.6	393	5	Q30757 p64-k4.	1.60e-104
30	187	47.6	836	7	Q45604 Sequence of single ch	1.60e-104
31	185	47.1	333	9	Q55917 Humanised light chain	3.50e-103
32	185	47.1	407	4	Q26047 V-region of L-chain o	3.50e-103
33	184	46.8	334	11	Q73749 Light chain variable	1.64e-102
34	183	46.6	333	14	Q82818 Murine NM-01 variable	7.67e-102
35	183	46.6	336	16	Q96285 Human IgE receptor-bi	7.67e-102
36	179	45.5	333	12	Q70376 Chimeric anti HIV ant	3.66e-99
37	179	45.5	333	11	Q65558 Mouse-human chimeric	3.66e-99
38	179	45.5	336	16	Q96283 Human IgE receptor-bi	3.66e-99
39	179	45.5	783	17	T08490 Anti-G5 MAb N19/8 scf	3.66e-99
40	177	45.0	363	10	Q56686 Sequence of the monoc	7.99e-98
41	176	44.8	336	2	Q10379 Chimeric MAb 9.2.27 1	3.73e-97
42	176	44.8	451	1	Q04694 Light chain variable	3.73e-97
43	176	44.8	717	18	T04019 Anti-EGFR single chai	3.73e-97
44	175	44.5	363	10	Q56688 Sequence of the monoc	1.74e-96
45	173	44.0	363	6	Q37472 Sequence encoding the	3.78e-95

## ALIGNMENTS

RESULT 1  
ID Q83520 standard; cDNA; 393 BP.  
AC Q83520;  
DT 20-SEP-1995 (first entry)  
DE Humanized antibody 3B9 light chain.  
KW Humanized antibody; antibody engineering; monoclonal antibody;  
KW MAB; interleukin-4; IL-4; allergy; ds.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT CDS  
FT /\*tag= a  
PN W09507301-A.  
PD 16-MAR-1995.  
PF 07-SEP-1994; U10308.  
PR 07-SEP-1993; US-117366.  
PR 14-OCT-1993; US-136783.  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
PA (SMIK ) SMITHKLINE BEECHAM PLC.  
PI Gross MS, Holmes SD, Sylvester DR;  
DR WFI; 95-123387/16.  
PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived from high affinity mAbs - useful in treatment of IL-4-mediated

PT and IgE-mediated allergic conditions  
 PS Disclosure; Page 71-72; 97pp; English.  
 CC A humanized antibody light chain variable region and signal  
 CC sequence is given in R75355. The signal sequence is also  
 CC provided in R70194. The sequences of the 3 CDRs  
 CC are identical to mouse anti-human IL-4 Mab 3B9 light chain  
 CC CDRs (given in R70195-97).  
 SQ Sequence 393 BP; 97 A; 98 C; 105 G; 93 T;

Query Match 99.0%; Score 389; DB 14; Length 393;  
 Best Local Similarity 99.5%; Pred. No. 7.09e-242;  
 Matches 391; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 1 atgggatgagctgtatcatctcttctgttagcaacagctacaggtgtccactccgat 60  
 |||||||  
 Qy 1 ATGGGATGAGCTGTATCATCTCTTCTGTAGCAACAGCTACAGGTGCCACTCCGAT 60  
 |||||||  
 Db 61 atcgtgatgaccagctctccagactcgctagctgtctctggcgagagggccaccatc 120  
 |||||||  
 Qy 61 ATCTGTGATGACCCAGCTCTCCAGACTCGCTAGCTGTCTCTCTGGCGCAGAGGCCACCATC 120  
 |||||||  
 Db 121 aactgcaaggctcccaagdtgttattatgatgtgatagttatatgaactggtatcag 180  
 |||||||  
 Qy 121 AACTGCAAGGCCCTCCAAAGCTTGTATGATGCTGATAGTTATATCAATCACTGGTATCAG 180  
 |||||||  
 Db 181 cagaacccggcgagctcctcctaagttgctcattacgctgcacccaatcagaatctggg 240  
 |||||||  
 Qy 181 CAGAAACCCGGCGAGCCTCTTAAGTGTCTCAATTAGCGTCGATCCCAATCTAGAAATCTGGG 240  
 |||||||  
 Db 241 gtacctgaccagcttcagtgccagcggtctgggacagagatttcactctcaccatcagcagc 300  
 |||||||  
 Qy 241 GTACCTGACCGAATTCACTGCGACGGGGTCTGGGACAGAGATTTCACCTCAACATCAGCAGC 300  
 |||||||  
 Db 301 ctgagagctgaagatggcagatatactactgtcagcaagtaagtgaagatcctccgagc 360  
 |||||||  
 Qy 301 CTCGAGGCTCAAGATGTGGCAGTATACTACTGTCCAGCAAGTAATGAGGATCTCCGAGG 360  
 |||||||

## RESULT 2

ID Q73986 standard; cDNA; 393 BP.  
 AC Q73986;  
 DT 20-SEP-1995 (first entry)  
 DE Humanized antibody 3B9 light chain.  
 KW Humanized antibody; antibody engineering; monoclonal antibody;  
 KW Mab; interleukin-4; IL-4; allergy; ds.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT CDS 1..393  
 FT /\*tag= a  
 FT sig\_peptide 1..60  
 FT /\*tag= b  
 FT mat\_peptide 61..393  
 FT /\*tag= c  
 PN W09507301-A.  
 PD 16-MAR-1995.  
 PF 07-SEP-1994; U10308.  
 PR 07-SEP-1993; US-117366.  
 PR 14-OCT-1993; US-136783.  
 PA (SWIK ) SMITHKLINE BEECHAM CORP.  
 PA (SWIK ) SMITHKLINE BEECHAM PLC.

PI Grosse MS, Holmes SD, Sylvester DR;  
 DR WPI; 95-123387/16.  
 DR P-PSDB; R75355.  
 PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived  
 PT from high affinity mAbs - useful in treatment of IL-4-mediated  
 PT and IgE-mediated allergic conditions  
 PS Disclosure; Fig.5; 97pp; English.  
 CC A humanized antibody light chain variable region and signal  
 CC sequence is given in R75355. The signal sequence is also  
 CC provided in R70194. The sequences of the first 2 CDRs  
 CC are identical to mouse anti-human IL-4 Mab 3B9 light chain  
 CC CDRs (given in R70195-96), but the third (R70201) differs  
 CC by a single amino acid from the native mouse CDR (R70197).  
 SQ Sequence 393 BP; 97 A; 96 C; 108 G; 92 T;

Query Match 99.0%; Score 389; DB 14; Length 393;  
 Best Local Similarity 99.5%; Pred. No. 7.09e-242;  
 Matches 391; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 1 atgggatgagctgtatcatctcttctgttagcaacagctacaggtgtccactccgat 60  
 |||||||  
 Qy 1 ATGGGATGAGCTGTATCATCTCTTCTGTAGCAACAGCTACAGGTGCCACTCCGAT 60  
 |||||||  
 Db 61 atcgtgatgaccagctctccagactcgctagctgtctctggcgagagggccaccatc 120  
 |||||||  
 Qy 61 ATCTGTGATGACCCAGCTCTCCAGACTCGCTAGCTGTCTCTCTGGCGCAGAGGCCACCATC 120  
 |||||||  
 Db 121 aactgcaaggcgagcccaagdtgttattatgatgtgatagttatatgaactggtatcag 180  
 |||||||  
 Qy 121 AACTGCAAGGCCCTCCAAAGCTTGTATGATGCTGATAGTTATATCACTGGTATCAG 180  
 |||||||  
 Db 181 cagaacccggcgagcctcctcctaagttgctcattacgctgcacccaatcagaatctggg 240  
 |||||||  
 Qy 181 CAGAAACCCGGCGAGCCTCTTAAGTGTCTCAATTAGCGTCGATCCCAATCTAGAAATCTGGG 240  
 |||||||  
 Db 241 gtacctgaccagcttcagtgccagcggtctgggacagagatttcactctcaccatcagcagc 300  
 |||||||  
 Qy 241 GTACCTGACCGAATTCACTGCGACGGGGTCTGGGACAGAGATTTCACCTCAACATCAGCAGC 300  
 |||||||  
 Db 301 ctgagagctgaagatggcagatatactactgtcagcaagtaagtgaagatcctccgagc 360  
 |||||||  
 Qy 301 CTCGAGGCTCAAGATGTGGCAGTATACTACTGTCCAGCAAGTAATGAGGATCTCCGAGG 360  
 |||||||

## RESULT 3

ID Q44828 standard; DNA; 339 BP.  
 AC Q44828;  
 DT 05-OCT-1994 (first entry)  
 DE Humanised light chain variable region PfHzlcl-2.  
 KW Monoclonal antibody; Plasmodium falciparum; CDR;  
 KW complementarity determining region; fusion protein;  
 KW murine; variable; light; heavy; chain; malaria; ds.  
 OS Synthetic.  
 FH Key Location/Qualifiers  
 FT misc feature 70..120  
 FT /\*tag= a  
 FT /label= CDR1  
 FT misc feature 166..186  
 FT /\*tag= b  
 FT /label= CDR2



```
FT misc feature 283..309
FT /*tag= c
FT /label= CDR3
PN W09405690-A.
PD 17-MAR-1994.
PF 08-SEP-1993; U08435.
PR 09-SEP-1992; US-941654.
PA (SMIK ) SMITHKLINE BEECHAM CORP.
PA (USNA ) US SEC OF ARMY.
PA (USNA ) US SEC OF NAVY.
PI Charoenvit Y, Hoffman S, Hurle M, Rosenberg M;
PI Sadoff JC, Sylvester DR, Gross MS;
DR WPI; 94-101115/12.
DR P-PSDB; R50314.
PT New engineered antibodies and fusion proteins for preventing
PT Plasmodium infection - contg. murine antibody CDR sequences, and
PT corresp. nucleic acid, vectors and transformed cells
PS Claim 5; Fig 3; 98pp; English.
CC Naturally-occurring (Q44841-42) and synthetic (Q44825-28)
CC variable light chain and variable heavy chain sequences
CC derived from murine mAb NFS2 are provided. Murine mAb NFS2,
CC its variable chain peptides, CDRs, functional fragments,
CC Fab fragments, and analogs are useful in prodn. of fusion
CC proteins, esp. engineered antibodies. These prods. are
CC used to protect humans against Plasmodium infections.
SQ Sequence 339 BP; 84 A; 86 C; 93 G; 76 T;

Query Match 56.7%; Score 223; DB 10; Length 339;
Best Local Similarity 87.3%; Pred. No. 9.30e-129;
Matches 296; Conservative 0; Mismatches 37; Indels 6; Gaps 5;

Db 1 gatatcgtgatgaccagctccagactcgtcagctgctgtctctggcgagagggccacc 60
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Qy 58 GATATCGTGATGCCAGCTCCAGACTCGCTAGCTGTGTCTCTGGCGAGAGGGCCACC 117
|||||

Db 61 atcaactgcaagagctctcagagccttttatactcagcagcaatcaaaagaattactggcc 120
|||||
Qy 118 ATCAACTGCAAGGCTCCCAAGTGTGATTA-T-GATGG-TGATA-G--TTATATGAAC 171
|||||

Db 121 tggatcagcagaaccggcgagctcctaagttgctcatttactggcgctgactagg 180
|||||
Qy 172 TGGTATCAGCAGAACCCGGCGAGCGCTCCTAGTTGCTCATTTACGCTGCATCAATCTA 231
|||||

Db 181 gaatctgggtacctgaccgattcagtgccagcgggtctgtgggacagatttcaactctcacc 240
|||||
Qy 232 GAATCTGGGTTACCTGACCCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACCTCTCACC 291
|||||

Db 241 atcagcagctcagcgtgaagatgtggcagtgatactactcagcaatattagctat 300
|||||
Qy 292 ATCAGCAGCTCAGGCTGAAGATGTGCAGTATACTACTGTGCAGCAAGTAATGAGGAT 351
|||||

Db 301 ccgcggagctcggcgagggaccaggtggagatcaaa 339
|||||
Qy 352 CTCGCGAGGTTCCGGCGGAGGACCAAGTGGAGATCAAA 390
|||||
```

## RESULT 4

```
ID Q44827 standard; DNA; 339 BP.
AC Q44827;
DT 05-OCT-1994 (first entry)
DE Humanised light chain variable region Pfhlcl-1.
KW Monoclonal antibody; Plasmodium falciparum; CDR;
KW complementarity determining region; fusion protein;
KW murine; variable; light; heavy; chain; malaria; ds.
```

```
OS Synthetic.
FH Key Location/Qualifiers
FT misc feature 70..120
FT /*tag= a
FT /label= CDR1
FT misc feature 166..186
FT /*tag= b
FT /label= CDR2
FT misc feature 283..309
FT /*tag= c
FT /label= CDR3
PN W09405690-A.
PD 17-MAR-1994.
PF 08-SEP-1993; U08435.
PR 09-SEP-1992; US-941654.
PA (SMIK ) SMITHKLINE BEECHAM CORP.
PA (USNA ) US SEC OF ARMY.
PA (USNA ) US SEC OF NAVY.
PI Charoenvit Y, Hoffman S, Hurle M, Rosenberg M;
PI Sadoff JC, Sylvester DR, Gross MS;
DR WPI; 94-101115/12.
DR P-PSDB; R50313.
PT New engineered antibodies and fusion proteins for preventing
PT Plasmodium infection - contg. murine antibody CDR sequences, and
PT corresp. nucleic acid, vectors and transformed cells
PS Claim 5; Fig 2; 98pp; English.
CC Naturally-occurring (Q44841-42) and synthetic (Q44825-28)
CC variable light chain and variable heavy chain sequences
CC derived from murine mAb NFS2 are provided. Murine mAb NFS2,
CC its variable chain peptides, CDRs, functional fragments,
CC Fab fragments, and analogs are useful in prodn. of fusion
CC proteins, esp. engineered antibodies. These prods. are
CC used to protect humans against Plasmodium infections.
SQ Sequence 339 BP; 85 A; 85 C; 92 G; 77 T;

Query Match 56.2%; Score 221; DB 10; Length 339;
Best Local Similarity 87.0%; Pred. No. 2.08e-127;
Matches 295; Conservative 0; Mismatches 38; Indels 6; Gaps 5;

Db 1 gatatcgtgatgaccagctccagactcgtcagctgctgtctctggcgagagggccacc 60
|||||
Qy 58 GATATCGTGATGCCAGCTCCAGACTCGCTAGCTGTGTCTCTGGCGAGAGGGCCACC 117
|||||

Db 61 atcaactgcaagagctctcagagccttttatactcagcagcaatcaaaagaattactggcc 120
|||||
Qy 118 ATCAACTGCAAGGCTCCCAAGTGTGATTA-T-GATGG-TGATA-G--TTATATGAAC 171
|||||

Db 121 tggatcagcagaaccggcgagctcctaagttgctcatttactggcgctgactagg 180
|||||
Qy 172 TGGTATCAGCAGAACCCGGCGAGCGCTCCTAGTTGCTCATTTACGCTGCATCAATCTA 231
|||||

Db 181 gaatctgggtacctgaccgattcagtgccagcgggtctgtgggacagatttcaactctcacc 240
|||||
Qy 232 GAATCTGGGTTACCTGACCCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACCTCTCACC 291
|||||

Db 241 atcagcagctcagcgtgaagatgtggcagtgatactactcagcaatattagctat 300
|||||
Qy 292 ATCAGCAGCTCAGGCTGAAGATGTGCAGTATACTACTGTGCAGCAAGTAATGAGGAT 351
|||||

Db 301 ccgcggagctcggcgagggaccaggtggagatcaaa 339
|||||
Qy 352 CTCGCGAGGTTCCGGCGGAGGACCAAGTGGAGATCAAA 390
|||||
```

RESULT 5  
ID T34110 standard; DNA; 5703 BP.  
AC T34110;  
DE Anti-IL-5 humanised antibody light chain plasmid pCNIL5H2L1C1.0.  
KW Antibody engineering; humanised antibody; chimeric antibody; Fab; Interleukin-5; IL-5; eosinophil; asthma; allergic rhinitis;  
KW atopic dermatitis; therapy; diagnosis; light chain; VI;  
KW monoclonal antibody; Mab; plasmid pCNIL5H2L1C1.0; ds; cyclic.  
OS Synthetic.  
PN WO9621000-A2.  
PD 11-JUL-1996.  
PF 22-DEC-1995; U17082.  
PR 23-DEC-1994; US-363131.  
PR 06-JUN-1995; US-470110.  
PR 06-JUN-1995; US-467420.  
PA (SMIK) SMITHKLINE BEECHAM CORP.  
PA (SMIK) SMITHKLINE BEECHAM PLC.  
PI Ames RS, Appelbaum ER, Chaiken IM, Cook RM, Gross MS;  
PI Holmes SD, McMillan LJ, Thiesen TW;  
DR WI1; 96-333976/33.  
PT New monoclonal antibody to human interleukin-5 - used to produce  
PT products for the treatment and diagnosis of conditions associated  
PT with excess eosinophil prodn., e.g. asthma etc.  
PS Example 4; Page 76-81; 120pp; English.  
CC pCNIL5H2L1C1.0 (T34110) is a pUC19-based plasmid that incorporates  
CC a DNA sequence (see also T34094) coding for a humanised light chain  
CC (R98489) of murine anti-human interleukin-5 (IL-5) monoclonal  
CC antibody 2B6 as well as a beta-lactamase gene, an SV40 replication  
CC origin, a cytomegalovirus promoter, a signal sequence (see also  
CC T34108), a polyA signal from bovine growth hormone (BGH), a  
CC beta-globin promoter, a dihydrofolate-reductase gene and another  
CC BGH polyA signal. pCNIL5H2L1C1.0 and pCDIL5H2H1C1.0 (T34109) coding  
CC for the humanised heavy chain were co-transfected into COS cells  
CC for prodn. of humanised 2B6 antibody. This can be used for the  
CC diagnosis and treatment of IL-5-mediated conditions, e.g. asthma,  
CC allergic rhinitis and atopic dermatitis.  
SQ Sequence 5703 BP; 1361 A; 1450 C; 1495 G; 1397 T;

Query Match 55.5%; Score 218; DB 22; Length 5703;  
Best Local Similarity 85.0%; Pred. No. 2.21e-125;  
Matches 301; Conservative 0; Mismatches 47; Indels 6; Gaps 4;  
Db 1062 ggtgctacggggtatcgtagaccagctctccagactcgtagctgtgtctctggcc 1121  
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Qy 46 CGTCTCCACTCCGATATCGTGTGATCCAGCTCCAGACTCGTAGCTGTCTCTGGCC 105  
Db 1122 gagagggccaccatcaactgcaagagctctcagagctgtgttaaacagtggaatcaaaag 1181  
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Qy 106 GAGAGGGCCACCATCAACTCAAGGCTCCCAAGT--GTTGATTA-TGATGTGTAGT 162  
Db 1182 aactactggctggtatcagcagaacccggcgagcctcctcaagtgtcattacggg 1241  
||||| ||| ||||||||||||||||||||||||||||||||||||||||||||||||  
Qy 163 TA-TA--TGACTGGTATCAGCAGAAACCCGGCGAGCTCTTAAGTTCGTCATTAACCT 219  
Db 1242 gcgtcgactagggaatctgggtacctgacqattcagtgagcggggtctgggacagat 1301  
||||| ||| ||||||||||||||||||||||||||||||||||||||||||||||||  
Qy 220 GCATCCCAATTAAGATCTGGGGTACTGACCGGATTCAGTGGCAGCGGTCTGGGACAGAT 279  
Db 1302 ttcaactcaccatcagcagcctgcaggctgaagatgtggcagatactactgtcagaat 1361  
||||| ||| ||||||||||||||||||||||||||||||||||||||||||||||||  
Qy 280 TTCACTCTCACCATCAGCAGCTGCAGGCTGAAGATGTGGCAGTACTACTGTGAGCA 339  
Db 1362 gttcatagttttccattcaactgttcggggaggaccagaagtggagatcaaacgt 1415

Qy 340 ACTAATCAGGATCCTCCGAGGTTCCGGCGAGGACCAAGGTGGAGATCAAACT 393  
||||| ||| ||||||||||||||||||||||||||||||||||||||||||||||||  
RESULT 6  
ID Q83490 standard; cDNA; 396 BP.  
AC Q83490;  
DT 20-SEP-1995 (first entry)  
DE Mouse Mab 3B9 light chain.  
KW Chimeric antibody; humanized antibody; antibody engineering; monoclonal antibody; Mab; interleukin-4; IL-4; allergy; ds.  
OS Mus sp.  
FH Key Location/Qualifiers  
FT CDS 1..396  
FT /\*tag= a  
FT sig\_peptide 1..60  
FT /\*tag= b  
FT mat\_peptide 61..396  
FT /\*tag= c  
PN WO9507301-A.  
PD 16-MAR-1995.  
PF 07-SEP-1994; U10308.  
PR 07-SEP-1993; US-117366.  
PR 14-OCT-1993; US-136783.  
PA (SMIK) SMITHKLINE BEECHAM CORP.  
PA (SMIK) SMITHKLINE BEECHAM PLC.  
PI Gross MS, Holmes SD, Sylvestre DR;  
DR WI1; 95-123387/16.  
DR P-PDOB; R70189.  
PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived  
PT from high affinity mAbs - useful in treatment of IL-4-mediated  
PT and IgE-mediated allergic conditions  
PS Disclosure; Fig.1; 97pp; English.  
CC Spleen cells from mice immunized with human IL-4 were used to prepare  
CC hybridomas, which were screened for anti-IL-4 Mab secretion. Only  
CC clone 3B9 was positive. cDNA clones of the 3B9 light and heavy  
CC chains were cloned into pGEM7f+ and transformed into E. coli  
CC DH5-alpha. The clones were sequenced (Q83490-91), and used for  
CC antibody engineering.  
SQ Sequence 396 BP; 99 A; 103 C; 103 G; 91 T;

Query Match 54.7%; Score 215; DB 14; Length 396;  
Best Local Similarity 82.1%; Pred. No. 2.33e-123;  
Matches 275; Conservative 0; Mismatches 60; Indels 0; Gaps 0;  
Db 61 gacattgtgtgacccaatctccagctttttggctgtctctctagggcagagggccacc 120  
||||| ||| ||||||||||||||||||||||||||||||||||||||||||||||||  
Qy 58 GATATCTGATGACCCAGTCTCCAGACTCGCTAGCTGTCTCTGGCGAGAGGGCCACC 117  
Db 121 atctcctgcaagggccagccaaagtgttgattgatgtgtagtatgatgaactggtag 180  
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Qy 118 ATCAACTGCAAGGGCTCCCAAGTGTGATTATGATGATGATTATATGAACCTGGTAT 177  
Db 181 caacagaaccaggacagccaccacaaactcctcatctatgtcgatcccaatctagaatct 240  
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Qy 178 CAGCAGAAACCCGGCGAGCTCTCAAGTTCGCTTACGCTGCATCCCAATCTAGAACT 237  
Db 241 gggatcccgacagggtttagtggcagtggtgtgtggacagactccacctcaacatccat 300  
||||| ||| ||||||||||||||||||||||||||||||||||||||||||||||||  
Qy 238 GGGGTACCTGACCGATTTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGC 297  
Db 301 cctgtgaggaggaggtgctgcaacctattactgtcagcaaatgaatgaggatcctccg 360  
||||| ||| ||||||||||||||||||||||||||||||||||||||||||||||||  
Qy 298 AGCTGCAGGCTGAAGATGTGGCAGTATACTACTCTCAGCAAGTATGAGGATCTCTCCG 357

Db 361 acgttcggtggaggcaccacagctggaatcaaacg 395  
 | | | | | | | | | | | | | | | | | | | |  
 Qv 358 AGGTTCCGGCGGAGGGACCAAGGTGGAGATCAAAAG 392

## RESULT 7

ID T34094 standard; DNA; 339 BP.

AC T34094;

DT 12-OCT-1996 (first entry)

DE Humanised 2B6 antibody light chain variable region DNA.

KW Antibody engineering; humanised antibody; chimeric antibody; Fab;

KW interleukin-5; IL-5; eosinophil; asthma; allergic rhinitis;

KW atopic dermatitis; therapy; diagnosis; light chain; VL;

KW monoclonal antibody; MAB; *es*.

QS Synthetic.

PN W09621000-A2.

PD 11-JUL-1996.

PF 22-DEC-1995; U17082.

PR 23-DEC-1994; US-363131.

PR 06-JUN-1995; US-470110.

PR 06-JUN-1995; US-467420.

PA (SMIK ) SMITHKLINE BEECHAM CORP.

PA (SMIK ) SMITHKLINE BEECHAM PLC.

PI Ames RS, Appelbaum ER, Chaiken IM, Cook RM, Gross MS;

PI Holmes SD, McMillan LJ, Theisen TW;

DR WPI; 96-333976/33.

DR P-PSDB; R98489.

PT New monoclonal antibody to human interleukin-5 - used to produce

PT products for the treatment and diagnosis of conditions associated

PT with excess eosinophil prodn., e.g asthma etc.

PS Example 4; Page 54-55; 120pp; English.

CC A DNA sequence (T34094) codes for the light chain variable region

CC (R98489) of humanised antibody 2B6, comprising complementarity

CC determining regions (see also R98484-86) derived from murine

CC monoclonal antibody 2B6 VL (see also R98479) and framework region

CC from the Bence-Jones protein (LEN). Murine 2B6 is specific for

CC human interleukin-5 (IL-5). The construct, in vector pCNIL5H2LC1

CC (T34110), was used to produce humanised 2B6 VL in COS cells.

CC Humanised 2B6 VH was also produced (see also T34093). Humanised

CC 2B6 can be used for the diagnosis and treatment of IL-5-mediated

CC conditions, e.g. asthma, allergic rhinitis and atopic dermatitis.

SO Sequence 339 BP; 85 A; 93 G; 78 T;

Query Match 54.2%; Score 213; DB 22; Length 339;  
Best Local Similarity 85.8%; Pred. No. 5.20e-122;  
Matches 291; Conservative 0; Mismatches 42; Indels

Db 1 gatatcgtgatgaccagctccagactcgtagctgtgtctctggcgagagggccacc 60

Qy 58 GATATCGTATGATGACCCAGTCTCCAGACTCGCTAGTGTGTCTCTGGCGAGAGGGCCACC 117

Db           61 atcaactgcaagagtctcagagtctgttaaacagtggaaatcaaagaactacttgccc  
|||||  
|||  
  
G:  
119 ATCAATACAAAGCCCTCCCCAAGT---ATTTCATA-TCATCCTCATACTTA TA--TCAAC 171

118 ATCAACATGCAAGGCCCTCCCAAGAGT--GTTGATTA-AGATGGAGATAGTAA-7A--1GATAC 177

121 TGGTATCAAGCAGAAAGCCCGGAGCGCTCTAAGTTGCTCTATTACGGGGCCTCAGTAgg 180

Qy 172 TGGTATCAGCAGAAACCGGGAGCGCTCTAAGTTGCTCATTTACGTCATCCAAATCTA 231

Db 181 gaatctgggtacctgaccgattcagtagcagcgggtctggacagatttcactctcacc 240

Qy 232 GAATCTGGGGTACCTGACCGATTCACTGGCAGCGGCTCTGGACAGATTTCACCTCACC 291

Db	241	atcagcagcctcgagctggaagtggcagtcatactctcgaagtgttcatagtttt	300
Qy	292	ATCAGAGCCTCGAGGCTCAGATGTGGCAGTATCTACTTCACCAAGTATCAGGAT	351
Db	301	ccattcagctgcaggaggaaccaagtgtgagatcaaa	339
Qy	352	CCTCCGAGGTTCCGGCGAGGACCAAGGTCGAGATCAAA	390

## RESULT

RESOLUTION  
ID Q70372 standard; cDNA to mRNA; 333 BP.  
AC Q70372;  
DT 09-MAR-1995 (first entry)  
DE Anti HIV antibody light chain variable region.  
KW Antibody; heavy chain; light chain; human immunodeficiency virus;  
KW HIV; acquired immune deficiency syndrome; AIDS; treatment;  
KW prophylaxis; Mus musculus; Homo sapiens; ss.

Location/Qualifiers	1.333
FT CDS	
FH Key	

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FT /*tag= a
FT /product= Antibody light chain variable region.
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PN W09415969-A.

21-III-1994

14 JAN 1963  
15 JAN 1963  
16 JAN 1963

PF 14-JAN-1993; J00039

PR 14-JAN-1993; AU-032671.

PR 14-JAN-1993: WO-J00039.

DA (KACA) CHENO SEPO THER

PA (KAGA) / CHEMO SERO THERAPEUTIC RES INST.

PI Eda Y, Kimachi K, Maeda H, Osatomi K, Shiosaki K,

PI Tokivoshi S:

WPT: 94-249145/30

DR  
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DR p-PSDB; R60302.  
PT Recombinant chimeric anti HIV antibody - useful for the treatment  
PT and prevention of HIV

Claim 15: Figure 4: 51mm: Japanese

FS Cram 13; Figure 4; jipb; Japanese.  
CC The recombinant antibody light chain has neutralising activity  
CC against HIV. Chimeric antibodies comprising both mouse and human  
CC sequences are useful in the treatment/prevention of AIDS caused by  
CC HIV. This sequence is obtained from the mu5.5 anti HIV monoclonal  
CC antibody producing cell.

CC	antibody producing cell	76 T;
SQ	Sequence	83 C; 86 G;
	333 BP;	88 A;

Query Match 52.7%; Score 207; DB 12; Length 333;  
Best Local Similarity 81.1%; Pred. No. 5.75e-118;  
Matches 270; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

Db 1 gacattgtgctgaccaatctccagcttctttggctgtgtctctagggcagagggccacc 60

Qy 58 GATATCGTATGACCCAGTCTCCAGACTCGCTAGCTGTGTCTCTGGCGGAGAGGGCCACC 117

Dbb  
61 atctcctgcaaggccagccaaagtgttgattatgatggtagtatttatgaactgggtac 177

118 ATCAACTGCAAGGCGTCCCAAGTGTTCATTATGATGGTGATAGTATAATGAACTGGAT 177  
QY  
121 caacanaaacannacagcaccscaactcctcatctatcgtcgatccaatctagaatct 180  
nb

178 CACCAGAAACCGGCAGCCTCCTAAGTTGCTCATTTAGCGTGCATCCAACTAGAAATCT 237

Db 181 gggatccagccaggtttagtggcagtggtctgggacagacttcaccctcaacatccat 240

Qy 238 GGGTACCTGACCGATTCA GTGGCAGCGGGCTTGGGACAGATTCACTCTCACCATCAGC 297

Db 241 cctgtgaggaggagatggtgcaacctattactgtcagcaagaataatgaggaatccgtgg 300

Db 241 cctatgagagagagatggtgcaacctattactgtcagcaaatgataagagatccgtgg 300

337

D**b** 241 g

[illegible]

RESULT	11	
ID	N80498 standard; DNA; 619 BP.	
AC	N80498;	
DT	03-DEC-1990 (first entry)	
DE	Encodes V region of L chain of anti-P.aeruginosa exotoxin Ab #1.	
KW	Pseudomonas aeruginosa; anti-exotoxin antibody; L chain; V region; ds.	
OS	Homo sapiens.	
FX	Key	Location/Qualifiers
FT	sig_peptide	1..49
FT	/*tag= a	
FT	sig_peptide	269..279
FT	/*tag= b	
FT	intron	50..268
FT	/*tag= c	
PN	EP-270077-A.	
PD	08-JUN-1988.	
PF	01-DEC-1987; 117760.	
PR	03-DEC-1986; JP-288340.	
PR	26-NOV-1987; JP-298513.	
PA	(SUMO) Sumitomo Chem Ind KK.	
PI	Nakatani T, Nomura N, Horigome K, Noguchi H.;	
DR	WPI; 88-156310/23.	
DR	P-PSDB; P80894.	
PT	New gene encoding for antibody to Pseudomonas aeruginosa exotoxin - plus recombinant vectors and host cells, useful for treating	
PT	infections.	
PS	Claim 5; page 26; 39pp; English.	
CC	Sequence encodes variable region of light chain of anti-exotoxin	
CC	antibody. The signal sequence contains an intron which is spliced	
CC	out prior to translation.	
CC	See also N80495-N80496, N80499 and N80941-2.	
SQ	Sequence 619 BP; 177 A; 139 C; 134 G; 169 T;	

Query Match	52.2%	Score 205	DB 1	Length 619	
Best Local Similarity	82.9%	Pred. No. 1.28e-116			
Matches	296	Conservative 0	Mismatches 55	Indels 6	Gaps 5
Db	263	ctacaggtgctacgggggacatcgtgatgaccaggtctccagactccctggctggtgtctc	322		
Qy	41	CTACAGGTGTCACCTCCGATATGGTGATGCCACGCTCCAGACTCGCTAGCTGTGTCTC	100		
Db	323	tggcgagagggccaccatcaactgacgtccaccacgagtgttttatacagctcccaaca	382		
Qy	101	TGGCGGAGAGGGCCACCATCAACTGCAAGGCTCCCAAGTGTGTGATTATCATGTGTC--	157		
Db	383	ataagaactaactagtctggtaccagagaaacccagagacagctcctaagctgctcatitt	442		
Qy	158	ATAGTTA-TA-TGAAC-TGGTATCAGCAGAAACCCGGGACGCTCTCTAAGTTGTCATTT	214		
Db	443	actgggcatctaccggggaatccggggtccctgaccgattcagtgggcaggggtctggga	502		

Qy 215 ACGTGCATCAATCTAGANCTCTGGGGTACTGACCATTCAGTGGCAGCGGGTCTGGGA 274

Db 503 CAGATTCACCTCTCACCATCAGCAGCCTCAGGCGTGAAGTGTGCGAGTTTATLactgtc 562

Qy 275 CAGATTTCACCTCTCACCATCAGCAGCCTCGAGGCTGAAGATCTGGCAGTATACTACTGTC 334

Db 563 AGCAATATTATTAGTACTCCTCGTCACTTCGGCCAGGAGGCAAGTGTGAATCAaac 619

Ov 335 AGCAAAAGTAATCAGGATCTCCGAGGTTCTCGCGAGGGACCAAGGTGGAGNCTAAAC 391

RESULT	12	
ID	Q56735	standard; DNA; 1088 BP.
AC	Q56735;	
DT	02-SEP-1994	(first entry)
DE	Sequence of Hum4VL gene ClaI-HindIII segment in pRL1001	
KW	Antibody; Hum4VL; variable light; single chain Fv immunoglobulin; ds.	
OS	Synthetic.	
FR	Key	Location/Qualifiers
FT	exon	448..496
FT	*tag= a	
FT	Intron	497..715
FT	*tag= b	
FT	exon	716..1065
FT	*tag= c	
FN	WO9404691-A.	
PD	03-MAR-1994.	
PF	20-AUG-1993; U07918.	
PR	21-AUG-1992; US-933695.	
PA	(DOWC ) DOW CHEM CO.	
PI	Affholter JA, Kotite NJ, Mezes PS, Richard RA;	
DR	WPI; 94-083206/10.	
DR	P-PSDB; R48633.	
PT	Dimer and multimer forms of single chain antibody polypeptide(a)	
PT	- used in vivo and in vitro in diagnostics, therapy, imaging and	
PT	bio:sensors	
PS	Example; Fig 5; 99pp; English.	
CC	Hum4VL was obt'd. by PCR DNA amplification using pRL1001 as a	
CC	template and oligos UNIH1 and UNIH2(-) as primers. The DNA sequence	
CC	in pRL1001 coding for the Hum4VL is given in Q56735, and the	
CC	AA sequence it encodes in R48633. Human C-kappa is found to the 3'	
CC	end of the coding strand of Q56735.	
SO	Sequence	1088 BP; 299 A; 230 G; 341 T;

Query Match	52.2%	Score 205;	DB 10;	Length 1088;
Best Local Similarity	82.1%;	Pred. No. 1.28e-116;		
Matches	297;	Conservative 0;	Mismatches 56;	Indels 6; Gaps 5;
Db	710	ctacagtgctcaaggaggacatcgtgatgacccactctccagacctccctggctgtgtctc	769	
Qy	41	CTACAGGTGCCACTCCGCATATCGTGATGACCCAGCTCTCCAGACTCGCTAGCTGTGTCTC	100	
Db	770	tgggcgagggccaccatcaactcaaggtccagccagagtggtttatacacgctccaaca	829	
Qy	101	TGGCGCAGAGGGGCCACCACTCAACTGCAAGGCCCTCCCAAAGTGTGTATT-GATGTG---	157	
Db	830	ataagaactacttaagcttggtaccagagaaacccaggacgacctcaagctgctcattt	889	
Qy	158	ATAGTTA-TA-TCAACT--GGTATCAGCAAAACCCGGCAGCCTCTTAAGTGTGCTCATTT	214	
Db	890	actbgygcactcaaccgggaatccgggggtccctgaaccgattcaatggcagcggtctggga	949	
Qy	215	ACCGTCCCAATCTAGAACTCTGGGGTACTCTGACCGATTACTGGCAGCGGGGTGCGGA	274	



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Qy 358 AGGTTCCGGCGGAGGCCAAGGTGGAGATCAACGT 393
      | | | | | | | | | | | | | | | | | | | |
Search completed: Wed Mar 19 08:07:45 1997
Job time : 47 secs.

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## 15

ID	Q25658 standard; DNA; 733 BP.
AC	Q25658;
DT	08-DEC-1992 (first entry)
DE	Mouse 0.5beta anti-HIV antibody Light chain.
KW	Heavy; light; CDR; HIV; AIDS; FR; framework region; ds.
OS	Synthetic.
FH	Key
FT	Location/Qualifiers
FT	primer_bind complement (77..106)
FT	/*tag= a
FT	/note= "binding site for the primer
FT	represented Q30550"
FT	primer_bind 709..730
FT	/*tag= b
FT	/note= "binding site for the primer
FT	represented Q30551"
PN	J04141095-A.
PD	14-MAY-1992.
PF	02-OCT-1990; 266091.
PR	02-OCT-1990; JP-266091.
PA	(KAGA ) KAGAKU OYOBI KESSEI RYOHO.
DR	WPI; 92-212765/26.
PT	New recombinant modified anti-HIV antibodies - comprise human x
PT	mouse modified antibody H and L chains
PS	Discloure; Fig 4; 15pp; Japanese.
CC	Recombinant modified anti-HIV antibodies comprise framework regions
CC	derived from human antibody and CDRs derived from mouse monoclonal
CC	antibody 0.5beta. The anti-HIV modified antibody can be used for
CC	the prophylaxis and treatment of AIDS.
SC	Sequence 733 BP; 194 A; 162 C; 161 G; 216 T;

Query Match 50.9%; Score 200; DB 4; Length 733;  
Best Local Similarity 79.8%; Pred. No. 2.96e-113;  
Matches 268; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

Db	382	gacattgtgtgaccacaatctccagctcttttggctgtctcttagggcagagggccacc	441
Qy	58	CATATCGTGATGACCCAGTCTCCAGACTCGCTAGCTGTGTCTCTGGCGAGAGGGCCACC	117
Db	442	atctctgcaaggccagccaaagtgttgattgatggtgatagttatgaactgggtac	501
Qy	118	ATCACTGCAAGGCTCCCAAAAGTGTGATATGATGCTGATAGTTATATGAAGACTGGTAT	177
Db	502	caacagaaacaggacagcagccaccaactccctcatctatgctgcacccaatctagaatct	561
Qy	178	CAGCAGAAACCGGGCAGCGCTCCTAAAGTGTGCTCATTTACGCTGCATCCAAATCTAGAATCT	237
Db	562	gggatccagccaggttttagtgagcagtggtctaggacagaacttcacccctcaacatccat	621
Qy	238	GGGTACTCTGACCGATTTCAGTGGCAGGGGCTCGGACAGATTTCACTCTCACCATCAGC	297
Db	622	cctgtggagaggaggatgctgcaacctattactgcagcaagttaatgaggatccattc	681
Qy	298	AGCCTGCAGGCTGAGATGTGGCATTACTACTCTCAGCAAAAGTAATGAGGATCTCCG	357
Db	682	acgttcggctcggggacaaagtctggaataaaaacct	717









Db	301	acgttcggtggaggcaccagctgggaatcaacgt	336
Qy	358	AGGTTGGCGGAGGACCAAGCTGGAGATCAACGT	393
RESULT	5		
LOCUS	MUSL711KVK	354 bp	mRNA
DEFINITION	Mouse hybridoma Ig rearranged kappa-chain mRNA V-region, partial cds.	ROD	29-OCT-1994
ACCESSION	M97875		
NTID	g198677		
KEYWORDS	protein; immunoglobulin light chain; immunoglobulin-kappa; processed gene.		
SOURCE	Mus musculus (strain BALB/c, sub_species domesticus) SP20-BALB/c fusion hybridoma cDNA to mRNA.		
ORGANISM	Mus musculus		
REFERENCE	1 (bases 1 to 354)		
AUTHORS	Lohman,K.L., Buck,D.W., Carrillo,M.A. and Kennedy,R.C.		
TITLE	Characterization of murine monoclonal anti-CD4; epitope recognition, idiotope expression, and variable gene sequence Unpublished (1992)		
JOURNAL	Location/Qualifiers		
FEATURES	source		
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	Best Local Similarity 80.9%; Pred. No. 9.37e-172;		
	Matches 271; Conservative 0; Mismatches 64; Indels 0; Gaps 0;		
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Qy	58	GATATCGTATGATCCAGCTCTCCAGCTCGCTAGCTGTGTCTTGGCGAGAGGCCACC	117
Db	61	atctctgcaaggccagccaaagtgtgattgatgtgtatgaactatgaactggatc	120
Qy	118	ATCACTGCACAGGCTCCCAAGTGTGATTATGATGTGTACTATATCACTCGTAT	177
Db	121	caacagaaacaggagacagccaccacaaactcctcatctatgctgcattccaatctagaatc	180
Qy	178	CAGCAGAAACCCGGGAGCCCTCTTAAGTGTGCTATTACGCTGCATCCAAATCTAGAA	237
Db	181	gggatccagccaggttgggtggcagtggtctgggacagacttcacccctcaacatccat	240
Qy	238	GGGGTACCTGACCATTCAGTGGCAGCGGGTCTGGCAGACAGATTCATCTCACCAT	297
Db	241	cctgtggaggaggagatgctgcaacctattactgtcagcaaatgaatcaggaatcctcc	300
Qy	298	AGCCTGCAGGCTCAAGATGTGGCAGTATACTACTGTGCAGCAAGTAATGAGGATCCTCG	357
Db	301	atgttcggaggggggaccagctggagataaaacg	335

Qy	358	AGGTTCCGGCGGACCAAGCTGGATCAAACC	392
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RESULT	6	MUSL202IGK	363 bp	mRNA	ROD	29-OCT-1994
LOCUS		Mouse hybridoma Ig rearranged kappa-chain mRNA V-region, partial cds.				
DEFINITION		K97869				
ACCESSION		g198667				
NID		V-region; immunoglobulin light chain; immunoglobulin-kappa;				
KEYWORDS		processed gene.				
SOURCE		Mus musculus (strain BALB/c, sub_species domesticus) SP20-BALB/c fusion hybridoma cDNA to mRNA.				
ORGANISM		Mus musculus				
REFERENCE		Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.				
AUTHORS		1 (bases 1 to 363)				
TITLE		Lohman,K.L., Buck,D.W., Carrillo,M.A. and Kennedy,R.C.				
JOURNAL		Characterization of murine monoclonal anti-CD4; epitope recognition, idiotope expression, and variable gene sequence Unpublished (1992)				
FEATURES		Location/Qualifiers				
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		/map="6"				
BASE COUNT	93 a	96 c	92 g	82 t		
ORIGIN						
Query Match		52.7%;	Score 207;	DB 67;	Length 363;	
Best Local Similarity		80.9%;	Pred. No. 9.37e-172;			
Matches	271;	Conservative	0;	Mismatches 64;	Indels 0;	Gaps 0;
Db	1	gacattgtctgaccgaatctccagttcttttgctgtgtctctggcgaggagggccacc	60			
Qy	58	GATATCCTGATGACCCAGCTCCAGACTCGCTAGCTGTCTCTGGCGAGAGGCCACC	117			
Db	61	atctcttcgaagccagcgcacaaagtgttgattatgatgtgtgatgtatatgaactggtaac	120			
Qy	118	ATCAACTGCAGGCCCTCCCMAAGTGTTCATTATGATGCTGATAGTTATGAACCTGGTAT	177			
Db	121	caacagaacacaggacagcacccaccaaactctcatctatgtcgatccaatctagsaatct	180			
Qy	178	CAGCAGAAACCCGGCAGCGCTCTTAAGTGCTCATTTACGCTGCATCCCAATCTAGAATCT	237			
Db	181	gggatccccagcaggttttgtgcagtggtgtggacagacttcacctcaacatccat	240			
Qy	238	GGGTACCTGTGCCATTCAGTGGCAGCGGGCTGGGACAGATTCACTCTCACCATCAGC	297			
Db	241	cctgtgagagaggagatgctgcaacctattactgtcagcaagttaacgagatccccc	300			
Qy	298	AGCCTGACGCTGAAGATGTGGCAGTATTAATACTGTGAGCAAGTAATGAGGATCCTCGG	357			
Db	301	acgtctcgaggggggaccaagctggagataaaaacg	335			
Qy	358	AGGTTCCGGCGGACCAAGCTGGATCAAACC	392			



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QY 358 AGTTTCGGCGGAGGACCAAGTGCAGATCAAA 390

RESULT 9 HUMIGKAW 405 bp mRNA PRI 04-JAN-1995
LOCUS Human Ig rearranged kappa-chain mRNA V-JL-region, hybridoma AE6-5,
DEFINITION 5' end.
ACCESSION M29467
NID g185920
KEYWORDS J-region; V-region; immunoglobulin-kappa; processed gene;
variable region subgroup VK-IV.
SOURCE Human (patient POP) hybridoma AE6-5 DNA, clone phiUCVK, derived
from B-CLL cell line UC729-5.
ORGANISM Homo sapiens
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Primates; Haplorhini; Catarrhini; Hominoidea.
REFERENCE 1 (bases 1 to 405)
AUTHORS Spatz, L.A., Wong, K.K., Williams, M., Desai, R., Golier, J.,
Berman, J.E., Alt, F.W. and Latov, N.
TITLE Cloning and sequence analysis of the VH and VL regions of an
anti-myelin/DNA antibody from a patient with peripheral neuropathy
and chronic lymphocytic leukemia
JOURNAL J. Immunol. 144 (7), 2821-2828 (1990)
MEDLINE 90203623
COMMENT Draft entry and printed sequence for [1] kindly submitted by
L.A.Spatz, 28-OCT-1989, for release after publication. Columbia
University, Department of Neurology BB-322, 630 W. 168th street,
New York, NY 10032.
FEATURES
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sig_peptide   1..60
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RESULT 10
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DEFINITION immunoglobulin M light chain V region-anti-lipid A antibody [human,
hybridoma cell line HR78, mRNA Partial, 460 nt].
ACCESSION S50732
NID g261239
KEYWORDS human hybridoma cell line HR78.
ORGANISM Homo sapiens
Unclassified.
REFERENCE 1 (bases 1 to 460)
AUTHORS Dorai, H., Bubbers, J.E. and Gillies, S.D.
TITLE Cloning and reexpression of a functional human IgM anti-lipid A
antibody
JOURNAL Hybridoma 11 (5), 667-675 (1992)
MEDLINE 93093632
REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI gibbsq 120606] from the original journal article.
This sequence comes from Fig. 3A.
FEATURES
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RESULT	15
LOCUS	HSIGKVBD 339 bp RNA PRI 02-FEB-1995
DEFINITION	H.sapiens mRNA for immunoglobulin V-region of kappa chain.
ACCESSION	Z18328
NID	G33300
KEYWORDS	anti-lamine antibody; cardiolipin/g2glycoprotein antibody; immunoglobulin light chain; kappa chain; monoclonal antibody; myelin-associated glycoprotein antibody; V-region. human.
SOURCE	

ORGANISM *Homo sapiens*

Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Hominidae; Homo.

REFERENCE. 1 (bases 1 to 339)

1 (pages 1 to 55)  
**AUTHORS** Mariette, X., Tsapis, A. and Brouet, J.C.  
**TITLE** Nucleotide Sequence Analysis Of The Variable Domains Of Four Human Monoclonal IgM With An Antibody Activity To Mvelin-Associated

JOURNAL OF THE  
CRYOPROTECTANT SOCIETY OF AMERICA

COOKMAN		CONFIDENTIAL
REFERENCE	2	(b)(7)C
		2301

REFERENCE	7 (bases I
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**AUTHORS** Mariette, X.

**TITLE** Direct Submission

**JOURNAL** Submitted (29-OCT-1992) to the EMBL/GenBank/DBJ databases. Xavier Mariette, Laboratoire d'Immunopathologie, Hôpital Saint-Louis, 1, avenue Claude Vellefaux, Paris, 75010, France

## FEATURES

FEATURE	SOURCE
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Page 21

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Search completed: Wed Mar 19 08:06:38 1997

Job time : 297 sec



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5	648	69.8	111	5	KV3L_MOUSE	IG KAPPA CHAIN V-III	5.19e-122
6	643	69.3	133	5	KV4B_HUMAN	IG KAPPA CHAIN PRECUR	7.86e-121
7	637	68.6	110	5	KV3P_MOUSE	IG KAPPA CHAIN V-III	2.04e-119
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9	622	67.0	111	5	KV3H_MOUSE	IG KAPPA CHAIN V-III	6.99e-116
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AC P06314;  
DT 01-JAN-1988 (REL. 06, CREATED)  
DT 01-APR-1988 (REL. 07, LAST SEQUENCE UPDATE)  
DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)  
DE IG KAPPA CHAIN PRECURSOR V-IV REGION (B17).  
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OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; PRIMATES.  
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RP SEQUENCE FROM N.A.  
RX MEDLINE; 86041854.  
RA MARSH P., MILLS F., GOULD H.;  
RL NUCLEIC ACIDS RES. 13:6531-6544 (1985).  
RN [2]  
RP REVISION TO 76.  
RA MARSH P.;  
RL SUBMITTED (OCT-1986) TO EMBL/GENBANK/DBJ DATA BANKS.  
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Query Match 67.5%; Score 626; DB 5; Length 134;  
Best Local Similarity 75.0%; Pred. No. 7.99e-117;  
Matches 96; Conservative 12; Mismatches 18; Indels 2; Gaps 1;  
Db 7 vfiailwlsagvgdivmtqspaslavslqgraticrascasqldydgdsymwvqqkpgppklliyaaanles 66  
Qy 6 IILFLVATGTVHSDIVMTQSPDSLAVSLGERATINCKASQSDYDGDGS--YNNWYQQKPG 63  
Db 67 gppklliyawstresvdpdfsgsgtdftltieslqaedvavyyccqynlpwtfgq 126  
||||||| || ||||||||||||||||||||||||||||||||||| : ||

Qy 64 GQPKLLIYAASNLES GVPDRFSGSGGTFTLTITSSLAQEDVAVYYCQSNEDPFRFG 123  
Db 127 gtkveikr 134  
Qy 124 GTKVEIKR 131

RESULT 9  
ID KV3H MOUSE STANDARD; PRT; 111 AA.  
AC P01660;  
DT 21-JUL-1986 (REL. 01, CREATED)  
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)  
DE IG KAPPA CHAIN V-III REGION (PC 3741 AND TEPC 111).  
OS MUS MUSCULUS (MOUSE).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; RODENTIA.  
RN [1]  
RP SEQUENCE (PC 3741).  
RX MEDLINE; 79073152.  
RA WEIGERT M., GATMAITAN L., LOH E., SCHILLING J., HOOD L.E.;  
RL NATURE 276:785-790 (1978).  
RN [2]  
RP SEQUENCE (TEPC 111).  
RX MEDLINE; 79012520.  
RA MCKEAN D.J., BELL M., POTTER M.;  
RL PROC. NATL. ACAD. SCI. U.S.A. 75:3913-3917 (1978).  
CC -/- THE PC 3741 AND TEPC 111 SEQUENCES ARE IDENTICAL.  
DR PIR; A01934; KVM37.  
DR HSP; P01679; IGGB.  
KW IMMUNOGLOBULIN V REGION.  
FT DOMAIN 1 23 FRAMEWORK 1.  
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING 1.  
FT DOMAIN 39 53 FRAMEWORK 2.  
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING 2.  
FT DOMAIN 61 92 FRAMEWORK 3.  
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING 3.  
FT DOMAIN 102 111 FRAMEWORK 4.  
FT DISULFID 23 92 BY SIMILARITY.  
FT NON TER 111 111  
SQ SEQUENCE 111 AA; 12099 MW; 76502E89 CRC32;  
Query Match 67.0%; Score 622; DB 5; Length 111;  
Best Local Similarity 78.4%; Pred. No. 6.99e-116;  
Matches 87; Conservative 15; Mismatches 9; Indels 0; Gaps 0;  
Db 1 divltqspaslavslqgraticrascasqldydgdsymwvqqkpgppklliyaaanles 60  
Qy 20 DIVMTQSPDSLAVSLGERATINCKASQSDYDGDGYNNWYQQKPGPPKLLIYAASNLES 79  
Db 61 giparfsgsgtdftlnihpveedaatyqhge-edpwtfgsgtkleik 111  
Qy 80 GVPDRFSGSGGTFTLTITSSLAQEDVAVYYCQSNEDPFRFGGKTKVEIK 130

RESULT 10  
ID KV3G MOUSE STANDARD; PRT; 112 AA.  
AC P01659;  
DT 21-JUL-1986 (REL. 01, CREATED)  
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)  
DE IG KAPPA CHAIN V-III REGION (TEPC 124).  
OS MUS MUSCULUS (MOUSE).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

OC	EUTHERIA; RODENTIA.	
1]	SEQUENCE.	
RR	MEDLINE; 73140225.	
RR	MCKEAN D.J., POTTER M., HOOD L.E.;	
RR	BIOCHEMISTRY 12:760-771(1973).	
RR	PIR; A01933; KVM632.	
DR	HSP; P01679; 1GGR.	
DR	IMMUNOGLOBULIN V REGION.	
RR	DOMAIN 1	23
RR	DOMAIN 24	38
FT	DOMAIN 39	53
FT	DOMAIN 54	60
FT	DOMAIN 61	92
FT	DOMAIN 93	101
FT	DOMAIN 102	111
FT	DISULFID 23	92
FT	NON TER 112	112
SO	SEQUENCE 112 AA; 12339 MW; 4504DD0E CRC32;	

Query Match 66.9%; Score 621; DB 5; Length 112;  
Best Local Similarity 67.0%; Pred. No. 1.20e-115;  
Matches 27; Mismatches 10; Indels 0; Gaps 0;

1 divltgpaaslavslqgratiscraazsvmvgnsfmzwyzzkpgzpkklliyraenlzs 60  
 ||||| ||||| ||||| ||||| ||||| :||:||||| ||||| ||||| |||||  
 20 divmtospdnlavsigerratnckasodvdygdpsymnytookgoppklliyaasnles 79

61 giparfsqgqartbftlibpwzabdvatycfzszbzrapwrfqgqtkleir 112  
1-1 111111 1:111111::111 1::1: 1 11:111:1111

80 gypdfsgsgsgtdtlttisslonedvavyvcoosnedpprfgggtkveikr 131

	RESULT	11			
ID	KV3F MOUSE	STANDARD;	PRT;	132 AA.	
AC	P01658;				
DT	21-JUL-1986	(REL. 01, CREATED)			
DT	21-JUL-1986	(REL. 01, LAST SEQUENCE UPDATE)			
DT	01-OCT-1993	(REL. 27, LAST ANNOTATION UPDATE)			
DE	IG KAPPA CHAIN PRECURSOR V-II REGION (MOPC 321).				
OS	MUS MUSCULUS ('MOUSE').				
OC	EUKARYOTA; METAZOA; VERTEBRATA; TETRAPODA; MAMMALIA;				
OC	EUTHERIA; RODENTIA.				
RN	[1]				
RP	SEQUENCE OF 1-37.				
RX	MEDLINE; 78235887.				
RA	BURSTEIN Y.; SCHECHTER I.;				
RL	BIOCHEMISTRY 17:2392-2400(1978).				
RN	[2]				
RP	SEQUENCE OF 21-132.				

RA MEDLINE; 75140224.  
 RA MCKEAN D.J., POTTER M., HOOD L.E.;  
 RL BIOCHEMISTRY 12:749-759(1973).  
 CC -!- THE PARTIAL SEQUENCE OF THE C REGION OF THIS BENGE-JONES PROTEIN  
 CC WAS ALSO DETERMINED. IT DIFFERS FROM THAT REPORTED FOR MOUSE  
 CC MOPC 21 ONLY IN THE TRANSPOSITION OF TWO NEARBY RESIDUES.

CC	MOPC 21 ONLY IN THE TRANSPOSITION OF TWO NEARBY RESIDUES.
DR	PIR; A01933; KVMG32.
DR	HSP; P01679; 1GG8.
KW	TM210GLOBULIN V REGION: BENGE-JONES PROTEIN; SIGNAL.

ANALYSE	PROTEIN	MOLECULAR WEIGHT	ISODENSITY	ISOPHORE	ISOELECTRIC POINT	AMPHOTERICITY	COMPLEMENTARITY	DETERMINATION
1	FT	20	1	1	1	1	1	1
2	FT	20	1	1	1	1	1	1
3	FT	20	1	1	1	1	1	1
4	FT	20	1	1	1	1	1	1
5	FT	20	1	1	1	1	1	1
6	FT	20	1	1	1	1	1	1
7	FT	20	1	1	1	1	1	1
8	FT	20	1	1	1	1	1	1
9	FT	20	1	1	1	1	1	1
10	FT	20	1	1	1	1	1	1
11	FT	20	1	1	1	1	1	1
12	FT	20	1	1	1	1	1	1
13	FT	20	1	1	1	1	1	1
14	FT	20	1	1	1	1	1	1
15	FT	20	1	1	1	1	1	1
16	FT	20	1	1	1	1	1	1
17	FT	20	1	1	1	1	1	1
18	FT	20	1	1	1	1	1	1
19	FT	20	1	1	1	1	1	1
20	FT	20	1	1	1	1	1	1
21	FT	20	1	1	1	1	1	1
22	FT	20	1	1	1	1	1	1
23	FT	20	1	1	1	1	1	1
24	FT	20	1	1	1	1	1	1
25	FT	20	1	1	1	1	1	1
26	FT	20	1	1	1	1	1	1
27	FT	20	1	1	1	1	1	1
28	FT	20	1	1	1	1	1	1
29	FT	20	1	1	1	1	1	1
30	FT	20	1	1	1	1	1	1
31	FT	20	1	1	1	1	1	1
32	FT	20	1	1	1	1	1	1
33	FT	20	1	1	1	1	1	1
34	FT	20	1	1	1	1	1	1
35	FT	20	1	1	1	1	1	1
36	FT	20	1	1	1	1	1	1
37	FT	20	1	1	1	1	1	1
38	FT	20	1	1	1	1	1	1
39	FT	20	1	1	1	1	1	1
40	FT	20	1	1	1	1	1	1
41	FT	20	1	1	1	1	1	1
42	FT	20	1	1	1	1	1	1
43	FT	20	1	1	1	1	1	1
44	FT	20	1	1	1	1	1	1
45	FT	20	1	1	1	1	1	1
46	FT	20	1	1	1	1	1	1
47	FT	20	1	1	1	1	1	1
48	FT	20	1	1	1	1	1	1
49	FT	20	1	1	1	1	1	1
50	FT	20	1	1	1	1	1	1
51	FT	20	1	1	1	1	1	1
52	FT	20	1	1	1	1	1	1
53	FT	20	1	1	1	1	1	1
54	FT	20	1	1	1	1	1	1
55	FT	20	1	1	1	1	1	1
56	FT	20	1					

	74	80	
FT DOMAIN	81	112	COMPLEMENTARITY-DETERMINING 2. FRAMEWORK 3.
FT DOMAIN	113	121	COMPLEMENTARITY-DETERMINING 3. FRAMEWORK 4.
FT DOMAIN	122	131	BY SIMILARITY.
FT DISULFID	43	112	
FT NON TER	132	132	
SO SEQUENCE	132 AA:	14523 MW:	E572F824 CRC32:

Query Match 66.7%; Score 619; DB 5; Length 132;  
Best Local Similarity 65.5%; Pred. No. 3.55e-115;  
Matches 76; Conservative 28; Mismatches 12; Indels 0; Gaps 0;

Db	17	gsgdvlvtgspaelavlsgratiscraaksvntynqsfmwyzzkpgzpkllyras	76
QY	16	GVHSDIIVTGTSPDSLAVSLGERATINCKASQSDVDGDSVMNYYQKPGQPCKLIYAAS	75
Db	77	nlzsgiparfesagrsrbftltlbpvzabdvatyfczbezbbpwtfgegktleikr	132
QV	76	NLGSVPRTSGSGSTGFTLTITSSLAQEDAVVYQQSNEDPFRGGTKVEIKR	131

RESULT	12	
ID	KV4A	HUMAN
		STANDARD:
		PRT: 114 AA.

AC	21-JUL-1986 (REL. 01, CREATED)	
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)	
DT	01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)	
DE	IG KAPPA CHAIN V-IV REGION (LEN).	
OS	HOMO SAPIENS (HUMAN).	
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;	
OC	EUTHERIA; PRIMATES.	
RN	[1]	
RP	SEQUENCE.	
RX	MEDLINE: 76004342.	
RA	SCHNEIDER M., HILLSCHMANN N.;	
RL	HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 356:507-557(1975).	
CC	-1- THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.	
CC	-1- THIS IS A BENCE-JONES PROTEIN.	
CC	PIR; A01903; K4HULN.	
DR	HSP; P01607; IMCP.	
DR	IMMUNOGLOBULIN V REGION: BENCE-JONES PROTEIN.	

KW	IMMUNOGLOBULIN V REGION; BENCE-JONES PROTEIN.	1	23	FRAMEWORK 1.
FT	DOMAIN	24	40	COMPLEMENTARITY-DETERMINING 1.
FT	DOMAIN	41	55	FRAMEWORK 2.
FT	DOMAIN	56	62	COMPLEMENTARITY-DETERMINING 2.
FT	DOMAIN	63	94	FRAMEWORK 3.
FT	DOMAIN	95	101	COMPLEMENTARITY-DETERMINING 3.
FT	DOMAIN	102	113	FRAMEWORK 4.
FT	DISULFID	23	94	BY SIMILARITY.
FT	NON TER	114	114	
SO	SEQUENCE	114 AA:	12639 MW:	3C34761A CRC32:

Query Match	66.2%;	Score 614;	DB 5;	Length 114;
Best Local Similarity	81.6%;	Pred. No. 5.33e-114;		
Matches	93;	Conservative	6;	Mismatches 13;
			Indels	2;
			Gaps	1;

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Db      1 dlvmtqspnslavslgeratlnckseqgsvlyssnknlyawyqqkpgqpkllylwast 60
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
C"     20 dlvmtqspnslavslcprattncaksoqvdvngds--ymnwvookpgppkllyaaasl 77

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Db 61 esgypdrfgsgsgtdftltislsqaedvavyvcqgypstpsfgagktleir 114  
|||||  
78 fscvndfscscgcmfwtstsiatfnvavyvcqsnedprrfggtkveir 131  
|||||

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RESULT 13
ID KV3J MOUSE STANDARD; PRT; 131 AA.
AC P01661;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN PRECURSOR V-III REGION (MOPC 63).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE OF 1-35.
RX MEDLINE; 78235887.
RA BURSTEIN Y., SCHECHTER I.;
RL BIOCHEMISTRY 17:2392-2400(1978).
RN [2]
RP SEQUENCE OF 21-131.
RX MEDLINE; 73140225.
RA MCKEAN D.J., POTTER M., HOOD L.E.;
RL BIOCHEMISTRY 12:760-771(1973).
RN [3]
RP REVISIONS.
RX MEDLINE; 79012520.
RA MCKEAN D.J., BELL M., POTTER M.;
RL PROC. NATL. ACAD. SCI. U.S.A. 75:3913-3917(1978).
DR PIR; A01935; KYMSM6.
DR HSP; P01679; IACY.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 20
FT CHAIN 21 131 IG KAPPA CHAIN V-III REGION (MOPC 63).
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 58 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 59 73 FRAMEWORK 2.
FT DOMAIN 74 80 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 81 112 FRAMEWORK 3.
FT DOMAIN 113 121 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 122 131 FRAMEWORK 4.
FT DISULFID 43 112 BY SIMILARITY.
FT NON TER 131 131
SQ SEQUENCE 131 AA; 14291 MW; 9D55A06B CRC32;

Query Match 65.9%; Score 612; DB 5; Length 131;
Best Local Similarity 74.8%; Pred. No. 1.58e-113;
Matches 86; Conservative 16; Mismatches 13; Indels 0; Gaps 0;

Db 17 getgnivltgsaelavslgratiscrasevdygnsmfhwgkqgppklllylaas 76
| :||:||||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 16 GVHSDIVMTQSPDSLAVSLGERATINCKASQSDYDGDSDYNNWYQKQGPQPKLLIYAAS 75

Db 77 nlesygarfsgsgstftltidpveadtaatyccqnnedpwtfgggtkleik 131
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 76 NLESYVDRFSGSGSTFTLTITSSLAQEDVAVYYCQSNEDPPRFGGGTRKEIK 130

RESULT 14
ID KV3J MOUSE STANDARD; PRT; 111 AA.
AC P01662;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (ABPC 22 AND PC 9245).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
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OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE (ABPC 22).
RX MEDLINE; 79012520.
RA MCKEAN D.J., BELL M., POTTER M.;
RL PROC. NATL. ACAD. SCI. U.S.A. 75:3913-3917(1978).
RN [2]
RP SEQUENCE (PC 9245).
RX MEDLINE; 79073152.
RA WEIGERT M., GATMAITAN L., LOH E., SCHILLING J., HOOD L.E.;
RL NATURE 276:785-790(1978).
CC -|- THE ABPC22 AND PC9241 SEQUENCES ARE IDENTICAL.
DR PIR; A01935; KYMSM6.
DR HSP; P01679; IACY.
KW IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 39 53 FRAMEWORK 2.
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 61 92 FRAMEWORK 3.
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 102 111 FRAMEWORK 4.
FT DISULFID 23 92 BY SIMILARITY.
FT NON TER 111 111
SQ SEQUENCE 111 AA; 12041 MW; 711C554A CRC32;

Query Match 65.7%; Score 610; DB 5; Length 111;
Best Local Similarity 76.6%; Pred. No. 4.65e-113;
Matches 85; Conservative 15; Mismatches 11; Indels 0; Gaps 0;

Db 1 nivltqspaslavslgratiscrasevdygnsmfhwgkqgppklllylaas 60
|:||||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 20 DIVMTQSPDSLAVSLGERATINCKASQSDYDGDSDYNNWYQKQGPQPKLLIYAAS 79

Db 61 gparfsgsgstftltidpveadtaatyccqnnedpwtfgggtkleik 111
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 80 GVPDRFSGSGSTFTLTITSSLAQEDVAVYYCQSNEDPPRFGGGTRKEIK 130

RESULT 15
ID KV3K MOUSE STANDARD; PRT; 111 AA.
AC P01663;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (PC 4050).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE.
RX MEDLINE; 79073152.
RA WEIGERT M., GATMAITAN L., LOH E., SCHILLING J., HOOD L.E.;
RL NATURE 276:785-790(1978).
DR PIR; A01935; KYMSM6.
DR HSP; P01679; IACY.
KW IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 39 53 FRAMEWORK 2.
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 61 92 FRAMEWORK 3.
FT DOMAIN 93 101 FRAMEWORK 4.
FT DOMAIN 102 111
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FT NON TER

Matches 83; Conservative 17; Mismatches 11; Indels

Qy 20 DIVMTQSPDSLAVSLGERATINCKASQSDYDGD SYMNWYQQKGPCKLLIYAASNLES 79

Qy 80 GVPDRFSGSGGTFTLTISSLQAEDVAVYCCQSNEDPPRFGGGTKVEIK 130

Job time : 17 secs.

Result	No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	676	72.8	112	5	S19971	Ig kappa chain V reg	1.40e-61	
2	674	72.6	131	5	PH1226	Ig kappa chain precu	2.39e-61	
3	664	71.6	111	2	KWMS43	Ig kappa chain V reg	3.43e-60	
4	662	71.3	111	2	KWMS83	Ig kappa chain V reg	5.84e-60	
5	660	71.1	111	2	KWMS68	Ig kappa chain V reg	9.95e-60	
6	650	70.0	111	2	KWMS69	Ig kappa chain V reg	1.42e-58	
7	648	69.8	111	2	KWMS61	Ig kappa chain V reg	2.42e-58	
8	646	69.6	112	5	S19976	Ig kappa chain V reg	4.13e-58	
9	643	69.3	133	2	K4HUJ1	Ig kappa chain precu	9.16e-58	
10	640	69.0	112	5	S19972	Ig kappa chain V reg	2.03e-57	
11	637	68.6	110	2	KWMS10	Ig kappa chain V reg	4.51e-57	
12	635	68.4	127	14	S21680	Ig heavy chain precu	7.67e-57	

## ALIGNMENTS

Query Match 72.8%; Score 676; DB 5; Length 112;  
Best Local Similarity 82.1%; Pred. No. 1.40e-61;











Mar 18 10:06

US-08-612-929-14.rpr

11

#journal Eur. J. Immunol. (1993) 23:846-851  
#title Nucleotide sequence analysis of the variable domains of four human monoclonal IgM with an antibody activity to myelin-associated glycoprotein.

#accession S34003  
##status preliminary

##molecule\_type mRNA

##residues 1-113 ##label MAR

SUMMARY #length 113 #molecular-weight 12312 #checksum 3087

Query Match 67.3%; Score 625; DB 11; Length 113;  
Best Local Similarity 83.2%; Pred. No. 1.09e-55;  
Matches 94; Conservative 6; Mismatches 11; Indels 2; Gaps 1;

Db 1 divmtqspdelavclgeratincsksgvlysenknkylawycqkagppklliywastr 60

Qy 20 DIVMTQSPDSELAVALGERATINCASQSDYDGDGDS--YMMWYQQRPGQPPKLLIYAASNL 77

Db 61 esgvpdrfsgsgsgtdftltislaqaedvavvyccqylttptfgggtkveik 113

Qy 78 ESGVPDRFSGSGSGTDFTLTISLQAEDEVAVVYCCQSNEDPPRFGGGTKEIK 130

Search completed: Tue Mar 18 10:08:28 1997  
Job time : 24 secs.

(TM)

Result No.	Score	Query		DB	ID	Description	Pred. No.
		Match	Length				
1	928	100.0	131	13	R75355	Humanized antibody 3B	1.38e-62
2	917	98.8	131	13	R70202	Humanized antibody 3B	1.02e-61
3	701	75.5	132	13	R70189	Mouse Mab 389 light c	1.02e-44
4	679	73.2	233	6	R30777	pH52-9.0 humanised mu	5.39e-43
5	674	72.6	131	6	R32123	Anti-CD4 antibody MT	1.33e-42
6	671	72.3	131	1	R04132	Anti-Leu 3a light cha	2.28e-42
7	669	72.1	127	1	P90918	Light chain antibody	3.27e-42
8	669	72.1	233	4	R22794	Reshaped CAMPATH-1 an	3.27e-42
9	666	71.8	124	11	R59943	Anti-VIA4 rAb humanis	5.61e-42
10	665	71.7	111	11	R60302	Anti HIV antibody lig	6.71e-42
11	665	71.7	111	10	R53123	Mouse anti-HIV mu5.5	6.71e-42
12	664	71.6	112	5	R24575	Human x mouse modifie	8.04e-42

RESULT	1
ID	R75355; standard; Protein; 131 AA.
AC	R75355;
DT	20-SEP-1995 (first entry)
DE	Humanized antibody 389 light chain.
DE	Humanized antibody; antibody engineering; monoclonal antibody;
KW	MAB; interleukin-4; IL-4; allergy.

PI Gross MS, Holmes SD, Sylvester DR;  
DR WPI; 95-123387/16.  
DR N-PSDB; Q73986.  
PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived  
PT from high affinity mAbs - useful in treatment of IL-4-mediated  
PT and IgE-mediated allergic conditions  
PS Disclosure; Fig.5; 97pp; English.  
CC A humanized antibody light chain variable region and signal  
CC sequence is given in R75355. The signal sequence is also  
CC provided in R70194. The sequences of the first 2 CDRs  
CC are identical to mouse anti-human IL-4 Mab 3B9 light chain  
CC CDRs (given in R70195-96), but the third (R70201) differs  
CC by a single amino acid from the native mouse CDR (R70197).  
SQ Sequence 131 AA;

Query Match 100.0%; Score 928; DB 13; Length 131;  
Best Local Similarity 100.0%; Pred. No. 1.38e-62;  
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 mqwscilflvatatgvhsdivmtqpsdlsavlsgeratincasqsvdydgsymwyq 60  
QY 1 MQMSCILFLVATATGVRHSDIVMTQSPDSLAVSLGERATINCKASQSDYDGSYMNWYQ 60  
Db 61 qkpggppklliyaanlesgvdpdfrfsgsgtdftltiselaedvavyyccqsgnedprr 120  
QY 61 QKPGQPPLLIYAASNLESGVDPDRFSGSGGTDTFTLTISLQAEDVAVYYCQSQSNEDPPR 120  
Db 121 fgggtkveikr 131  
QY 121 FGGGTRVEIKR 131

## RESULT 2

ID R70202 standard; Protein; 131 AA.  
AC R70202;  
DT 20-SEP-1995 (first entry)  
DE Humanized antibody 3B9 light chain.  
KW Humanized antibody; antibody engineering; monoclonal antibody;  
KW Mab; interleukin-4; IL-4; allergy.  
OS Homo sapiens.  
PN WO9507301-A.  
PD 16-MAR-1995.  
PF 07-SEP-1994; U10308.  
PR 07-SEP-1993; US-117366.  
PR 14-OCT-1993; US-136783.  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
PA (SMIK ) SMITHKLINE BEECHAM PLC.  
PI Gross MS, Holmes SD, Sylvester DR;  
DR WPI; 95-123387/16.  
DR N-PSDB; Q83520.  
PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived  
PT from high affinity mAbs - useful in treatment of IL-4-mediated  
PT and IgE-mediated allergic conditions  
PS Disclosure; Page 71-72; 97pp; English.  
CC A humanized antibody light chain variable region and signal  
CC sequence is given in R75355. The signal sequence is also  
CC provided in R70194. The sequences of the 3 CDRs  
CC are identical to mouse anti-human IL-4 Mab 3B9 light chain  
CC CDRs (given in R70195-97).  
SQ Sequence 131 AA;

Query Match 98.8%; Score 917; DB 13; Length 131;  
Best Local Similarity 99.2%; Pred. No. 1.02e-61;  
Matches 130; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 mqwscilflvatatgvhsdivmtqpsdlsavlsgeratincasqsvdydgsymwyq 60  
QY 1 MQMSCILFLVATATGVRHSDIVMTQSPDSLAVSLGERATINCKASQSDYDGSYMNWYQ 60  
Db 61 qkpggppklliyaanlesgvdpdfrfsgsgtdftltiselaedvavyyccqsgnedprr 120  
QY 61 QKPGQPPLLIYAASNLESGVDPDRFSGSGGTDTFTLTISLQAEDVAVYYCQSQSNEDPPR 120  
Db 121 fgggtkveikr 131  
QY 121 FGGGTRVEIKR 131

## RESULT 3

ID R70189 standard; Protein; 132 AA.  
AC R70189;  
DT 20-SEP-1995 (first entry)  
DE Mouse Mab 3B9 light chain.  
KW Chimeric antibody; humanized antibody; antibody engineering;  
KW monoclonal antibody; Mab; interleukin-4; IL-4; allergy.  
OS Mus sp.  
FH Key Location/Qualifiers  
FT Peptide 1..20  
FT /label= Sig\_peptide  
FT Region 44..58  
FT /label= CDR  
FT /note= "complementarity determining region"  
FT Region 74..80  
FT /label= CDR  
FT /note= "complementarity determining region"  
FT Region 113..121  
FT /label= CDR  
FT /note= "complementarity determining region"  
PN WO9507301-A.  
PD 16-MAR-1995.  
PF 07-SEP-1994; U10308.  
PR 07-SEP-1993; US-117366.  
PR 14-OCT-1993; US-136783.  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
PA (SMIK ) SMITHKLINE BEECHAM PLC.  
PI Gross MS, Holmes SD, Sylvester DR;  
DR WPI; 95-123387/16.  
DR N-PSDB; Q83490.  
PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived  
PT from high affinity mAbs - useful in treatment of IL-4-mediated  
PT and IgE-mediated allergic conditions  
PS Disclosure; Fig.1; 97pp; English.  
CC Spleen cells from mice immunized with human IL-4 were used to prepare  
CC hybridomas, which were screened for anti-IL-4 Mab secretion. Only  
CC clone 3B9 was positive. cDNA clones of the 3B9 light and heavy  
CC chains were cloned into pGEM7f+ and transformed into E. coli  
CC DH5-alpha. The clones were sequenced (Q83490-91), and used for  
CC antibody engineering.  
SQ Sequence 132 AA;

Query Match 75.5%; Score 701; DB 13; Length 132;  
Best Local Similarity 78.7%; Pred. No. 1.02e-44;  
Matches 100; Conservative 11; Mismatches 15; Indels 1; Gaps 1;

Db 6 illwvlllwyvgstgdivltqpsaslavlsgratincasqsvdydgsymwyqktpg 65  
QY 6 IILFLVATATGVRHSDIVMTQSPDSLAVSLGERATINCKASQSDYDGSYMNWYQKQPG 64

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5

Db 66 qpklliyaanleagiparfsgsgtdftlnihpveedaatyccqnedpdtfgg 125  
 Qy 65 QPKLLIYAASNLGSGVDPDRFSGSGGTDFTLTITSSIQAEADVAVYCCQSNEDPPRFGG 124  
 Db 126 tkleikr 132  
 Qy 125 TKVEIKR 131

# RESULT 4

ID R30777 standard; protein; 233 AA.  
 AC R30777;  
 DT 12-MAY-1993 (first entry)  
 DE pH52-9.0 humanised murine anti-CD18 antibody light chain.  
 KW Humanisation; rapid; monoclonal antibody.  
 OS Mus musculus.  
 PN W09222653-A.  
 PD 23-DEC-1992.  
 PF 15-JUN-1992; 005126.  
 PR 14-JUN-1991; US-715272.  
 PA (GETH ) GENENTECH INC.  
 PI Carter PJ, Presta LG.  
 DR WPI; 93-018139/02.  
 PT Humanisation of antibodies - by molecular modelling of the variable domains and alteration by gene conversion mutagenesis  
 PS Disclosure; Fig 6B; 126pp; English.  
 CC The sequence is that of the humanised light chain sequence of murine anti-CD18 antibody pH52-9.0.  
 SQ Sequence 233 AA;

Query Match 73.2%; Score 679; DB 6; Length 233;  
 Best Local Similarity 74.0%; Pred. No. 5.39e-43;  
 Matches 97; Conservative 13; Mismatches 17; Indels 4; Gaps 2;  
 Db 1 mgwecillflvatatgvdhsgvpsrfsgsgtdytltselqpedfatyccqngtlppt 116  
 Qy 1 MGSICILFLVATATGVDHSDIVMTQSPDSLAVSLGERATINCKASQVDYDGSYNNYQ 60  
 Db 57 qkpgkapklliyvtetlsgvpsrfsgsgtdytltselqpedfatyccqngtlppt 116  
 Qy 61 QKPGKPKLLIYAASNLGSGVDPDRFSGSGGTDFTLTITSSIQAEADVAVYCCQSNEDPPR 120  
 Db 117 fqggtkveikr 127  
 Qy 121 FGGGTRKVEIKR 131

# RESULT 5

ID R32123 standard; Protein; 131 AA.  
 AC R32123;  
 DT 02-JUN-1993 (first entry)  
 DE Anti-CD4 antibody MT 3.10 light chain variable region.  
 KW immunosuppression; tissue transplantation; graft; L chain; V region;  
 KW T-helper cell inhibition; transplant rejection; Mab;  
 KW interleukin-2 receptor.  
 FH Key Location/Qualifiers  
 FT Peptide 1..20  
 FT /label= signal  
 FT Region 21..120  
 FT /label= Variable  
 FT Region 121..131  
 FT /label= J1  
 PN DE4143214-A.  
 PD 28-JAN-1993.

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6

PF 30-DEC-1991; 143214.  
 PR 25-JUL-1991; DE-124759.  
 PR 30-DEC-1991; DE-143214.  
 PA (BOEF ) BOEHRINGER MANNHEIM GMBH.  
 PI Kaluza B, Rietmueller G, Scheuer W, Weidle U;  
 DR WPI; 93-037582/05.  
 DR N-PSDB; Q36609.  
 PT Synergistic antibody compsn. for use as immunosuppressant - comprises monoclonal anti-CD4 antibodies and monoclonal anti-IL2R  
 PT alpha- or anti-IL2R beta antibodies  
 PS Claim 5; Page 11; 18pp; German.  
 CC This sequence is the light chain variable region of a preferred anti-CD4 monoclonal antibody for use in the claimed synergistic composition. Mab MT 3.10 is deposited as clone 3.101/sB10 (ECACC 90090702). The anti-CD4 antibody is used with at least one anti-IL2R alpha or beta antibody. Individually the antibodies are strongly inhibiting and when used together their immunosuppressive properties are improved; they synergistically inhibit T-helper cell proliferation to effectively inhibit transplant rejection at low doses without significantly reducing the general immune response.  
 CC See also Q36608-Q36616.  
 SQ Sequence 131 AA;

Query Match 72.6%; Score 674; DB 6; Length 131;  
 Best Local Similarity 75.4%; Pred. No. 1.33e-42;  
 Matches 95; Conservative 15; Mismatches 15; Indels 1; Gaps 1;  
 Db 6 illwvlllwpvgstgdivltgpaelpmslqgratiscasqeldydgaymwyqkpg 65  
 Qy 6 IILF-LVATATGVHSDIVMTQSPDSLAVSLGERATINCKASQVDYDGSYNNYQKPG 64  
 Db 66 qpklliyaanleagiparfsgsgtdftlnihpveedaatyccqsedpdtfgg 125  
 Qy 65 QPKLLIYAASNLGSGVDPDRFSGSGGTDFTLTITSSIQAEADVAVYCCQSNEDPPRFGG 124  
 Db 126 tkleikr 131  
 Qy 125 TKVEIKR 130

# RESULT 6

ID R04132 standard; protein; 131 AA.  
 AC R04132;  
 DT 06-SEP-1990 (first entry)  
 DE Anti-Leu 3a light chain variable region gene product, 206 Vx.  
 KW HIV; AIDS; anti-Leu3A; vaccine; ds.  
 OS Mus musculus.  
 PN EP-365209-A.  
 PD 25-APR-1990.  
 PF 11-OCT-1989; 010415.  
 PR 17-OCT-1988; US-260558.  
 PA (BECT) Becton Dickinson Co.  
 PI Hinton R, Oi VT;  
 DR WPI; 90-126329/17.  
 DR N-PSDB; Q04039.  
 PT New chimeric variants of murine antibody anti-leucine - contg. human antibody regions, and DNA encoding sequences.  
 PS Claim 1; Fig 2; 12pp; English.  
 CC Variants of murine monoclonal anti-CD4 antibody, anti-leu3A can be used to form chimeric mouse-variable, human-constant region Abs suggested as being useful as a vaccine to HIV.  
 SQ Sequence 131 AA;

Query Match 72.3%; Score 671; DB 1; Length 131;







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FT /label= CDR1 39..53
FT Region
FT /label= FR2 54..60
FT Region
FT /label= CDR2 61..92
FT Region
FT /label= FR3 93..101
FT Region
FT /label= CDR3 102..111
FT Region
FT /label= FR4
FT J06125783-A.
PN 10-MAY-1994.
PF 28-DEC-1991; 359808.
PR 28-DEC-1991; JP-359808.
PA (KAGA-) ZH KAGAKU KESSEI-RYOHO KENKYUSHO.
DR WPI; 94-187942/23.
DR N-PSDB; Q65554.
PT Mouse-human chimeric anti-HIV antibody heavy and light chains -
PT and recombinant antibody consisting of the H- and L-chains,
PT useful in AIDS therapy
PS Example 3; Fig 4; 22pp; Japanese.
CC Murine monoclonal antibodies mu 39.1 and mu 5.5 both neutralise HIV.
CC The heavy and light chain variable regions from these antibodies
CC were sequenced (R55120-R55123). The murine anti-HIV CDRs were
CC introduced into human framework regions to construct chimeric
CC antibodies (R55124-R55127).
SQ Sequence 111 AA;

Query Match 71.7%; Score 665; DB 10; Length 111;
Best Local Similarity 84.7%; Pred. No. 6.71e-42;
Matches 94; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

Db 1 divltqpsaslavlqgratiscasqsdvdygdsmymwyqqkpgkpklliyaaenles 60
QY 20 DIVMTQSPDLSAVSISGERATINCKASQSDVDYGDSDYNNWYQKPGKPKLLIYAASNLES 79

Db 61 giparfegsgtdftlnlhvveedgatyyccqnedpwtfgggtkleik 111
QY 80 GVPDRFSGSGTDFLTITISSLAQEDVAVYYCQSNEDPPRFGGGKTKVEIK 130

RESULT 12
ID R24575 standard; Protein; 112 AA.
AC R24575;
DT 08-DEC-1992 (first entry)
DE Human x mouse modified anti-HIV antibody Light chain R10.5beta.
KW Heavy; light; CDR; HIV; AIDS; REI; 0.5beta.
OS Synthetic.
FH Key Location/Qualifiers
FT Region 1..23
FT /label= FR1
FT Region 24..38
FT /label= CDR1
FT Region 39..53
FT /label= FR2
FT Region 54..60
FT /label= CDR2
FT Region 61..92
FT /label= FR3
FT Region 93..101
FT /label= CDR3
FT Region 102..112
FT /label= FR4
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PN J04141095-A.
PD 14-MAY-1992.
PF 02-OCT-1990; 266091.
PR 02-OCT-1990; JP-266091.
PA (KAGA ) KAGAKU OYOBI KESSEI RYOHO.
DR WPI; 92-212765/26.
PT New recombinant modified anti-HIV antibodies - comprise human x
PT mouse modified antibody H and L chains
PS Disclosure; Fig 2; 15pp; Japanese.
CC The framework regions (FR) are derived from the human antibody
CC REI. The CDRs are mouse monoclonal antibody 0.5beta derived
CC sequences. The anti-HIV modified antibody can be used for the
CC prophylaxis and treatment of AIDS.
CC Specific examples of the H chain are given in R24556-58 and
CC R24560-62. A specific example of the L chain is given in R24575.
SQ Sequence 112 AA;

Query Match 71.6%; Score 664; DB 5; Length 112;
Best Local Similarity 83.9%; Pred. No. 8.04e-42;
Matches 94; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

Db 1 divltqpsaslavlqgratiscasqsdvdygdsmymwyqqkpgkpklliyaaenles 60
QY 20 DIVMTQSPDLSAVSISGERATINCKASQSDVDYGDSDYNNWYQKPGKPKLLIYAASNLES 79

Db 61 gyparfegsgtdftlnlhvveedgatyyccqnedpwtfgggtkveikr 112
QY 80 GVPDRFSGSGTDFLTITISSLAQEDVAVYYCQSNEDPPRFGGGKTKVEIKR 131

RESULT 13
ID R40180 standard; Protein; 127 AA.
AC R40180;
DT 14-FEB-1994 (first entry)
DE Humanised antibody CMX5-3 light chain variable region.
KW Primer; polymerase chain reaction; amplify; PCR; human; kappa; L;
KW constant region; heavy; H; chain; pUC19; humanised; antibody;
KW light; REI; VL3 fragment; CMX5-1; CMX5-3.
OS Synthetic.
FH Key Location/Qualifiers
FT Peptide 1..19
FT /note= "Secretory leader peptide"
FT Protein 20..127
FT /note= "CMX5-3 light chain variable region"
PN W09316184-A.
PD 19-AUG-1993.
PF 04-FEB-1993; U00759.
PR 06-FEB-1992; US-832842.
PA (SCHE ) SCHERING CORP.
PI Abrams JS, Chou C, Jenh C, Murgolo NJ, Petro ME;
PI Silver JE, Tindall S, Windsor WT, Zavodny RJ;
DR WPI; 93-272888/34.
PT Humanised monoclonal antibody - comprises variable animal region
PT and constant human region, binds to human interleukin-5
PS Example; Page 92-93; 118pp; English.
CC The sequences given in R40179-80 represent the variable regions of
CC the heavy and light chains of the humanised antibody CMX5-3
CC respectively. These sequences were based on the humanised antibody
CC CMX5-1. These sequences were generated using the primer sequences
CC given in Q48068-71. These primers were based on sequences derived
CC from antibody JES1-39D10 and human LAY VH framework sequences. The
CC amplification products were used to replace the VH1 and VH3 fragments
CC of CMX5-1 H chain cDNA in pSV.Sport (see also R40175).
SQ Sequence 127 AA;
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Query Match          71.2%; Score 661; DB 8; Length 127;
Best Local Similarity 71.0%; Pred. No. 1.38e-41;
Matches 93; Conservative 19; Mismatches 15; Indels 4; Gaps 2;

Db 1 mqwscilflvfatgthsdgtdgtspslsvsgdvrtitclasegi---s-sylawyq 56
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Qy 1 MGCWSCIILFLVATATGVHSDIVMTQSPDSLAVSLGERATINCKASQSDYDGD SYMNYQ 60

Db 57 qkpglapklliyganslqtgvprfsgsgtgdtftltisslqpediatyycqsykfnt 116
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 61 QKPGQPKLLIYAASNLSEGVDPDRFSGSGSGTDTLTITISSIQAEDVAVYYCQSQSNEDPPR 120

Db 117 fqggtkvdkr 127
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 121 FGGGTRKEIKR 131

RESULT 14
ID R40176 standard; Protein; 127 AA.
AC R40176;
DT 14-FEB-1994 (first entry)
DE Humanised antibody CMX5-1 light chain variable region.
KW Heavy; light; chain; anti-human; monoclonal; antibody; JES1-39D10;
KW complementarity determining region; CDR; loop analysis; IL-5; human;
KW Kabat determination; grafting; CMX5-1; CMX5-2.
OS Synthetic.
FH Key Location/Qualifiers
FT Peptide 1..19
FT /note= "Secretory leader peptide"
FT Protein 20..127
FT /note= "CMX5-1 light chain variable region"
PN W09316184-A.
PD 19-AUG-1993.
PF 04-FEB-1993; U00759.
PR 06-FEB-1992; US-832842.
PA (SCHE ) SCHERING CORP.
PI Abrams JS, Chou C, Jenh C, Murgolo NJ, Petro ME;
PI Silver JE, Tindall S, Windsor WT, Zavodny PJ;
PI WPI; 93-272888/34.
PT Humanised monoclonal antibody - comprises variable animal region
PT and constant human region, binds to human interleukin-5
PS Example; Page 103; 118pp; English.
CC The sequences given in R40183-84 represent the heavy and light chain
CC variable regions of the humanised antibody CMX5-5. The DNA encoding
CC these fragments was generated by polymerase chain reaction. The VL
CC region was generated by replacing VL3 of CMX5-1 in pSR5 to form CMX5-5
CC VL, using CMX5-1 L as a template. CMX5-5 VH was constructed using
CC the primers given in Q48078-81. Two amplification products were
CC produced and these were used to replace the SpeI/BamHI fragments in
CC the VH cDNA of antibody CMX5-1 (see R40175).
SQ Sequence 127 AA;

Query Match          71.1%; Score 660; DB 8; Length 127;
Best Local Similarity 71.0%; Pred. No. 1.65e-41;
Matches 93; Conservative 19; Mismatches 15; Indels 4; Gaps 2;

Db 1 mqwscilflvfatgthsdgtdgtspslsvsgdvrtitclasegi---s-sylawyq 56
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Qy 1 MGCWSCIILFLVATATGVHSDIVMTQSPDSLAVSLGERATINCKASQSDYDGD SYMNYQ 60

Db 57 qkpglapklliyganslqtgvprfsgsgtgdtftltisslqpediatyycqsykfnt 116
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 61 QKPGQPKLLIYAASNLSEGVDPDRFSGSGSGTDTLTITISSIQAEDVAVYYCQSQSNEDPPR 120

Db 117 fqggtkvdkr 127
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 121 FGGGTRKEIKR 131
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Job time : 17 secs.

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RESULT 15
ID R40184 standard; Protein; 127 AA.
AC R40184;
DT 14-FEB-1994 (first entry)
DE Humanised antibody CMX5-5 light chain variable region.
KW Primer; polymerase chain reaction; amplifiy; PCR; humanised antibody;
KW human; CMX5-4; pSR5; variable; V; light; L; region; chain; CMX5-1.
OS Synthetic.
FH Key Location/Qualifiers
FT Peptide 1..19
FT /note= "Secretory leader peptide"
FT Protein 20..127
FT /note= "CMX5-5 light chain variable region"
PN W09316184-A.
PD 19-AUG-1993.
PF 04-FEB-1993; U00759.
PR 06-FEB-1992; US-832842.
PA (SCHE ) SCHERING CORP.
PI Abrams JS, Chou C, Jenh C, Murgolo NJ, Petro ME;
PI Silver JE, Tindall S, Windsor WT, Zavodny PJ;
PI WPI; 93-272888/34.
PT Humanised monoclonal antibody - comprises variable animal region
PT and constant human region, binds to human interleukin-5
PS Example; Page 103; 118pp; English.
CC The sequences given in R40183-84 represent the heavy and light chain
CC variable regions of the humanised antibody CMX5-5. The DNA encoding
CC these fragments was generated by polymerase chain reaction. The VL
CC region was generated by replacing VL3 of CMX5-1 in pSR5 to form CMX5-5
CC VL, using CMX5-1 L as a template. CMX5-5 VH was constructed using
CC the primers given in Q48078-81. Two amplification products were
CC produced and these were used to replace the SpeI/BamHI fragments in
CC the VH cDNA of antibody CMX5-1 (see R40175).
SQ Sequence 127 AA;

Query Match          71.1%; Score 660; DB 8; Length 127;
Best Local Similarity 71.0%; Pred. No. 1.65e-41;
Matches 93; Conservative 19; Mismatches 15; Indels 4; Gaps 2;

Db 1 mqwscilflvfatgthsdgtdgtspslsvsgdvrtitclasegi---s-sylawyq 56
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 1 MGCWSCIILFLVATATGVHSDIVMTQSPDSLAVSLGERATINCKASQSDYDGD SYMNYQ 60

Db 57 qkpglapklliyganslqtgvprfsgsgtgdtftltisslqpediatyycqsykfnt 116
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 61 QKPGQPKLLIYAASNLSEGVDPDRFSGSGSGTDTLTITISSIQAEDVAVYYCQSQSNEDPPR 120

Db 117 fqggtkvdkr 127
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 121 FGGGTRKEIKR 131
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(TM)

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Result No.	Score	Query		ID	Description	Pred. No.
		Match	Length			
c 1	21	46.7	380 128	T97605	ye55d07.s1 Homo sapie	1.73e-06
c 2	21	46.7	387 128	T98507	ye60g02.s1 Homo sapie	1.73e-06
c 3	21	46.7	413 74	R09757	yf27f09.s1 Homo sapie	1.73e-06
c 4	20	44.4	246 33	H87767	y875b05.s1 Homo sapie	2.74e-05
c 5	19	42.2	315 138	H0MT0800	Human STS UTR800.	4.03e-04
c 6	19	42.2	330 6	CELK121G3F	C.elegans cDNA clone	4.03e-04
c 7	19	42.2	339 2	CELK002DYF	C.elegans cDNA clone	4.03e-04
c 8	19	42.2	362 174	HS690296	human STS SHGC-6155 c	4.03e-04
c 9	19	42.2	362 134	G17690	human STS SHGC-6155 c	4.03e-04
c 10	19	42.2	427 66	N63295	yz88h06.s1 Homo sapie	4.03e-04
c 11	19	42.2	427 160	HS295292	yz88h06.s1 Homo sapie	4.03e-04
c 12	19	42.2	442 88	R59112	yh03h11.r1 Homo sapie	4.03e-04
c 13	19	42.2	497 86	R51415	ygt72d03.r1 Homo sapie	4.03e-04
c 14	19	42.2	520 118	T63218	ycl5b007.r1 Homo sapie	4.03e-04
c 15	19	42.2	600 122	T77507	ycl94h02.r1 Homo sapie	4.03e-04
c 16	18	40.0	182 108	T25334	ESN060 Homo sapiens c	5.44e-03
c 17	18	40.0	227 125	T88534	12230 Arabidopsis tha	5.44e-03
c 18	18	40.0	297 87	R54253	ygt74f04.r1 Homo sapie	5.44e-03
c 19	18	40.0	299 22	HS2906	SW3TC4S58SK Brugia ma	5.44e-03
c 20	18	40.0	305 136	HSB344YE5	H.sapiens (D20S893) D	5.44e-03
c 21	18	40.0	305 174	HSB344YE5	H.sapiens (D20S893) D	5.44e-03
c 22	18	40.0	309 112	T41640	10221 Arabidopsis tha	5.44e-03
c 23	18	40.0	313 1	ATTS2998	A. thaliana transcrib	5.44e-03
c 24	18	40.0	334 48	H0M224A03B	Human aorta cDNA 5'-e	5.44e-03
c 25	18	40.0	344 135	HS299YF1	H. sapiens (D18S476)	5.44e-03
c 26	18	40.0	354 129	G00573	fruit fly STS Dm0285	5.44e-03
c 27	18	40.0	385 107	T19193	cd08013t Homo sapiens	5.44e-03
c 28	18	40.0	391 132	G09820	human STS CHLC.CCT11H	5.44e-03
c 29	17	37.8	158 137	H0MSWS2017	human STS sWS2017.	6.69e-02
c 30	17	37.8	188 158	HS098360	za79f12.r1 Soares fet	6.69e-02
c 31	17	37.8	188 147	W05098	za79f12.r1 Soares fet	6.69e-02
c 32	17	37.8	240 102	RIC51121A	Rice cDNA, partial se	6.69e-02
c 33	17	37.8	270 107	T20181	D193F Homo sapiens cd	6.69e-02
c 34	17	37.8	292 131	G06364	human STS WI-7035.	6.69e-02
c 35	17	37.8	303 98	R00210	16565 Arabidopsis tha	6.69e-02
c 36	17	37.8	326 138	H0MT8005B	Human STS UTR8005, 3'	6.69e-02
c 37	17	37.8	329 113	T44985	8248 Arabidopsis tha	6.69e-02
c 38	17	37.8	339 37	HS05H012	H. sapiens partial cd	6.69e-02
c 39	17	37.8	344 73	R05096	pk41a04.s1 Caenorhabd	6.69e-02
c 40	17	37.8	353 174	HSA046VB1	H.sapiens (D17S1873)	6.69e-02
c 41	17	37.8	400 135	G19182	human STS SHGC-18387	6.69e-02
c 42	17	37.8	416 51	MT8296	EST00444 Homo sapiens	6.69e-02



Liver and spleen from a 20 week-post conception male fetus. 1st strand cDNA was primed with a Pac I - oligo (dT) primer [5' AACTGGAGAAATTAATAAGATCTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo.

## ORGANISM

Homo sapiens

Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 (bases 1 to 413)

## AUTHORS

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.

## TITLE

The WashU-Merck EST Project

## JOURNAL

Unpublished (1995)

## COMMENT

Contact: Wilson RK

WashU-Merck EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@wustl.edu

High quality sequence stops: 270

Source: IMAGE Consortium, LLNL

This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

## FEATURES

source

1..413

/organism="Homo sapiens"

/clone="128105"

/note="human"

BASE COUNT 127 a 81 c 82 g 120 t 3 others

## ORIGIN

Query Match 46.7%; Score 21; DB 74; Length 413;  
Best Local Similarity 76.9%; Pred. No. 1.73e-06;  
Matches 30; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Db 102 tcattactctgaccatcataatcattcttttctgtgg 140

||||| ||||| ||||| ||||| ||||| ||||| |||||

Cp 43 TCATATAACTATCACCATCATATCAACACTTTTGGCTGG 5

## RESULT

4

LOCUS H87767

DEFINITION ys75b5.s1 Homo sapiens cDNA clone 220593 3'.

ACCESSION H87767

NID g1069346

KEYWORDS EST.

SOURCE

human clone=220593 primer=Promega -21ml3 library=Soares retina N2b4HR vector=pT73D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) Reite1=Not I Reite2=Eco RI 1st strand cDNA was primed with a Not I - oligo (dT) primer [5'-TCTTACCAATCTGAAGTGGAGCGCGCGCTTTTTTTTTTTTTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). The retinas were obtained from a 55 year old Caucasian male and total cellular poly(A)+ RNA was extracted 6 hrs after their removal. The retina RNA was kindly provided by Roderick R. McInnes M.D. Ph.D. from the

University of Toronto. Library constructed by Bento Soares and M.Fatima Bonaldo.

## ORGANISM

Homo sapiens

Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 (bases 1 to 246)

## AUTHORS

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.

## TITLE

The WashU-Merck EST Project

## JOURNAL

Unpublished (1995)

## COMMENT

Contact: Wilson RK

WashU-Merck EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@wustl.edu

High quality sequence stops: 236

Source: IMAGE Consortium, LLNL

This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

## FEATURES

source

1..246

/organism="Homo sapiens"

/clone="220593"

/note="human"

BASE COUNT 67 a 47 c 51 g 73 t 8 others

## ORIGIN

Query Match 44.4%; Score 20; DB 33; Length 246;  
Best Local Similarity 74.4%; Pred. No. 2.74e-05;  
Matches 29; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Db 105 tcattgactctgncatcataatcattcttttctgtgg 143

||||| ||||| ||||| ||||| ||||| ||||| |||||

Cp 43 TCATATAACTATCACCATCATATCAACACTTTTGGCTGG 5

## RESULT

5

LOCUS HUMUT8000

DEFINITION Human STS UT8000.

ACCESSION L30320

NID g605352

KEYWORDS

PCR primer; STS sequence; microsatellite DNA;

microsatellite marker; sequence tagged site;

trinucleotide repeat.

SOURCE

Homo sapiens DNA.

ORGANISM

Homo sapiens

Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;

Eutheria; Primates; Haplorhini; Catarrhini; Hominidae.

## REFERENCE

1 (bases 1 to 315)

## AUTHORS

Gerken, S.C., Matsunami, N., Plaetke, R., Albertsen, H., Ballard, L., Mellis, R., Lawrence, E., Moore, M., Holik, P.R., Carlson, M., Zhao, X., Robertson, M., Bradley, P., Eisner, T., Fingey, A., Lalouel, J.-M. and White, R.

## TITLE

Genetic and physical mapping of simple sequence repeat containing sequence tagged sites from the human genome

JOURNAL COMMENT  
 Unpublished (1994) See COMMENT for author address  
 Submitted by: Utah Center for Human Genome Research University of  
 Utah, Dept. of Human Genetics  
 2160 Eccles Institute of Human Genetics  
 Salt Lake City, UT 84112  
 e-mail: sts@corona.med.utah.edu  
 Primer A: TCATTCTGGATGATCCCTA  
 Primer B: GCAGAGACAAGGACAGAT  
 End to Label: Primer A  
 PCR Profile:  
 Initial Denaturation: 94C 300sec  
 Cycles Denaturation Annealing Extension 5  
 C 10 sec. 56 C 10 sec. 72 C 20 sec. 30 94 C 10 sec.  
 52 C 10 sec. 72 C 20 sec. Mg++: 1.00 mM  
 Gel: Acrylamide 7%, Formamide 32%, Urea 34%  
 Alleles: 1.

```

FEATURES
  source      Location/Qualifiers
              1..315
                /organism="Homo sapiens"
                /sequenced_mol="DNA"
  STS         127..311
                /standard_name="STS UT8000"
  primer_bind 127..146
                /evidence=experimental
  primer_bind complement(293..311)
                /evidence=experimental

BASE COUNT   91 a    74 c    62 g    88 t
ORIGIN
Query Match   42.2%; Score 19; DB 138; Length 315;
Best Local Similarity 78.8%; Pred. No. 4.03e-04;
Matches 26; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Db 169 atcaacctcatcatcatcatcacactggct 201
    || ||||| ||||| ||||| ||||| |||||
Cp 39 ATAACATCACCATCAVAAATCAACACTTGGCT 7

```

6

CELK121G3F 330 bp mRNA EST 07-DEC-1995  
C.elegans cDNA clone yk121g3 : 5' end, single read.  
D70633  
ql106595  
EST(expressed sequence tag).  
Caenorhabditis elegans (strain CB1489 him-8(e1489), ) (library:  
Yuji kohara unpublished cDNA) Hermaphrodite, male varied whole  
animal cDNA to mRNA.  
Caenorhabditis elegans  
Eukaryotae; mitochondrial eukaryotes; Metazoa; Nematoda;  
Secernenteae; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea;  
Rhabditidae; Caenorhabditis.  
1 (bases 1 to 330)  
Kohara, Y., Motohashi, T., Tabara, H., Sugimoto, A., Watanabe, H. and  
Nishigaki, A.  
Toward an expression map of the C.elegans genome  
Unpublished (1995)  
Submitted (23-Aug-1995) to DDBJ by:  
Yuji Kohara  
Gene Library Lab.  
National Institute of Genetics  
Yata 1111, Mishima Shizuoka  
411 Japan  
Phone: 0559-81-6854  
Fax : 0559-81-6855

```

Email:ykohara@dbj.nig.ac.jp.
Location/Qualifiers
    source
        1..330
            /organism="Caenorhabditis elegans"
            /strain="CB1489 him-8(e1489)"
            /dev_stage="varied"
            /sequenced_mol="cDNA to mRNA"
            /sex="Hermaphrodite, male"
            /tissue_type="whole animal"
            /clone_lib="Yuji kohara unpublished cDNA"
BASE COUNT      76 a   90 c   74 g   83 t   7 others
ORIGIN
Query Match          42.2%; Score 19; DB 6; Length 330;
Best Local Similarity 77.1%; Pred. No. 4.03e-04;
Matches      27; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Db      105 ctttcaacatccccaatcatcacttggtgacctt 139
       ||||| ||||| ||||| ||||| |||||
Cp     35 CTATCAACCATCAATCAACACTTTGGCTGCCCTT 1

```

7	CEK002DYF	339 bp	mRNA	EST	18-NOV-1995
LOCUS	C.elegans cDNA clone yk2dl1 : 5' end, single read.				
DEFINITION	D7216				
ACCESSION	G521324				
NID	EST (expressed sequence tag).				
KEYWORDS	Caenorhabditis elegans (strain CH489 him-8(e1489), ) (library: Yuiji Kohara unpublished cDNA) Hermaphrodite, male varied whole animal cDNA to mRNA.				
SOURCE	Caenorhabditis elegans				
ORGANISM	Eukaryotae; mitochondrial eukaryotes; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae; Caenorhabditis.				
REFERENCE	1 (bases 1 to 339)				
AUTHORS	Kohara, Y., Mitsuki, H., Nishigaki, A., Motohashi, T., Sugimoto, A. and Tabara, H.				
TITLE	Toward an expression map of the C.elegans genome				
JOURNAL	Unpublished (1994)				
COMMENT	Submitted (22-Dec-1993) to DDBJ by:				

```

FEATURES
source
1..339
Location/Qualifiers
/organism="Caenorhabditis elegans"
/strain="CB1489 him-8(e1489)"
/dev_stage="varied"
/sequenced_mol="cDNA to mRNA"
/sex="Hermaphrodite, male"
/tissue_type="whole animal"
/clone_lib="yuji Kohara unpublished cDNA"
BASE COUNT      81 a      84 c      76 g      93 t      5 others
ORIGIN
Query Match      42.2%; Score 19; DB 2; Length 339;
Best Local Similarity 77.1%; Pred. No. 4.03e-04;

```



Matches 27; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Db 135 ctttcaacatcccaatcatcatcttggtgacatt 169  
 || ||| |||| ||||| ||||| || |||  
 Cp 35 CTATCACCATCATATCAACACTTTGGCTGGCGCTT 1

RESULT 8  
 ID HS690296 standard; DNA; STS; 362 BP.  
 AC G17690;  
 DT 07-MAR-1996 (Rel. 47, Created)  
 DE 07-MAR-1996 (Rel. 47, Last updated, Version 1)  
 DE human STS SHGC-6155 clone pG-2635.  
 KW primer; sequence tagged site; STS sequence.  
 OS Homo sapiens (human)  
 OC Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;  
 OC Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae.  
 RN [1]  
 RP 1-362  
 RA Myers R.M.;  
 RT ;  
 RL Unpublished.  
 CC Contact: Richard M. Myers Stanford Human Genome Center (SHGC)  
 CC Stanford University School of Medicine Department of Genetics,  
 CC M-344, Stanford, CA 94305, USA Tel: 4157259687 Fax: 4157259689  
 CC Email: myers@shgc.stanford.edu Primer A: TTGTCGCTATTTCACAGGAA  
 CC Primer B: GCTCAATGGCTTATCATCTG STS size: 268 PCR Profile: Initial  
 CC incubation: 94 degrees C for 90 seconds Denaturation: 94 degrees C  
 CC for 15 seconds Annealing: 62 degrees C for 23 seconds  
 CC Polymerization: 72 degrees C for 30 seconds PCR Cycles: 30 Thermal  
 CC Cycler: Perkin Elmer 9600 Protocol: Template: 25 ng Primer: each 1  
 CC uM dNTPs: each 200 uM Taq Polymerase: 0.05 units/ul Total Vol: 10  
 CC ul Buffer: MgCl2: 2.5 mM KCl: 50 mM Tris-HCl: 20 mM pH: 8.3  
 CC Chromosome 13. NCBI gi: 1215116  
 FH Key Location/Qualifiers  
 FT source  
 FT 1..362  
 FT /organism="Homo sapiens"  
 FT /note="human"  
 FT STS 52..319  
 FT /map="13"  
 FT primer\_bind 52..71  
 FT /map="13"  
 FT primer\_bind complement(300..319)  
 FT /map="13"  
 FT Sequence 362 BP; 104 A; 75 C; 54 G; 113 T; 16 other;

Query Match 42.2%; Score 19; DB 174; Length 362;  
 Best Local Similarity 76.5%; Pred. No. 4.03e-04;  
 Matches 26; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Db 21 tcanatcatcatcatcatcatcatcatcacttg 54  
 ||| || | |||| ||||| |||| ||||  
 Cp 43 TCATATACTATCACCATCATATCAACTTTG 10

RESULT 9  
 LOCUS G17690 362 bp DNA STS 05-MAR-1996  
 DEFINITION human STS SHGC-6155 clone pG-2635.  
 ACCESSION G17690  
 NID gi215116  
 KEYWORDS STS sequence; primer; sequence tagged site.  
 SOURCE human Plasmid clones, generated from a lymphoblastoid cell line  
 from a human male. Localized to human chromosome 13 by analysis on

the NIGMS Human/Rodent Somatic Cell Hybrid Panel #1, Coriell  
 Institute for Medical Research, Camden, NJ 08103.

ORGANISM Homo sapiens  
 Eukaryota; Eukaryota; Mitochondrial eukaryotes; Metazoa; Chordata;  
 Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata;  
 Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;  
 Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 362)  
 AUTHORS Myers, R.M.  
 JOURNAL Unpublished (1996)  
 COMMENT

Contact: Richard M. Myers  
 Stanford Human Genome Center (SHGC)  
 Stanford University School of Medicine  
 Department of Genetics, M-344, Stanford, CA 94305, USA  
 Tel: 4157259687  
 Fax: 4157259689  
 Email: myers@shgc.stanford.edu

Primer A: TTGTCGCTATTTCACAGGAA  
 Primer B: GCTCAATGGCTTATCATCTG  
 STS size: 268  
 PCR Profile:

Initial incubation: 94 degrees C for 90 seconds

Denaturation: 94 degrees C for 15 seconds  
 Annealing: 62 degrees C for 23 seconds  
 Polymerization: 72 degrees C for 30 seconds  
 PCR Cycles: 30

Thermal Cycler: Perkin Elmer 9600

Protocol:  
 Template: 25 ng  
 Primer: each 1 uM  
 dNTPs: each 200 uM  
 Taq Polymerase: 0.05 units/ul  
 Total Vol: 10 ul

Buffer:  
 MgCl2: 2.5 mM  
 KCl: 50 mM  
 Tris-HCl: 20 mM  
 pH: 8.3

Chromosome 13.  
 Location/Qualifiers  
 1..362  
 /organism="Homo sapiens"  
 /note="human"  
 STS 52..319  
 /map="13"  
 primer\_bind 52..71  
 /map="13"  
 primer\_bind complement(300..319)  
 /map="13"

BASE COUNT 104 a 75 c 54 g 113 t 16 others  
 ORIGIN

Query Match 42.2%; Score 19; DB 134; Length 362;  
 Best Local Similarity 76.5%; Pred. No. 4.03e-04;  
 Matches 26; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Db 21 tcanatcatcatcatcatcatcatcacttg 54  
 ||| || | |||| ||||| |||| ||||

Cp 43 TCATATACTATCACCATCATATCAACTTTG 10



REFERENCE  
AUTHORS

1 (bases 1 to 442)  
 Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
 Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,  
 Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,  
 Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P. and  
 Wilson, R.

TITLE  
JOURNAL  
COMMENT

The WashU-Merck EST Project  
 Unpublished (1995)

GDB: G00-414-804

Contact: Wilson RK

WashU-Merck EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence stops: 344

Source: IMAGE Consortium, LLNL

This clone is available royalty-free through LLNL ; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.

## FEATURES

source

Location/Qualifiers

1..442

/organism="Homo sapiens"

/clone="42263"

/note="human"

BASE COUNT 93 a 89 c 119 g 136 t 5 others

## ORIGIN

Query Match 42.2%; Score 19; DB 88; Length 442;

Best Local Similarity 85.2%; Pred. No. 4.03e-04;

Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 123 accatctttatctacacttggtggc 149

||||| I ||| ||||| |||||

Cp 30 ACCATCATATCAACACTTTGGCTGGC 4

## RESULT 13

LOCUS R51415 497 bp mRNA EST 18-MAY-1995

DEFINITION Yg72d03.r1 Homo sapiens cDNA clone 38881 5'.

ACCESSION R51415

NTD g813317

KEYWORDS EST.

SOURCE human clone=38881 library=Soares infant brain INTB vector=Lafmid BA  
 host=BH10B (ampicillin resistant) primer=M13RPI Rsite1=Not I  
 Rsite2=Hind III Whole brain from a 73 days post natal female. 1st  
 strand cDNA was primed with a Not I - oligo(dT) primer [5'  
 AACTGCAAGATTCCGGCCGACGAGTAATTTTTTTTTTTT 3']; double-stranded  
 cDNA was ligated to Hind III adaptors (Pharmacia), digested with  
 Not I and directionally cloned into the Not I and Hind III sites of  
 the Lafmid BA vector. Library went through one round of  
 normalization. Library constructed by Bento Soares and M.Fatima  
 Bonaldo.

## ORGANISM

Homo sapiens

Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;

Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;

Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;

Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 497)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,

Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,

Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,

Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P. and

TITLE  
JOURNAL  
COMMENT

The WashU-Merck EST Project  
 Unpublished (1995)

GDB: G00-411-422

Contact: Wilson RK

WashU-Merck EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence stops: 413

Source: IMAGE Consortium, LLNL

This clone is available royalty-free through LLNL ; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.

## FEATURES

source

Location/Qualifiers

1..497

/organism="Homo sapiens"

/clone="38881"

/note="human"

BASE COUNT 103 a 102 c 135 g 154 t 3 others

## ORIGIN

Query Match 42.2%; Score 19; DB 86; Length 497;

Best Local Similarity 85.2%; Pred. No. 4.03e-04;

Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 154 accatctttatctacacttggtggc 180

||||| I ||| ||||| |||||

Cp 30 ACCATCATATCAACACTTTGGCTGGC 4

## RESULT 14

LOCUS T63218 520 bp mRNA EST 17-FEB-1995

DEFINITION Yc15b07.r1 Homo sapiens cDNA clone 80725 5'.

ACCESSION T63218

NTD 9667083

KEYWORDS EST.

SOURCE human clone=80725 library=Stratagene lung (#937210)

vector=pBluescript SK- host=SOIR cells (kanamycin resistant)

primer=M13RPI Rsite1=EcoRI Rsite2=XhoI Normal lung tissue from a 72

year old male. Cloned unidirectionally. Primer: Oligo dT. Average

insert size: 1.0 kb; Uni-ZAP XR Vector; 5' adaptor sequence:

5'-GAATTCGGCAGG-3'; 3' adaptor sequence:

5'-CTCGAGTTTTTTTTTTTTTTT-3'.

## ORGANISM

Homo sapiens

Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;

Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 520)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,

Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,

Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevasakis, E.,

Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.

WashU-Merck EST Project

Unpublished (1995)

## TITLE

JOURNAL

COMMENT

Contact: Wilson RK

WashU-Merck EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence stops: 360  
Source: IMAGE Consortium, LLNL  
This clone is available royalty-free through LLNL ; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.

# FEATURES

source  
1..520  
/organism="Homo sapiens"  
/clone="80725"  
/note="human"

BASE COUNT 113 a 104 c 133 g 161 t 9 others  
ORIGIN

Query Match 42.2%; Score 19; DB 118; Length 520;  
Best Local Similarity 85.2%; Pred. No. 4.03e-04;  
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 221 accatctttatctacacttggctggc 247  
||||| | ||| ||||| |||||  
Cp 30 ACCATCATAATCAACACTTTGGCTGGC 4

## RESULT 15

LOCUS T77507 600 bp mRNA EST 06-MAR-1995  
DEFINITION yc94h02.r1 Homo sapiens cDNA clone 23907 5'.  
ACCESSION T77507  
NID 9694710  
KEYWORDS EST.  
SOURCE human clone=23907 library=Soares infant brain LNIB vector=Lafmid BA  
host=DH10B (ampicillin resistant) primer=M13RP1 Rsite1=Not I  
Rsite2=Hind III Whole brain from a 73 days post natal female. 1st  
strand cDNA was primed with a Not I - oligo(dT) primer [5'  
AATCGAAGATTCGGCGCCGAGGAATTTTTTTTTTTTTTTT 3']; double-stranded  
cDNA was ligated to Hind III adaptors (Pharmacia), digested with  
Not I and directionally cloned into the Not I and Hind III sites of  
the Lafmid BA vector. Library went through one round of  
normalization. Library constructed by Bento Soares and M.Fatima  
Bonaldi.

## ORGANISM

Homo sapiens  
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;  
Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

AUTHORS  
1 (bases 1 to 600)  
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,  
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,  
Parsons,J., Rifkin,L., Rohlffing,T., Soares,M., Tan,F.,  
Trevaaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and  
Wilson,R.

TITLE  
The WashU-Merck EST Project  
JOURNAL  
Unpublished (1995)

GDB: G00-396-254

Contact: Wilson RK  
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High quality sequence stops: 454

Source: IMAGE Consortium, LLNL

This clone is available royalty-free through LLNL ; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.

## FEATURES

source  
1..600  
/organism="Homo sapiens"

/clone="23907"  
/note="human"

BASE COUNT 142 a 123 c 148 g 181 t 6 others  
ORIGIN

Query Match 42.2%; Score 19; DB 122; Length 600;  
Best Local Similarity 85.2%; Pred. No. 4.03e-04;  
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 319 accatctttatctacacttggctggc 345  
||||| | ||| ||||| |||||  
Cp 30 ACCATCATAATCAACACTTTGGCTGGC 4

Search completed: Wed Mar 19 08:15:31 1997  
Job time : 76 secs.

\*\*\*\*\*

W A P S E R E H

(TM)

\*\*\*\*\*

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MPerch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed Mar 19 08:13:33 1997; MasPar time 11.66 Seconds  
Tabular output not generated. 336.606 Million cell updates/sec

Title: >US-08-612-929-15  
Description: (1-45) from US08612929.seq  
Perfect Score: 45  
N.A. Sequence: 1 AAGCGACGCAAGCTGATTATGATGGTGATGATATATGAAAC 45  
Comp: TTCCGTCGGTTTCACACTAATACCTACCACTACATATATCTTC

Scoring table: TABLE default  
Gap 10

Nmatch STD : Dbase 0; Query 0

Searched: 113505 seqs, 43611913 bases x 2

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: n-geneseq25  
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13  
14:part14 15:part15 16:part16 17:part17 18:part18  
19:part19 20:part20 21:part21 22:part22

Statistics: Mean 6.151; Variance 4.302; scale 1.430

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query Match	Length	ID	Description	Pred. No.
1	45	100.0	333 12	Q70376	Chimeric anti HIV ant 1.41e-13
2	45	100.0	333 12	Q70372	Anti HIV antibody lig 1.41e-13
3	45	100.0	333 11	Q65554	Mouse anti-HIV mu5.5 1.41e-13
4	45	100.0	333 11	Q65558	Mouse-human chimeric 1.41e-13
5	45	100.0	334 1	N90492	Gene fragment of immu 1.41e-13
6	45	100.0	393 14	Q73986	Humanized antibody 3B 1.41e-13
7	45	100.0	396 14	Q83490	Mouse MAb 3B9 light c 1.41e-13
8	45	100.0	733 4	Q25658	Mouse 0.3beta anti-HI 1.41e-13

9	45	100.0	780 1	N90495	A V chi region gene. 1.41e-13
10	45	100.0	900 1	Q04039	Anti-Leu 3a light cha 1.41e-13
11	43	95.6	393 6	Q36609	Anti-CD4 antibody MT 1.73e-12
12	43	95.6	717 18	T04019	Anti-EGFR single chai 1.73e-12
13	41	91.1	393 14	Q83520	Humanized antibody 3B 2.10e-11
14	41	91.1	397 1	Q04041	Anti-Leu 3a light cha 2.10e-11
15	40	88.9	63 14	Q83508	IL-4 CDRI gene fragme 7.27e-11
16	40	88.9	67 14	Q83507	IL-4 CDRI gene fragme 7.27e-11
17	28	62.2	312 3	Q20309	B cell hybridoma 4:3. 1.36e-04
18	28	62.2	451 1	Q04694	Light chain variable 1.36e-04
19	28	62.2	7305 18	T15933	Anti-IgE VL expressio 1.36e-04
20	26	57.8	91 9	Q51746	Oligonucleotide probe 1.36e-03
21	26	57.8	333 18	T15726	3B1 light chain varia 1.36e-03
22	26	57.8	339 18	T04015	Anti-EGFR antibody li 1.36e-03
23	26	57.8	339 18	T04013	Anti-EGFR antibody li 1.36e-03
24	26	57.8	1797 18	T15733	3B1 single chain anti 1.36e-03
25	24	53.3	333 14	Q82818	Murine NM-01 variable 1.30e-02
26	24	53.3	334 9	Q55002	Murine anti-CD18 Ab 6 1.30e-02
27	24	53.3	334 9	Q55000	Humanised anti-CD18 A 1.30e-02
28	24	53.3	336 2	Q10379	Chimeric MAb 9.2.27 1 1.30e-02
29	24	53.3	336 16	Q96285	Human IgE receptor-bi 1.30e-02
30	24	53.3	363 10	Q56686	Sequence of the monoc 1.30e-02
31	24	53.3	393 5	Q30757	p64-k4. 1.30e-02
32	23	51.1	91 9	Q51746	Oligonucleotide probe 3.94e-02
33	22	48.9	122 4	Q26782	Oligomer ma6 used to 1.18e-01
34	22	48.9	261 17	T04628	Mouse derived light c 1.18e-01
35	22	48.9	336 16	Q96283	Human IgE receptor-bi 1.18e-01
36	22	48.9	363 6	Q37472	Sequence encoding the 1.18e-01
37	22	48.9	396 7	Q42987	Mouse 4C10 anti-idiot 1.18e-01
38	22	48.9	632 10	Q56690	Genomic sequence of t 1.18e-01
39	22	48.9	632 10	Q56691	Genomic sequence of t 1.18e-01
40	22	48.9	783 17	T08490	Anti-c5 MAb N19/8 scF 1.18e-01
41	21	46.7	333 11	Q63908	Light chain variable 3.48e-01
42	21	46.7	334 11	Q73749	Light chain variable 3.48e-01
43	21	46.7	363 10	Q56688	Sequence of the monoc 3.48e-01
44	20	44.4	336 2	Q12684	Murine 1B4 light chai 1.01e+00
45	19	42.2	336 16	Q74148	Human thyroid stimula 2.88e+00

## ALIGNMENTS

RESULT 1  
ID Q70376 standard; cDNA to mRNA; 333 BP.  
AC Q70376;  
DT 13-MAR-1995 (first entry)  
DE Chimeric anti HIV antibody light chain variable region.  
KW Antibody; heavy chain; light chain; human immunodeficiency virus;  
KW HIV; acquired immune deficiency syndrome; AIDS; treatment;  
KW prophylaxis; Mus musculus; Homo sapiens; ss.  
OS Chimeric Homo sapiens  
FH Chimeric Mus musculus.  
FT Key Location/Qualifiers  
FT CDS 1..333  
FT /\*tag= a  
FT /product= Antibody light chain variable region.  
PN W09415969-A.  
PD 21-JUL-1994.  
PF 14-JAN-1993; J00039.  
PR 14-JAN-1993; AU-032671.  
PR 14-JAN-1993; WO-100039.  
PA (KAGA ) CEMO SERO THERAPEUTIC RES INST.  
PI Eda Y, Kimachi K, Maeda H, Osatomi K, Shiosaki K;  
PI Tokiyoshi S;  
DR WPI; 94-249145/30.

Mar 19 08:12

US-08-612-929-15.rmg

3

DR P-PSDB; R60306.  
PT Recombinant chimeric anti HIV antibody - useful for the treatment  
PT and prevention of HIV  
PS Claim 14; Figure 12; 51pp; Japanese.  
CC The recombinant antibody light chain has neutralising activity  
CC against HIV. Chimeric antibodies comprising both mouse and human  
CC sequences are useful in the treatment/prevention of AIDS caused by  
CC HIV. This sequence is derived from the mu5.5 anti HIV monoclonal  
CC antibody producing cell.  
SQ Sequence 333 BP; 95 A; 90 C; 88 G; 60 T;

Query Match 100.0%; Score 45; DB 12; Length 333;  
Best Local Similarity 100.0%; Pred. No. 1.41e-13;  
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 70 aagggcagcaagtggtgattatgatggtgatgtatgatgatgaac 114  
|||||  
Qy 1 AAGGCCAGCCAAAGTGTGATTATGATGCGTAGTATATGAAC 45

## RESULT 2

ID Q70372 standard; cDNA to mRNA; 333 BP.

AC Q70372;  
DT 09-MAR-1995 (first entry)  
DE Anti HIV antibody light chain variable region.  
KW Antibody; heavy chain; light chain; human immunodeficiency virus;  
KW HIV; acquired immune deficiency syndrome; AIDS: treatment;  
KW prophylaxis; Mus musculus; Homo sapiens; ss.  
OS Mus musculus.

FH Key Location/Qualifiers  
FT CDS 1..333  
FT /tag= a

PT /product= Antibody light chain variable region.

PN W09415969-A.

PD 21-JUL-1994.  
PF 14-JAN-1993; J00039.  
PR 14-JAN-1993; AU-032671.  
PR 14-JAN-1993; WO-J00039.

PA (KAGA ) CHERO SERO THERAPEUTIC RES INST.  
PI Eda Y, Kimachi K, Maeda H, Osatomi K, Shiosaki K;  
PI Tokiyoshi S;  
DR WPI; 94-249145/30.  
DR P-PSDB; R60302.

PT Recombinant chimeric anti HIV antibody - useful for the treatment  
PT and prevention of HIV  
PS Claim 15; Figure 4; 51pp; Japanese.

CC The recombinant antibody light chain has neutralising activity  
CC against HIV. Chimeric antibodies comprising both mouse and human  
CC sequences are useful in the treatment/prevention of AIDS caused by  
CC HIV. This sequence is obtained from the mu5.5 anti HIV monoclonal  
CC antibody producing cell.  
SQ Sequence 333 BP; 88 A; 83 C; 86 G; 76 T;

Query Match 100.0%; Score 45; DB 12; Length 333;  
Best Local Similarity 100.0%; Pred. No. 1.41e-13;  
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 70 aagggcagcaagtggtgattatgatggtgatgtatgatgaac 114  
|||||  
Qy 1 AAGGCCAGCCAAAGTGTGATTATGATGCGTAGTATATGAAC 45

## RESULT 3

ID Q65554 standard; cDNA; 333 BP.

Mar 19 08:12

US-08-612-929-15.rmg

4

AC Q65554;  
DT 27-JAN-1995 (first entry)  
DE Mouse anti-HIV mu5.5 light chain variable region cDNA.  
KW Immunoglobulin; light chain; anti-HIV antibody; neutralisation;  
KW human immunodeficiency virus; variable region; VL chain; murine; ds.  
OS Mus musculus.

FH Key Location/Qualifiers  
FT misc\_feature 70..114  
FT /tag= a

FT /note= "encodes CDR1"

FT misc\_feature 160..180

FT /tag= b

FT /note= "encodes CDR2"

FT misc\_feature 277..303

FT /tag= c

FT /note= "encodes CDR3"

PN J06125783-A.

PD 10-MAY-1994.

PF 28-DEC-1991; 359808.

PR 28-DEC-1991; JP-359808.

PA (KAGA-) ZH KAGAKU KESSEI-RYOHO KENKYUSHO.

DR WPI; 94-187942/23.

DR P-PSDB; R55123.

PT Mouse-human chimeric anti-HIV antibody heavy and light chains -  
PT and recombinant antibody consisting of the H- and L-chains,  
PT useful in AIDS therapy  
PS Example 3; Fig 4; 22pp; Japanese.

CC Murine monoclonal antibodies mu 39.1 and mu 5.5 both neutralise HIV.  
CC The heavy and light chain variable regions from these antibodies  
CC were sequenced (Q65551-Q65554). The murine anti-HIV CDRs were  
CC introduced into human framework regions to construct chimeric  
CC antibodies (Q65555-Q65558).

SQ Sequence 333 BP; 88 A; 83 C; 86 G; 76 T;

Query Match 100.0%; Score 45; DB 11; Length 333;  
Best Local Similarity 100.0%; Pred. No. 1.41e-13;  
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 70 aagggcagcaagtggtgattatgatggtgatgtatgatgaac 114  
|||||  
Qy 1 AAGGCCAGCCAAAGTGTGATTATGATGCGTAGTATATGAAC 45

## RESULT 4

ID Q65558 standard; cDNA; 333 BP.

AC Q65558;

DT 30-JAN-1995 (first entry)

DE Mouse-human chimeric anti-HIV mu5.5-derived light chain V region.  
KW Immunoglobulin; heavy chain; anti-HIV antibody; neutralisation;  
KW human immunodeficiency virus; variable region; VL chain; murine;  
KW chimeric; humanised; ds.

OS Chimeric Mus musculus.

OS Chimeric Homo sapiens.

FH Key Location/Qualifiers

FT misc\_feature 70..114

FT /tag= a

FT /note= "encodes murine CDR1"

FT misc\_feature 160..180

FT /tag= b

FT /note= "encodes murine CDR2"

FT misc\_feature 277..303

FT /tag= c

FT /note= "encodes murine CDR3"

PN J06125783-A.

PD 10-MAY-1994.  
PF 28-DEC-1991; 359808.  
PR 28-DEC-1991; JP-359808.  
PA (KAGA-) ZH KAGAKU KESSEI-RYOHO KENKYUSHO.  
DR WPI; 94-187942/23.  
DR P-PSDB; R55127.  
PT Mouse-human chimeric anti-HIV antibody heavy and light chains -  
PT and recombinant antibody consisting of the H- and L-chains,  
PT useful in AIDS therapy  
PS Claim 5; Fig 12; 22pp; Japanese.  
CC Murine monoclonal antibodies mu 39.1 and mu 5.5 both neutralise HIV.  
CC The heavy and light chain variable regions from these antibodies  
CC were sequenced (065551-065554). The murine anti-HIV CDRs were  
CC introduced into human framework regions to construct chimeric  
CC antibodies (065555-065558).  
SQ Sequence 333 BP; 95 A; 90 C; 88 G; 60 T;  
Query Match 100.0%; Score 45; DB 11; Length 333;  
Best Local Similarity 100.0%; Pred. No. 1.41e-13;  
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 70 aagggcagcaagtggtgattgatgatgatgatgatgatgatgaac 114  
|||||  
QY 1 AAGGCCAGCCAAAGTGTGATTGATGATGATGATGATGATGATGAAC 45  
RESULT 5  
ID N90492 standard; DNA; 334 BP.  
AC N90492;  
DT 20-OCT-1989 (first entry)  
DE Gene fragment of immunoglobulin L chain variable region.  
KW Gene fragment; immunoglobulin; L chain variable region; HIV.  
OS Mus musculus  
FH Key Location/Qualifiers  
FT CDS 1..333  
FT /\*tag= a  
PN EP-327000-A.  
PD 09-AUG-1989.  
PF 30-JAN-1989; 101583.  
PR 30-JAN-1988; JP-20255.  
PR 08-JUL-1988; JP-171385.  
PA (KAGA ) The Chemo-Sero-Therapeutic Research Institute.  
PI Maeda H, Eda Y, Kimachi K, Tokiyoshi S, Matsushita S, Hattori T,  
PI Takatsuki K;  
DR WPI; 89-229050/32.  
PT Chimeric anti-human immune virus antibodies - contg. mouse variable  
PT regions and human constant regions for diagnosis, treatment and  
PT prevention of AIDS  
PS Claim 6; page 15; 33pp; English.  
CC The gene fragment encodes an L chain variable region from an  
CC immunoglobulin with anti-HIV neutralising activity. It is used, with an  
CC H chain variable region gene fragment (see N90491), to produce a chimeric  
CC anti-HIV antibody with mouse variable regions and human constant regions.  
CC The antibody retains its original specificity, but have much lower  
CC antigenicity to humans. See also P90541, N90493 and N90495.  
SQ Sequence 334 BP; 91 A; 83 C; 81 G; 79 T;  
Query Match 100.0%; Score 45; DB 1; Length 334;  
Best Local Similarity 100.0%; Pred. No. 1.41e-13;  
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 70 aagggcagcaagtggtgattgatgatgatgatgatgatgaac 114  
|||||  
QY 1 AAGGCCAGCCAAAGTGTGATTGATGATGATGATGATGATGATGAAC 45

RESULT 6  
ID Q73986 standard; cDNA; 393 BP.  
AC Q73986;  
DT 20-SEP-1995 (first entry)  
DE Humanized antibody 3B9 light chain.  
KW Humanized antibody; antibody engineering; monoclonal antibody;  
KW Mab; interleukin-4; IL-4; allergy; ds.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT CDS 1..393  
FT /\*tag= a  
FT sig\_peptide 1..60  
FT /\*tag= b  
FT mat\_peptide 61..393  
FT /\*tag= c  
PN W09507301-A.  
PD 16-MAR-1995.  
PF 07-SEP-1994; U10308.  
PR 14-OCT-1993; US-117366.  
PR 14-OCT-1993; US-136783.  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
PA (SMIK ) SMITHKLINE BEECHAM PLC.  
PI Gross MS, Holmes SD, Sylvester DR;  
DR WPI; 95-123387/16.  
DR P-PSDB; R75355.  
PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived  
PT from high affinity mAbs - useful in treatment of IL-4-mediated  
PT and IgE-mediated allergic conditions  
PS Disclosure; Fig.5; 97pp; English.  
CC A humanized antibody light chain variable region and signal  
CC sequence is given in R75355. The signal sequence is also  
CC provided in R70194. The sequences of the first 2 CDRs  
CC are identical to mouse anti-human IL-4 Mab 3B9 light chain  
CC CDRs (given in R70195-96), but the third (R70201) differs  
CC by a single amino acid from the native mouse CDR (R70197).  
SQ Sequence 393 BP; 97 A; 96 G; 108 C; 92 T;  
Query Match 100.0%; Score 45; DB 14; Length 393;  
Best Local Similarity 100.0%; Pred. No. 1.41e-13;  
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 127 aagggcagcaagtggtgattgatgatgatgatgatgaac 171  
|||||  
QY 1 AAGGCCAGCCAAAGTGTGATTGATGATGATGATGATGATGATGAAC 45  
RESULT 7  
ID Q83490 standard; cDNA; 396 BP.  
AC Q83490;  
DT 20-SEP-1995 (first entry)  
DE Mouse Mab 3B9 light chain.  
KW Chimeric antibody; humanized antibody; antibody engineering;  
KW monoclonal antibody; Mab; interleukin-4; IL-4; allergy; ds.  
OS Mus sp.  
FH Key Location/Qualifiers  
FT CDS 1..396  
FT /\*tag= a  
FT sig\_peptide 1..60  
FT /\*tag= b  
FT mat\_peptide 61..396  
FT /\*tag= c  
PN W09507301-A.

PD 16-MAR-1995.  
 PF 07-SEP-1994; U10308.  
 PR 07-SEP-1993; US-117366.  
 PR 14-OCT-1993; US-136783.  
 PA (SMIK ) SMITHKLINE BEECHAM CORP.  
 PA (SMIK ) SMITHKLINE BEECHAM PLC.  
 PI Gross MS, Holmes SD, Sylvester DR;  
 DR WPI; 95-123387/16.  
 DR P-PSDB; R70189.  
 PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived  
 PT from high affinity mAbs - useful in treatment of IL-4-mediated  
 PT and IgE-mediated allergic conditions  
 PS Disclosure; Fig.1; 97pp; English.  
 CC Spleen cells from mice immunised with human IL-4 were used to prepare  
 CC hybridomas, which were screened for anti-IL-4 MAb secretion. \*Only  
 CC clone 3B9 was positive. cDNA clones of the 3B9 light and heavy  
 CC chains were cloned into pCEM7f+ and transformed into E. coli  
 CC DH5-alpha. The clones were sequenced (Q83490-91), and used for  
 CC antibody engineering.  
 SQ Sequence 396 BP; 99 A; 103 C; 103 G; 91 T;  
 Query Match 100.0%; Score 45; DB 14; Length 396;  
 Best Local Similarity 100.0%; Pred. No. 1.41e-13;  
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 130 aaggccagccaaagtgtgattatgatgtgattatgatgaac 174  
 ||||||||||||||||||||||||||||||||||||||||  
 QY 1 AAGCCAGCCAAAGTGTGATTATGATGCTGCTAGTTATATGAAC 45

## RESULT 8

ID Q25658 standard; DNA; 733 BP.  
 AC Q25658;  
 DT 08-DEC-1992 (first entry)  
 DE Mouse 0.5beta anti-HIV antibody Light chain.  
 KW Heavy; light; CDR; HIV; AIDS; FR; framework region; ds.  
 OS Synthetic.  
 FH Key Location/Qualifiers  
 FT primer\_bind complement (77..106)  
 FT /\*tag= a  
 FT /note= "binding site for the primer  
 FT represented Q30550"  
 FT primer\_bind 709..730  
 FT /\*tag= b  
 FT /note= "binding site for the primer  
 FT represented Q30551"  
 PN J04141095-A.  
 PD 14-MAY-1992.  
 PF 02-OCT-1990; 266091.  
 PR 02-OCT-1990; JP-266091.  
 PA (KAGA ) KAGAKU OYOBI KESSEI RYOHO.  
 DR WPI; 92-212765/26.  
 PT New recombinant modified anti-HIV antibodies - comprise human x  
 PT mouse modified antibody H and L chains  
 PS Disclosure; Fig 4; 15pp; Japanese.  
 CC Recombinant modified anti-HIV antibodies comprise framework regions  
 CC derived from human antibody and CDRs derived from mouse monoclonal  
 CC antibody 0.3beta. The anti-HIV modified antibody can be used for  
 CC the prophylaxis and treatment of AIDS.  
 SQ Sequence 733 BP; 194 A; 162 C; 161 G; 216 T;

Query Match 100.0%; Score 45; DB 4; Length 733;  
 Best Local Similarity 100.0%; Pred. No. 1.41e-13;  
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 451 aaggccagccaaagtgtgattatgatgtgattatgatgaac 495  
 ||||||||||||||||||||||||||||||||||||||||  
 QY 1 AAGCCAGCCAAAGTGTGATTATGATGCTGCTAGTTATATGAAC 45

## RESULT 9

ID N90495 standard; DNA; 780 BP.  
 AC N90495;  
 DT 24-OCT-1989 (first entry)  
 DE A V chi region gene.  
 KW V chi region gene; immunoglobulin; L chain variable region; HIV.  
 OS Mus musculus  
 FH Key Location/Qualifiers  
 FT exon 119..167  
 FT /\*tag= a  
 FT exon 398..742  
 FT /\*tag= b  
 PN EP-327000-A.  
 PD 09-AUG-1989.  
 PF 30-JAN-1989; 101583.  
 PR 30-JAN-1988; JP-20255.  
 PR 08-JUL-1988; JP-171385.  
 PA (KAGA ) The Chemo-Sero-Therapeutic Research Institute.  
 PI Maeda H, Eda Y, Kimachi K, Tokiyoshi S, Matsushita S, Hattori T,  
 PI Takatsuki K;  
 DR WPI; 89-229050/32.  
 DR P-PSDB; P90543.  
 PT Chimeric anti-human immune virus antibodies - contg. mouse variable  
 PT regions and human constant regions for diagnosis, treatment and  
 PT prevention of AIDS  
 PS Disclosure; Fig 7; 33pp; English.  
 CC The sequence is a V chi region gene, encoding an L chain variable region  
 CC (see P90543). See also N90491-3.  
 SQ Sequence 780 BP; 205 A; 172 C; 171 G; 232 T;

Query Match 100.0%; Score 45; DB 1; Length 780;  
 Best Local Similarity 100.0%; Pred. No. 1.41e-13;  
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 478 aaggccagccaaagtgtgattatgatgtgattatgatgaac 522  
 ||||||||||||||||||||||||||||||||||||||||  
 QY 1 AAGCCAGCCAAAGTGTGATTATGATGCTGCTAGTTATATGAAC 45

## RESULT 10

ID Q04039 standard; DNA; 900 BP.  
 AC Q04039;  
 DT 06-SEP-1990 (first entry)  
 DE Anti-Leu 3a light chain variable region gene, 206 Vx.  
 KW HIV; AIDS; anti-Leu3A; vaccine; ds.  
 OS Mus musculus.  
 FH Key Location/Qualifiers  
 FT exon 259..307  
 FT /\*tag= a  
 FT intron 308..537  
 FT /\*tag= b  
 FT exon 538..882  
 FT /\*tag= c  
 PN EP-365209-A.  
 PD 25-APR-1990.  
 PF 11-OCT-1989; 010415.  
 PR 17-OCT-1988; US-260558.  
 PA (BECT) Becton Dickinson Co.



PI Hinton R, Oi VT;  
 DR WPI; 90-126329/17.  
 DR P-PSDB; R04132.  
 PT New chimeric variants of murine antibody anti-leucine -  
 PT contg. human antibody regions, and DNA encoding sequences.  
 PS Claim 1; Fig 2; 12pp; English.  
 CC Variants of murine monoclonal anti-CD4 antibody, anti-leu3A can be  
 CC used to form chimeric mouse-variable, human-constant region Abs  
 CC suggested as being useful as a vaccine to HIV.  
 SQ Sequence 900 BP; 261 A; 206 C; 187 G; 246 T;

Query Match 100.0%; Score 45; DB 1; Length 900;  
 Best Local Similarity 100.0%; Pred. No. 1.41e-13;  
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 618 aagccagcacaagtgtgattatgatgtgtagttatgatgaac 662  
 |||||  
 QY 1 AAGCCAGCCAAAGTGTGATTATGATGTTGATGTTATATGAAC 45

## RESULT 11

ID Q36609 standard; DNA; 393 BP.  
 AC Q36609;  
 DT 02-JUN-1993 (first entry)  
 DE Anti-CD4 antibody MT 3.10 light chain variable region.  
 KW immunosuppression; tissue transplantation; graft; L chain; V region;  
 KW T-helper cell inhibition; transplant rejection; MAb;  
 KW interleukin-2 receptor; ss.  
 FH Key Location/Qualifiers  
 FT sig\_peptide 1..60  
 FT /\*tag= a  
 FT mat\_peptide 61..393  
 FT /\*tag= b  
 FT /\*note= "J1 region begins at position 361"  
 PN D04143214-A.  
 PD 28-JAN-1993.  
 PF 30-DEC-1991; 143214.  
 PR 25-JUL-1991; DE-124759.  
 PR 30-DEC-1991; DE-143214.  
 PA (BOEF) BOEHRINGER MANNHEIM GMBH.  
 PI Kaluza B, Riethmuller G, Scheuer W, Weidle U;  
 DR WPI; 93-037582/05.  
 DR P-PSDB; R32123.  
 PT Synergistic antibody compen. for use as immunosuppressant -  
 PT comprises monoclonal anti-CD4 antibodies and monoclonal anti-IL2R  
 PT alpha- or anti-IL2R beta antibodies  
 PS Claim 5; Page 11; 18pp; German.  
 CC This sequence encodes the light chain variable region of a preferred  
 CC anti-CD4 monoclonal antibody for use in the claimed synergistic  
 CC composition. MAb MT 3.10 is deposited as clone 3.101/SB10 (ECACC  
 CC 90090702). The anti-CD4 antibody is used with at least one anti-IL2R  
 CC alpha or beta antibody. Individually the antibodies are strongly  
 CC inhibiting and when used together their immunosuppressive properties  
 CC are improved; they synergistically inhibit T-helper cell  
 CC proliferation to effectively inhibit transplant rejection at low  
 CC doses without significantly reducing the general immune response.  
 CC See Q36607-Q36616.  
 SQ Sequence 393 BP; 100 A; 105 C; 98 G; 90 T;

Query Match 95.6%; Score 43; DB 6; Length 393;  
 Best Local Similarity 97.8%; Pred. No. 1.73e-12;  
 Matches 44; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 130 aagccagcacaagtgtgattatgatgtgtagttatgatgaac 174

QY 1 AAGCCAGCCAAAGTGTGATTATGATGTTGATGTTATATGAAC 45  
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## RESULT 12

ID T04019 standard; cDNA; 717 BP.  
 AC T04019;  
 DT 02-JUL-1996 (first entry)  
 DE Anti-EGFR single chain antibody (Clone 4 B 2).  
 KW Single chain antibody; antibody; epidermal growth factor receptor;  
 KW EGFR; tumour; cancer; glioma; melanoma; carcinoma; diagnosis;  
 KW assessment; phage antibody library; ss.  
 OS Mus musculus.

FH Key Location/Qualifiers  
 FT CDS 1..717

FT /\*tag= a  
 FT /product= Single chain antibody.  
 PN W09525167-A1.  
 PD 21-SEP-1995.  
 PF 16-MAR-1995; E00978.  
 PR 17-MAR-1994; EP-104160.  
 PR 02-DEC-1994; EP-118970.  
 PA (MERE) MERCK PATENT GMBH.  
 PI Adan J, Ansell KH, Bendig MM, Blasco F, Guesow D;  
 PI Kettleborough AC, Mitjans F, Piulats J, Rosell E;  
 DR WPI; 95-336972/43.  
 DR P-PSDB; R79866.  
 PT Anti-EGFR antibodies and single chain Fv antibody fragments -  
 PT obtained from phage-antibody libraries, useful for diagnosis and  
 PT therapy of tumours  
 PS Claim 4; Page 57; 93pp; English.  
 CC Anti-epidermal growth factor receptor (EGFR) single chain antibodies  
 CC and antibodies constructed from anti-EGFR antibody fragments can be  
 CC used for diagnosis of tumours and assessment of tumour growth in  
 CC vitro and in vivo. They may also be used in a pharmaceutical  
 CC composition for the therapy of e.g. melanomas, gliomas and carcinomas.  
 CC The antibodies and fragments are derived from mice but are humanised  
 CC so as to cause minimum reaction against them. They are produced  
 CC using the phage antibody library. (See T04011-T04026 and  
 CC R79858-R79873)  
 SQ Sequence 717 BP; 165 A; 169 C; 213 G; 170 T;

Query Match 95.6%; Score 43; DB 18; Length 717;  
 Best Local Similarity 97.8%; Pred. No. 1.73e-12;  
 Matches 44; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 472 aagccagcacaagtgtgattatgatgtgtagttatgatgaac 516  
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 QY 1 AAGCCAGCCAAAGTGTGATTATGATGTTGATGTTATATGAAC 45

## RESULT 13

ID Q83520 standard; cDNA; 393 BP.  
 AC Q83520;  
 DT 20-SEP-1995 (first entry)  
 DE Humanized antibody 3B9 light chain.  
 KW Humanized antibody; antibody engineering; monoclonal antibody;  
 KW MAb; interleukin-4; IL-4; allergy; ds.  
 OS Homo sapiens.

FH Key Location/Qualifiers  
 FT CDS 1..393

FT /\*tag= a  
 PN W09507301-A.  
 PD 16-MAR-1995.

PF	07-SEP-1994; U10308.
PPR	07-SEP-1993; US-117366.
PR	14-OCT-1993; US-136783.
PPA	(SMIK ) SMITHKLINE BEECHAM CORP.
PPA	(SMIK ) SMITHKLINE BEECHAM PLC.
PPI	Gross MS, Holmes SD, Sylvestre RI;
PPI	WP1; 95-123387/16.
PPR	p-PSDB; R70202.
PPR	Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived
PPT	from high affinity mAbs - useful in treatment of IL-4-mediated
PPT	and IgE-mediated allergic conditions
PPT	Dioclosure; Page 71-72; 97pp; English.
CCC	A humanized antibody light chain variable region and signal
CCC	sequence is given in R75355. The signal sequence is also
CCC	provided in R70194. The sequences of the 3 CDRs
CCC	are identical to mouse anti-human IL-4 MAb 3B9 light chain
CCC	CDRs (given in R70195-97).
CC	Sequence 393 BF; 97 A; 98 C; 105 G; 93 T;

Query Match	91.1%;	Score 41;	DB 14;	Length 393;
Best Local Similarity	95.6%;	Pred. No. 2.10e-11;		
Matches	43;	Conservative 0;	Mismatches 2;	Indels 0; Gaps 0;

D <sub>b</sub>	127	aaggccctcccaagtgttgattatgatggatagttatatgaac	171
Q <sub>Y</sub>	1	AAGCCAGCCAAAGTGTGATTATCATGTGTAGTTATATGAAC	45

RESULT	14
ID	Q04041 standard; DNA; 397 BP.
AC	Q04041;
DT	06-SEP-1990 (first entry)
DE	Anti-Leu 3a light chain variable region gene, KOL/206 VL.
KW	HIV; AIDS; anti-Leu3a; vaccine; ds.

Key	Location/Qualifiers
FT exon	43..387

FT /\*tag= a  
PN EP-365209-A.

PD 25-APR-1990.  
PF 11-OCT-1989: 010415.

PR 17-OCT-1988; US-260558.

PA (BECT) Becton Dickinson Co.  
PI Hinton R. Qi VT;

DR WPI; 90-126329/17.

DR P-PSDB; RU4134.  
PT New chimeric va

PT. contg. human antibody regions, and DNA encoding sequences.

FS CLAIM 4; FIG 4; 12pp; ENGLISH.  
CC Variants of murine monoclonal

CC used to form chimeric mouse-variable, human-constant region Abs  
CC suggested as being useful as a vaccine to HIV

SQ	Sequence	397 BP;	105 A;	99 C;	84 G;	109 T;
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Query Match 91.1%; Score 41; DB 1; Length 397;  
Best Local Similarity 95.8%; Pred. No. 2.10e-11;  
Matches 43; Conservative 0; Mismatches 2; Indels

Db 120' aaagctagccaaagtgttgattatgatggtgatagttatatgaac 164

Qv 1 AAGGCCAGCCAAAGCTGTGATTATGATGGTGATAGTTATATGAAC 45

RESULT 15

ID	Q83508 standard; DNA; 63 BP.
AC	Q83508;
DT	20-SEP-1995 (first entry)
DE	IL-4 CDRI gene fragment.
KW	Humanized antibody; antibody engineering; monoclonal antibody;
KW	MAB; interleukin-4; IL-4; allergy; heavy chain; CDR;
KW	complementarity determining region; ss.
OS	Synthetic.
PN	W09507301-A.
PN	16-MAR-1995.
PF	07-SEP-1994; U10308.
PF	07-SEP-1993; US-117366.
PR	14-OCT-1993; US-136783.
PR	(SMIK ) SMITHKLINE BEECHAM CORP.
PA	(SMIK ) SMITHKLINE BEECHAM PLC.
PI	Gross MS, Holmes SD, Sylvester DR;
PT	WPI; 95-123387/16.
PT	Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived
PT	from high affinity mAbs - useful in treatment of IL-4-mediated
PT	and IgE-mediated allergic conditions
PT	Example 3; Page 28; 97pp; English.
CC	A humanized antibody was designed to contain mouse CDRs (from
CC	anti-IL-4 MAb 389 MAb) within a human antibody framework. A
CC	synthetic heavy chain was made using the oligonucleotides given
CC	in Q83498-502 and amplified by PCR using the primers given in
CC	Q83503-04. The construct was ligated into vector pCD, along
CC	with a signal sequence (Q83494) and an IgG1 human constant
CC	region. The CDR gene regions of a pre-existing light chain
CC	framework were replaced with synthetic IL-4 CDR genes constructed
CC	from oligonucleotides given in Q83505-08 (CDR1), Q83509-10 (CDR2)
CC	and Q83511-12 (CDR3). The synthetic VL (Q73986) was ligated into
CC	the vector. The anti-IL4 engineered antibody was expressed in
CC	COS and CHO cells.
SQ	Sequence 63 BP; 17 A; 16 C; 11 G; 19 T.

Query Match 88.9%; Score 40; DB 14; Length 63;  
Best Local Similarity 95.5%; Pred. No. 7.27e-11;  
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Db 19 gttcataactatcaccatcataatcaacactttggaggcct 62

Co 45 CTTTCATATAACTATCACCATCATATAATCAACACTTTGGCGCT 2

Search completed: Wed Mar 19 08:13:50 1997  
Job time : 17 secs.

Query Match 91.1%; Score 41; DB 1; Length 397;  
Best Local Similarity 95.8%; Pred. No. 2.10e-11;  
Matches 43; Conservative 0; Mismatches 2; Indels

Db 120' aaagctagccaaagtgttgattatgatggtgatagttatatgaac 164

Qv 1 AAGGCCAGCCAAAGCTGTGATTATGATGGTGATGATTATATGAAC 45

RESULT 15



Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 245)  
AUTHORS Mo, J.A., Bona, C.A. and Holmdahl, R.  
TITLE Variable region gene selection of immunoglobulin G expressing B cells with specificity for a defined epitope on type II collagen  
JOURNAL Eur. J. Immunol. (1993) In press  
REFERENCE 2 (bases 1 to 245)  
AUTHORS Mo, J.A.  
TITLE Direct Submission  
JOURNAL Submitted (02-AUG-1993) to the EMBL/GenBank/DBJ databases. John A Mo, Department of Medical and Physiological, Department of, Medical and Physiological Chemistry, Husargatan 3, Uppsala, 75123, Sweden

REFERENCE 3 (bases 1 to 245)  
AUTHORS Mo, J.A., Bona, C.A. and Holmdahl, R.  
TITLE Variable region gene selection of immunoglobulin G-expressing B cells with specificity for a defined epitope on type II collagen  
JOURNAL Eur. J. Immunol. 23 (10), 2503-2510 (1993)  
MEDLINE 94009207

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QY 1 AAGCCAGCCAAAGTCTTGATTATGATGCTAGTTATATGAAC 45

RESULT 2  
LOCUS MWIGKVRD 255 bp RNA ROD 13-OCT-1993  
DEFINITION M.musculus immunoglobulin kappa light chain (DBA/1) gene, v region.  
ACCESSION Z25448  
NID 9407836  
KEYWORDS Igk gene; immunoglobulin; light chain; variable region.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 255)  
AUTHORS Mo, J.A., Bona, C.A. and Holmdahl, R.  
TITLE Variable region gene selection of immunoglobulin G expressing B cells with specificity for a defined epitope on type II collagen  
JOURNAL Eur. J. Immunol. (1993) In press  
REFERENCE 2 (bases 1 to 255)  
AUTHORS Mo, J.A.  
TITLE Direct Submission  
JOURNAL Submitted (02-AUG-1993) to the EMBL/GenBank/DBJ databases. John A Mo, Department of Medical and Physiological, Department of, Medical and Physiological Chemistry, Husargatan 3, Uppsala, 75123, Sweden

REFERENCE 3 (bases 1 to 255)  
AUTHORS Mo, J.A., Bona, C.A. and Holmdahl, R.  
TITLE Variable region gene selection of immunoglobulin G-expressing B cells with specificity for a defined epitope on type II collagen  
JOURNAL Eur. J. Immunol. 23 (10), 2503-2510 (1993)  
MEDLINE 94009207

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RESULT 3  
LOCUS MWIGKVR 262 bp RNA ROD 13-OCT-1993  
DEFINITION M.musculus immunoglobulin kappa light chain (DBA/1) gene, v region.  
ACCESSION Z25450  
NID 9407838  
KEYWORDS Igk gene; immunoglobulin; light chain; variable region.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 262)  
AUTHORS Mo, J.A., Bona, C.A. and Holmdahl, R.  
TITLE Variable region gene selection of immunoglobulin G expressing B cells with specificity for a defined epitope on type II collagen

JOURNAL Eur. J. Immunol. (1993) In press  
REFERENCE 2 (bases 1 to 262)  
AUTHORS Mo,J.A.  
TITLE Direct Submission  
JOURNAL Submitted (02-AUG-1993) to the EMBL/GenBank/DBJ databases. John A Mo, Department of Medical and Physiological, Department of, Medical and Physiological Chemistry, Husargatan 3, Uppsala, 75123, Sweden  
REFERENCE 3 (bases 1 to 262)  
AUTHORS Mo,J.A., Bona,C.A. and Holmdahl,R.  
TITLE Variable region gene selection of immunoglobulin G-expressing B cells with specificity for a defined epitope on type II collagen  
JOURNAL Eur. J. Immunol. 23 (10), 2503-2510 (1993)  
MEDLINE 94009207  
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Qy 1 AAGGCCAGCCAAAGTTGATTATGATGCTGATAGTTATATGAAC 45  
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RESULT 4  
LOCUS MWIGKCVRI 264 bp RNA ROD 13-OCT-1993  
DEFINITION M.musculus immunoglobulin kappa light chain (DBA/1) gene, v region.  
ACCESSION 225458  
NID 9407844  
KEYWORDS Igk gene; immunoglobulin; light chain; variable region.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Mus.  
1 (bases 1 to 264)  
Mo,J.A., Bona,C.A. and Holmdahl,R.  
TITLE Variable region gene selection of immunoglobulin G expressing B cells with specificity for a defined epitope on type II collagen  
JOURNAL Eur. J. Immunol. (1993) In press  
REFERENCE 2 (bases 1 to 264)  
AUTHORS Mo,J.A.  
TITLE Direct Submission  
JOURNAL Submitted (02-AUG-1993) to the EMBL/GenBank/DBJ databases. John A Mo, Department of Medical and Physiological, Department of, Medical and Physiological Chemistry, Husargatan 3, Uppsala, 75123, Sweden

JOURNAL Submitted (02-AUG-1993) to the EMBL/GenBank/DBJ databases. John A Mo, Department of Medical and Physiological, Department of, Medical and Physiological Chemistry, Husargatan 3, Uppsala, 75123, Sweden  
REFERENCE 3 (bases 1 to 264)  
AUTHORS Mo,J.A., Bona,C.A. and Holmdahl,R.  
TITLE Variable region gene selection of immunoglobulin G-expressing B cells with specificity for a defined epitope on type II collagen  
JOURNAL Eur. J. Immunol. 23 (10), 2503-2510 (1993)  
MEDLINE 94009207  
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Qy 1 AAGGCCAGCCAAAGTTGATTATGATGCTGATAGTTATATGAAC 45  
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RESULT 5  
LOCUS MWIGKCVRC 266 bp RNA ROD 13-OCT-1993  
DEFINITION M.musculus immunoglobulin kappa light chain (DBA/1) gene, v region.  
ACCESSION 225446  
NID 9407834  
KEYWORDS Igk gene; immunoglobulin; light chain; variable region.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Mus.  
1 (bases 1 to 266)  
Mo,J.A., Bona,C.A. and Holmdahl,R.  
TITLE Variable region gene selection of immunoglobulin G expressing B cells with specificity for a defined epitope on type II collagen  
JOURNAL Eur. J. Immunol. (1993) In press  
REFERENCE 2 (bases 1 to 266)  
AUTHORS Mo,J.A.  
TITLE Direct Submission  
JOURNAL Submitted (02-AUG-1993) to the EMBL/GenBank/DBJ databases. John A Mo, Department of Medical and Physiological, Department of, Medical and Physiological Chemistry, Husargatan 3, Uppsala, 75123, Sweden  
REFERENCE 3 (bases 1 to 266)

AUTHORS Mo,J.A., Bona,C.A. and Holmdahl,R.  
TITLE Variable region gene selection of Immunoglobulin G-expressing B cells with specificity for a defined epitope on type II collagen  
JOURNAL Eur. J. Immunol. 23 (10), 2503-2510 (1993)  
MEDLINE 94009207  
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Qy 1 AAGGCCAGCCAAAGTGTGATTGATGATGCGTAGTTATATGAAC 45  
RESULT 6  
LOCUS MMIGKCVRF 270 bp RNA ROD 13-OCT-1993  
DEFINITION M.musculus immunoglobulin kappa light chain (DBA/1) gene, v region.  
ACCESSION Z25452  
NID 9407840  
KEYWORDS Igk gene; immunoglobulin; light chain; variable region.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;  
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;  
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;  
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;  
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 270)  
AUTHORS Mo,J.A., Bona,C.A. and Holmdahl,R.  
TITLE Variable region gene selection of immunoglobulin G expressing B cells with specificity for a defined epitope on type II collagen  
JOURNAL Eur. J. Immunol. (1993) In press  
REFERENCE 2 (bases 1 to 270)  
AUTHORS Mo,J.A.  
TITLE Direct Submission  
JOURNAL Submitted (02-AUG-1993) to the EMBL/GenBank/DBJ databases. John A Mo, Department of Medical and Physiological, Department of, Medical and Physiological Chemistry, Husargatan 3, Uppsala, 75123, Sweden  
REFERENCE 3 (bases 1 to 270)  
AUTHORS Mo,J.A., Bona,C.A. and Holmdahl,R.  
TITLE Variable region gene selection of immunoglobulin G-expressing B cells with specificity for a defined epitope on type II collagen  
JOURNAL Eur. J. Immunol. 23 (10), 2503-2510 (1993)

MEDLINE 94009207  
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ORIGIN  
Query Match 100.0%; Score 45; DB 64; Length 270;  
Best Local Similarity 100.0%; Pred. No. 2.65e-17;  
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 43 aagccagcacaagtggtgattgatgtgatgtatgatgaac 87  
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Qy 1 AAGGCCAGCCAAAGTGTGATTGATGATGCGTAGTTATATGAAC 45  
RESULT 7  
LOCUS MMIGKCVRB 270 bp RNA ROD 13-OCT-1993  
DEFINITION M.musculus immunoglobulin kappa light chain (DBA/1) gene, v region.  
ACCESSION Z25444  
NID 9407832  
KEYWORDS Igk gene; immunoglobulin; light chain; variable region.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;  
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;  
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;  
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;  
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 270)  
AUTHORS Mo,J.A., Bona,C.A. and Holmdahl,R.  
TITLE Variable region gene selection of immunoglobulin G expressing B cells with specificity for a defined epitope on type II collagen  
JOURNAL Eur. J. Immunol. (1993) In press  
REFERENCE 2 (bases 1 to 270)  
AUTHORS Mo,J.A.  
TITLE Direct Submission  
JOURNAL Submitted (02-AUG-1993) to the EMBL/GenBank/DBJ databases. John A Mo, Department of Medical and Physiological, Department of, Medical and Physiological Chemistry, Husargatan 3, Uppsala, 75123, Sweden  
REFERENCE 3 (bases 1 to 270)  
AUTHORS Mo,J.A., Bona,C.A. and Holmdahl,R.  
TITLE Variable region gene selection of immunoglobulin G-expressing B cells with specificity for a defined epitope on type II collagen  
JOURNAL Eur. J. Immunol. 23 (10), 2503-2510 (1993)  
MEDLINE 94009207  
FEATURES  
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1..270  
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/db_xref="PID:g407833"
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BASE COUNT      71 a      68 c      68 g      63 t
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 2.65e-17;  
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 43 aagccagcacaagtgtgattgatgtgatgtatgatgaac 87  
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Qy 1 AAGCCAGCCCAAGTGTGATTATGATGCGTGATGATTATGAAC 45

RESULT 8  
LOCUS MM1GKCVRG 270 bp RNA ROD 13-OCT-1993  
DEFINITION M.musculus immunoglobulin kappa light chain (DBA/1) gene, v region.  
ACCESSION Z25454  
NID g407842  
KEYWORDS Igk gene; immunoglobulin; light chain; variable region.  
SOURCE house mouse.  
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 270)  
Mo,J.A., Bona,C.A. and Holmdahl,R.  
Variable region gene selection of immunoglobulin G expressing B cells with specificity for a defined epitope on type II collagen Eur. J. Immunol. (1993) In press  
REFERENCE 2 (bases 1 to 270)  
Mo,J.A.  
Direct Submission  
Submitted (02-AUG-1993) to the EMBL/GenBank/DBSJ databases. John A Mo, Department of Medical and Physiological, Department of, Medical and Physiological Chemistry, Husarlgatan 3, Uppsala, 75123, Sweden  
REFERENCE 3 (bases 1 to 270)  
Mo,J.A., Bona,C.A. and Holmdahl,R.  
Variable region gene selection of immunoglobulin G-expressing B cells with specificity for a defined epitope on type II collagen Eur. J. Immunol. 23 (10), 2503-2510 (1993)  
JOURNAL 94009207  
MEDLINE  
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/db_xref="PID:g407843"
/translation="SLAVSLGQRATISCKASQSDYDGSYNNWYQKRPQPPKLLIY
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BASE COUNT      71 a      68 c      68 g      63 t
ORIGIN
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Query Match 100.0%; Score 45; DB 64; Length 270;  
Best Local Similarity 100.0%; Pred. No. 2.65e-17;  
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 43 aagccagcacaagtgtgattgatgtgatgtatgatgaac 87  
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Qy 1 AAGCCAGCCCAAGTGTGATTATGATGCGTGATGATTATGAAC 45

RESULT 9  
LOCUS MUSICKAANA 279 bp mRNA ROD 07-MAR-1995  
DEFINITION Mouse Igk chain mRNA, VJ5 region.  
ACCESSION M57978  
NID g196402  
KEYWORDS J-region; V-region; anti-cytochrome c antibody; immunoglobulin kappa-chain; immunoglobulin light chain.  
SOURCE Mouse (BALB/c) secondary B cell hybridoma 1C3 mRNA, clone 1C3.E3.  
ORGANISM Mus musculus

Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.  
REFERENCE 1 (bases 1 to 279)  
Goshorn,S.C., Retzel,E. and Jermerson,R.  
Common structural features among monoclonal antibodies binding the same antigenic region of cytochrome c  
J. Biol. Chem. 266 (4), 2134-2142 (1991)  
JOURNAL 91115823  
MEDLINE  
FEATURES  
Location/Qualifiers  
1..279  
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/clone="1C3.E3"  
/strain="BALB/c"  
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/tissue\_type="hybridoma"  
1..240  
/partial  
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1..279  
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/ note="CDR2"
220..246
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/ map="chromosome 6"
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241..279
/ gene="Igm"
/ map="chromosome 6"
/ note="J5"

misc_feature
75 a 73 c 69 g 62 t
ORIGIN      Chromosome 6.

Query Match      100.0%; Score 45; DB 66; Length 279;
Best Local Similarity 100.0%; Pred. No. 2.65e-17;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 13 aaggccagcaagtgttattatgatgtgatgttatgaac 57
|||||
Qy 1 AAGGCCAGCCAAAGTGTGATTATGATGCTGATGTTATATGAAC 45

RESULT 10
LOCUS      MMU29628      286 bp      mRNA      ROD      08-DEC-1995
DEFINITION Mus musculus anti-DNA antibody Ig kappa chain mRNA, V-J region,
hybridoma 52.60, partial cds.
ACCESSION U29628
NID      g896124
KEYWORDS .
SOURCE      house mouse.
ORGANISM      Mus musculus
Eukaryota; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 286)
AUTHORS      Ibrahim,S.M., Weigert,M., Basu,C., Erikson,J. and Radic,M.Z.
TITLE      Light chain contribution to specificity in anti-DNA antibodies
JOURNAL      J. Immunol. 155 (6), 3223-3233 (1995)
MEDLINE      95403997
REFERENCE 2 (bases 1 to 286)
AUTHORS      Ibrahim,S.M., Weigert,M., Basu,C., Erikson,J. and Radic,M.Z.
TITLE      Direct Submission
JOURNAL      Submitted (21-JUN-1995) Saleh M. Ibrahim, Molecular Biology,
Princeton University, Princeton, NJ 08544, USA
FEATURES
source
1..286
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/isolate="Hybridoma 52.60"
/chromosome="6"
<1..>286
/ note="V-J region"
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GQPKLLIYAASNLSCVPARFSGSGTDFTLINHPVEEDAATYYCQSSNEP"

CDS
820..857
/ gene="Igm"
/ map="chromosome 6"
/ note="CDR1"
820..857
/ gene="Igm"
/ map="chromosome 6"
/ note="CDR2"
858..885
/ gene="Igm"
/ map="chromosome 6"
/ note="CDR3"
886..913
/ gene="Igm"
/ map="chromosome 6"
/ note="J5"

BASE COUNT      74 a 75 c 69 g 68 t
ORIGIN
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Query Match      100.0%; Score 45; DB 65; Length 286;
Best Local Similarity 100.0%; Pred. No. 2.65e-17;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 70 aaggccagcaagtgttattatgatgtgatgttatgaac 114
|||||
Qy 1 AAGGCCAGCCAAAGTGTGATTATGATGCTGATGTTATATGAAC 45

RESULT 11
LOCUS      MMU29629      297 bp      mRNA      ROD      08-DEC-1995
DEFINITION Mus musculus anti-DNA antibody Ig kappa chain mRNA, V-J region,
hybridoma 52.468, partial cds.
ACCESSION U29629
NID      g896126
KEYWORDS .
SOURCE      house mouse.
ORGANISM      Mus musculus
Eukaryota; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 297)
AUTHORS      Ibrahim,S.M., Weigert,M., Basu,C., Erikson,J. and Radic,M.Z.
TITLE      Light chain contribution to specificity in anti-DNA antibodies
JOURNAL      J. Immunol. 155 (6), 3223-3233 (1995)
MEDLINE      95403997
REFERENCE 2 (bases 1 to 297)
AUTHORS      Ibrahim,S.M., Weigert,M., Basu,C., Erikson,J. and Radic,M.Z.
TITLE      Direct Submission
JOURNAL      Submitted (21-JUN-1995) Saleh M. Ibrahim, Molecular Biology,
Princeton University, Princeton, NJ 08544, USA
FEATURES
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BASE COUNT      78 a 77 c 72 g 70 t
ORIGIN

Query Match      100.0%; Score 45; DB 65; Length 297;
Best Local Similarity 100.0%; Pred. No. 2.65e-17;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 70 aaggccagcaagtgttattatgatgtgatgttatgaac 114
|||||
Qy 1 AAGGCCAGCCAAAGTGTGATTATGATGCTGATGTTATATGAAC 45

RESULT 12
LOCUS      MMU07207      333 bp      mRNA      ROD      08-OCT-1994
DEFINITION Mus musculus clone 31 anti-C5a Ig light chain V region mRNA,
partial cds.
ACCESSION U07207
NID      g459212
KEYWORDS .
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SOURCE mouse.  
ORGANISM Mus musculus  
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia; Eutheria; Rodentia; Myomorpha; Muridae; Mus.  
REFERENCE 1 (bases 1 to 333)  
AUTHORS Ames, R.S., Tornetta, M.A., Jones, C.S. and Tsui, P.  
TITLE Isolation of neutralizing anti-C5a monoclonal antibodies from a filamentous phage monovalent Fab display library [published erratum appears in J Immunol 1994 Jul 15;153(2):910]  
JOURNAL J. Immunol. 152 (9), 4572-4581 (1994)  
MEDLINE 94209678  
REFERENCE 2 (bases 1 to 333)  
AUTHORS Ames, R.S.  
TITLE Direct Submission  
JOURNAL Submitted (28-FEB-1994) Robert S. Ames, Molecular Genetics, SmithKline Beecham Pharmaceuticals, 709 Swedeland Road, PO Box 1539, King of Prussia, PA 19406-0939, USA

FEATURES  
Location/Qualifiers  
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/clone.lib="Combinatorial Fab library constructed in phage display vector pMKFabGene3"  
/organism="Mus musculus"  
/tissue type="spleen"  
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GOPPKLIYAASNLESIGIPAREFSGSGSRDTFTLINPVEDDVATYYCQOSHPDPTF  
GGGTKLEIK"

CDS  
89 a 86 c 81 g 77 t  
BASE COUNT  
ORIGIN  
Query Match 100.0%; Score 45; DB 64; Length 333;  
Best Local Similarity 100.0%; Pred. No. 2.65e-17;  
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 70 aagccagccaagtgtgattatgatgtgtagttatgaac 114  
|||||  
QY 1 AAGGCCAGCCAAAGTCTGATTATGATGCTAGTTATATGAAC 45

RESULT 13  
LOCUS MUSIGL5B 333 bp DNA ROD 01-NOV-1991  
DEFINITION Mouse IgL chain H2L2 V-region, partial cds.  
ACCESSION M80406  
NID g197577  
KEYWORDS V-region; immunoglobulin light chain.  
SOURCE Mus musculus (strain BALB/c, sub\_species domesticus) (library: lambda-gtl1) DNA.

ORGANISM Mus musculus  
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.  
REFERENCE 1 (bases 1 to 333)  
AUTHORS Matsushita, S., Maeda, H., Kimachi, K., Eda, Y., Maeda, T., Tokiyoshi, S. and Takatsuki, K.  
TITLE Characterization of a mouse/human chimeric monoclonal antibody (C-beta-1) to a principal neutralizing domain of the human immunodeficiency virus type 1 envelope protein

JOURNAL Unpublished (1991)  
FEATURES  
Location/Qualifiers  
1..333  
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/strain="BALB/c"  
/sub\_species="domesticus"  
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CDS  
1..333  
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/product="immunoglobulin light chain"  
/db\_xref="PID:g197578"  
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/note="FR2"  
160..180  
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/note="CDR2"  
181..276  
/gene="0.5 beta-VL"  
/note="FR3"  
277..303  
/gene="0.5 beta-VL"  
/note="CDR3"  
304..333  
/gene="0.5 beta-VL"  
/note="FR4"  
BASE COUNT 91 a 82 c 81 g 79 t  
ORIGIN

Query Match 100.0%; Score 45; DB 67; Length 333;  
Best Local Similarity 100.0%; Pred. No. 2.65e-17;  
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 70 aagccagccaagtgtgattatgatgtgtagttatgaac 114  
|||||  
QY 1 AAGGCCAGCCAAAGTCTGATTATGATGCTAGTTATATGAAC 45

RESULT 14  
LOCUS S42888 333 bp DNA ROD 09-NOV-1992  
DEFINITION Ig V kappa =immunoglobulin V kappa region [mice, hybridoma 54'CB1, Genomic, nt].  
ACCESSION S42888  
NID q254222  
KEYWORDS  
SOURCE mice hybridoma 54'CB1.  
ORGANISM Mus sp.  
Unclassified.  
REFERENCE 1 (bases 1 to 333)  
AUTHORS Matsushita, S., Maeda, H., Kimachi, K., Eda, Y., Maeda, Y., Murakami, T., Tokiyoshi, S. and Takatsuki, K.  
TITLE Characterization of a mouse/human chimeric monoclonal antibody (C beta 1) to a principal neutralizing domain of the human immunodeficiency virus type 1 envelope protein

JOURNAL AIDS Res. Hum. Retroviruses 8 (6), 1107-1115 (1992)

MEDLINE 92368728

REMARK GenBank staff at the National Library of Medicine created this entry [NCBI gibsseq 111883] from the original journal article. This sequence comes from Fig. 2.

## FEATURES

source Location/Qualifiers  
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/note="mice"  
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/gene="Ig V<kappa>"  
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GSGTKLEIK"

BASE COUNT 91 a 82 c 81 g 79 t

## ORIGIN

Query Match 100.0%; Score 45; DB 70; Length 333;  
Best Local Similarity 100.0%; Pred. No. 2.65e-17;  
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 70 aagggcagccaaagtgtgattgatggtgatgtatgatgaac 114

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Qy 1 AAGGCCAGCCAAAGTGTGATTGATGGTGATGATTATGAAC 45

## RESULT 15

LOCUS S54207 333 bp mRNA ROD 26-MAR-1993  
DEFINITION V kappa 21=immunoglobulin light chain variable region [mice, HIV-1  
BRU immunized BALB/c, mRNA Partial, 333 nt].

ACCESSION S54207

NID g264866

KEYWORDS

SOURCE mice HIV-1 BRU immunized BALB/c.

ORGANISM Mus sp.

Unclassified.

REFERENCE 1 (bases 1 to 333)

AUTHORS Pirofski, L.A., Thomas, E.K. and Scharff, M.D.

TITLE Variable region gene utilization and mutation in a group of  
neutralizing murine anti-human immunodeficiency virus type 1  
principal neutralizing determinant antibodies

JOURNAL AIDS Res. Hum. Retroviruses 9 (1), 41-49 (1993)

MEDLINE 93152285

REMARK GenBank staff at the National Library of Medicine created this  
entry [NCBI gibsseq 124489] from the original journal article.  
This sequence comes from Fig. 2.

## FEATURES

source Location/Qualifiers  
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1..333  
/partial  
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/note="Mismatch (62[1->M]); Description: immunoglobulin  
light chain variable region, anti-HIV-1 monoclonal  
antibody 110.3; Method: conceptual translation supplied  
by author. This sequence comes from Fig. 2. Author-given

protein sequence is in conflict with the conceptual  
translation. anti-HIV-1 monoclonal antibody 110.3"  
/codon\_start=1  
/product="immunoglobulin light chain variable region"  
/db\_xref="PID:g264867"  
/translation="DIVLTQSPASIVSLGQRATISCKASQSYVDGDSYMMYQQKP  
GPPKLLIHAASNLSVGPAREFGSGGRTDFTLNHPVEEDAATYYCQQSIEDPFTF  
GGGTKLEIK"

BASE COUNT 87 a 85 c 85 g 76 t

## ORIGIN

Query Match 100.0%; Score 45; DB 70; Length 333;  
Best Local Similarity 100.0%; Pred. No. 2.65e-17;  
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 70 aagggcagccaaagtgtgattgatggtgatgtatgatgaac 114

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Qy 1 AAGGCCAGCCAAAGTGTGATTGATGGTGATGATTATGAAC 45

## RESULT 16

LOCUS MUSICKAM 336 bp mRNA ROD 15-JUN-1990  
DEFINITION Mouse Ig rearranged kappa-chain mRNA V-J region, hybridoma BAT123,  
partial cds.

ACCESSION M31962

NID g196467

KEYWORDS J-region; V-region; immunoglobulin-kappa; processed gene.

SOURCE Mouse hybridoma BAT123, cDNA to mRNA.

ORGANISM Mus musculus

Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;  
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.

REFERENCE 1 (bases 1 to 336)

AUTHORS Liou, R.-S., Rosen, E.M., Fung, M.S.C., Sun, W.N.C., Sun, C., Gordon, W.,  
Chang, N.T. and Chang, T.-W.

TITLE A chimeric mouse-human antibody that retains specificity for HIV

gp120 and mediates the lysis of HIV-infected cells

JOURNAL J. Immunol. 143, 3967-3975 (1989)

MEDLINE 90078997

COMMENT The sequence presented is from a chimeric mouse-human antibody. The  
authors have reported the mouse portion of the kappa-chain V-region  
mRNA.

FEATURES Location/Qualifiers

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CDS <1..>336

/note="Ig kappa-chain V-region"

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GGGTKLEIK"

BASE COUNT 87 a 84 c 86 g 79 t

## ORIGIN

Query Match 100.0%; Score 45; DB 66; Length 336;  
Best Local Similarity 100.0%; Pred. No. 2.65e-17;  
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 70 aagggcagccaaagtgtgattgatggtgatgtatgatgaac 114

|||||  
Qy 1 AAGGCCAGCCAAAGTGTGATTGATGGTGATGATTATGAAC 45

## RESULT 17

Mar 19 15:51

US-08-612-929-15.rge

17

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LOCUS MUSIGKABBC 350 bp mRNA ROD 29-OCT-1994
DEFINITION Mouse Ig kappa chain mRNA, V-J region from hybridoma MOR8.2.1,
partial cds.
ACCESSION M92401
NID g196481
KEYWORDS J-region; V-region; immunoglobulin light chain;
immunoglobulin-kappa; morphine specific antibody; processed gene.
SOURCE Mus musculus (strain BALB/c, sub_species domesticus) B-lymphocyte
cDNA to mRNA.
ORGANISM Mus musculus
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE 1 (bases 1 to 350)
AUTHORS Sawada, J., Yamazaki, T. and Terao, T.
TITLE Molecular and biochemical analyses of combining sites of monoclonal
anti-morphine antibodies
JOURNAL Mol. Immunol. 30 (1), 77-86 (1993)
MEDLINE 93109376
FEATURES
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                /cell_type="hybridoma"
                /sequenced_mol="cDNA to mRNA"
                /tissue_type="B-lymphocyte"
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            /map="6"
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            /product="Igk"
            /db_xref="PID:g196482"
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            GQPLLIYAASNLIESGIPARFSGSGTFTLNHPVEEDAAITYCQRSNEDFTF
            GSGTKLEIKRAADAP"
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            /map="6"
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BASE COUNT 90 a 88 c 89 g 81 t 2 others
ORIGIN
Query Match 100.0%; Score 45; DB 66; Length 350;
Best Local Similarity 100.0%; Pred. No. 2.65e-17;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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LOCUS MUSICKAF 360 bp mRNA ROD 30-AUG-1991
DEFINITION Mouse Ig active kappa chain mRNA V-region (V-D-J).
ACCESSION M61046
NID g196679
KEYWORDS anti-CD4; immunoglobulin light chain; monoclonal antibody.
SOURCE Mouse, cDNA to mRNA.
ORGANISM Mus musculus
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE 1 (bases 1 to 360)
AUTHORS Attanasio, R., Dilley, D., Buck, D.W., Maino, V.C., Lohman, K.L.,
Kanda, P. and Kennedy, R.C.
TITLE Structural characterization of a cross-reactive idiotype shared by
monoclonal antibodies specific for the human CD4 molecule
JOURNAL J. Biol. Chem. 266, 14611-14619 (1991)
MEDLINE 91317827
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US-08-612-929-15.rge

18

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ORGANISM Mus musculus
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Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE 1 (bases 1 to 354)
AUTHORS Lohman, K.L., Buck, D.W., Carrillo, M.A. and Kennedy, R.C.
TITLE Characterization of murine monoclonal anti-CD4; epitope
recognition, idiotope expression, and variable gene sequence
JOURNAL Unpublished (1992)
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LOCUS MUSICKAF 360 bp mRNA ROD 30-AUG-1991
DEFINITION Mouse Ig active kappa chain mRNA V-region (V-D-J).
ACCESSION M61046
NID g196679
KEYWORDS anti-CD4; immunoglobulin light chain; monoclonal antibody.
SOURCE Mouse, cDNA to mRNA.
ORGANISM Mus musculus
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE 1 (bases 1 to 360)
AUTHORS Attanasio, R., Dilley, D., Buck, D.W., Maino, V.C., Lohman, K.L.,
Kanda, P. and Kennedy, R.C.
TITLE Structural characterization of a cross-reactive idiotype shared by
monoclonal antibodies specific for the human CD4 molecule
JOURNAL J. Biol. Chem. 266, 14611-14619 (1991)
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DEFINITION Mouse hybridoma Ig rearranged kappa-chain mRNA V-region, partial
          cds.
ACCESSION M97871
NID g198669
KEYWORDS V-region; immunoglobulin light chain; immunoglobulin-kappa;
          processed gene.
SOURCE Mus musculus (strain BALB/c, sub_species domesticus) SP20-BALB/c
          fusion hybridoma cDNA to mRNA.
ORGANISM Mus musculus
          Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
          Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE 1 (bases 1 to 363)
AUTHORS Lohman,K.L., Buck,D.W., Carrillo,M.A. and Kennedy,R.C.
TITLE Characterization of murine monoclonal anti-CD4; epitope
        recognition, idiotope expression, and variable gene sequence
JOURNAL Unpublished (1992)
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ACCESSION M97879
NID g198681
KEYWORDS V-region; immunoglobulin light chain; immunoglobulin-kappa;
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SOURCE Mus musculus (strain BALB/c, sub_species domesticus) SP20-BALB/c
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fusion hybridoma cDNA to mRNA.
Mus musculus
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE 1 (bases 1 to 363)
AUTHORS Lohman,K.L., Buck,D.W., Carrillo,M.A. and Kennedy,R.C.
TITLE Characterization of murine monoclonal anti-CD4; epitope
        recognition, idiotope expression, and variable gene sequence
JOURNAL Unpublished (1992)
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DEFINITION Mouse hybridoma Ig rearranged kappa-chain mRNA V-region, partial
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ACCESSION M97869
NID g198667
KEYWORDS V-region; immunoglobulin light chain; immunoglobulin-kappa;
          processed gene.
SOURCE Mus musculus (strain BALB/c, sub_species domesticus) SP20-BALB/c
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ORGANISM Mus musculus
          Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
          Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE 1 (bases 1 to 363)
AUTHORS Lohman,K.L., Buck,D.W., Carrillo,M.A. and Kennedy,R.C.
TITLE Characterization of murine monoclonal anti-CD4; epitope
        recognition, idiotope expression, and variable gene sequence
JOURNAL Unpublished (1992)
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US-08-612-929-15 rge

21

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DEFINITION Sequence 1 from patent EP 0365209.  
ACCESSION I08223  
NID g589062  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 900)  
AUTHORS Hinton,R. and Oi,V.T.  
TITLE Anti-leu 3A amino acid sequence  
JOURNAL Patent: EP 0365209-A2 1 25-APR-1990;

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Search completed: Wed Mar 19 15:53:40 1997  
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WUQ5REH (TM)

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MPerch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed Mar 19 08:17:42 1997; MasPar time 57.36 Seconds  
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Description: (1-21) from US08612929.seq  
Perfect Score: 21  
N.A. Sequence: 1 GCTGCATCCATCTAGAACTCT 21  
Comp: CGACGTAGTCTAGATCTTAGA

Scoring table: TABLE default  
Gap 10

Nmatch STD : Dbase 0; Query 0

Searched: 630489 seqs, 220513910 bases x 2

Post-processing: Minimum Match 0%  
Listing first 45 summaries

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166:STS38 167:STS39 168:STS40 169:STS41 170:STS42  
171:STS43 172:STS44 173:STS45 174:STS46

Statistics: Mean 6.496; Variance 1.216; scale 5.342

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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c 1	17	81.0	442	98	R91891	yq04d10.r1 Homo sapie	6.90e-06
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c 3	17	81.0	493	24	H59381	yl19b06.r1 Homo sapie	6.90e-06
c 4	15	71.4	265	154	W25331	zb70b03.r1 Soares fet	4.79e-03
c 5	15	71.4	265	160	H531330	zb70b03.r1 Soares fet	4.79e-03
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c 7	15	71.4	391	134	GI6692	human STS SHGC-1306 c	4.79e-03
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c 10	15	71.4	598	58	N38958	yv21b03.s1 Homo sapie	4.79e-03
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c 17	14	66.7	262	151	W17407	mb58b09.r1 Soares mou	1.03e-01
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c 19	14	66.7	291	16	H33946	EST110402 Rattus sp.	1.03e-01
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c 23	14	66.7	383	8	H08973	yl18g12.r1 Homo sapie	1.03e-01
c 24	14	66.7	384	24	H60570	yr41c04.s1 Homo sapie	1.03e-01
c 25	14	66.7	391	122	T78239	yr79a08.r1 Homo sapie	1.03e-01
c 26	14	66.7	396	105	T08896	EST06788 Homo sapiens	1.03e-01
c 27	14	66.7	400	174	HS883301	human STS SHGC-10649	1.03e-01
c 28	14	66.7	400	134	GI6583	human STS SHGC-10649	1.03e-01
c 29	14	66.7	415	75	R14485	yf83d06.r1 Homo sapie	1.03e-01
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c 31	14	66.7	422	169	WM1305	ma42f07.r1 Soares mou	1.03e-01
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c 41	13	61.9	405	106	T15301	5c05f10-t7 Zea mays c	1.88e+00
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ACCESSION H59381  
NID g1012213  
KEYWORDS EST.  
SOURCE human clone=205715 primer=M13R1 library=Soares fetal liver spleen  
INFLS vector=pT7T3D (Pharmacia) with a modified polylinker  
host=DH10B (ampicillin resistant) Reitel=Pac I Reite2=Eco RI Liver  
and spleen from a 20 week-post conception male fetus. 1st strand  
cDNA was primed with a Pac I - oligo(dT) primer [5'  
AACTGGAGATTAATTAAGATCTTTTTTTTTTTTTTT 3'], double-stranded  
cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac  
I and cloned into the Pac I and Eco RI sites of the modified pT7T3  
vector. Library went through one round of normalization. Library  
constructed by Bento Soares and M.Fatima Bonaldo.  
Homo sapiens  
ORGANISM  
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;  
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;  
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;  
Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.  
REFERENCE  
1 (bases 1 to 493)  
AUTHORS  
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,  
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,  
Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and  
Wilson, R.  
TITLE  
The WashU-Merck EST Project  
JOURNAL  
Unpublished (1995)  
COMMENT  
Contact: Wilson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
High quality sequence stops: 383  
Source: IMAGE Consortium, LINL  
This clone is available royalty-free through LINL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
FEATURES  
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REFERENCE  
1 (bases 1 to 265)  
AUTHORS  
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
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Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,  
Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and  
Wilson, R.  
TITLE  
The WashU-Merck EST Project  
JOURNAL  
Unpublished (1995)  
COMMENT  
Contact: Wilson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone is available royalty-free through LINL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Seq primer: mob.RECA+ET.  
NCBI gi: 1303223  
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double-stranded cDNA was size selected, ligated to Eco RI  
adapters (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of a modified pT7T3 vector  
(Pharmacia). Library went through one round of  
normalization to a Cot = 5. Library constructed by Bento  
Soares and M.Fatima Bonaldo. This library was constructed  
from the same fetus as the fetal heart library, Soares  
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/dev\_stage="19 weeks"  
/lab\_host="DH10B (ampicillin resistant)"  
mRNA  
72 a 46 c 57 g 88 t 2 others  
BASE COUNT  
ORIGIN  
Query Match 71.4%; Score 15; DB 154; Length 265;  
Best Local Similarity 89.5%; Pred. No. 4.79e-03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Db 141 gattctagtttgcagc 159  
||||| ||||| ||||| ||||| |||||  
Cp 20 GATTCTAGATTGGATGCAGC 2  
RESULT 5  
ID H5331330 standard; RNA; EST; 265 BP.  
AC W25331;  
DT 09-MAY-1996 (Rel. 47, Created)  
DT 09-MAY-1996 (Rel. 47, Last updated, Version 1)  
DE zb70b03.r1 Soares fetal lung NBHL19W Homo sapiens cDNA clone 308909  
DE 5'.  
KW EST.



OS Homo sapiens (human)  
OC Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;  
OC Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominoidea.  
RN [1]  
RP 1-265  
RA Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M.,  
RA Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M.,  
RA Parsons J., Rifkin L., Rohlfing T., Soares M., Tan F.,  
RA Trevaskis E., Waterston R., Williamson A., Wohlmann P., Wilson R.;  
RT "The WashU-Merck EST Project";  
RL Unpublished.  
CC Contact: Wilton RK WashU-Merck EST Project Washington University  
CC School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,  
CC MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email:  
CC est@wustl.edu This clone is available royalty-free through  
CC LNL; contact the IMAGE Consortium (info@image.llnl.gov) for  
CC further information. Seq primer: mob.REGA+ET. NCBI gi: 1303223  
FH Key Location/Qualifiers  
FH 1..265  
FT source  
FT /organism="Homo sapiens"  
FT /note="Organ: lung; Vector: pT7T3D (Pharmacia) with a  
FT modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st  
FT strand cDNA was primed with a Not I - oligo(dT) primer  
FT 15'-TGTTACCAATCTGAGTGGGAGCGGCCCAATTTTTTTTTTTT-3'),  
FT double-stranded cDNA was size selected, ligated to Eco RI  
FT adapters (Pharmacia), digested with Not I and cloned into  
FT the Not I and Eco RI sites of a modified pT7T3 vector  
FT (Pharmacia). Library went through one round of  
FT normalization to a Cot = 5. Library constructed by Bento  
FT Soares and M. Fatima Bonaldo. This library was constructed  
FT from the same fetus as the fetal heart library, Soares  
FT fetal heart NBH19W."  
FT /clone="308909"  
FT /clone\_lib="Soares fetal lung NBH19W"  
FT /dev stage="19 weeks"  
FT /lab host="DH10B (ampicillin resistant)"  
FT mRNA  
FT <1...>265  
SQ Sequence 265 BP; 72 A; 46 C; 57 G; 88 T; 2 other;  
  
Query Match 71.4%; Score 15; DB 160; Length 265;  
Best Local Similarity 89.5%; Pred. No. 4.79e-03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
DB 141 gattctagtttgatgcag 159  
||||||| |||||  
CP 20 GATTCTAGTGGATGCAG 2  
  
RESULT 6  
ID HS692294 standard; DNA; STS; 391 BP.  
AC G16692;  
DT 07-MAR-1996 (Rel. 47, Created)  
DT 07-MAR-1996 (Rel. 47, Last updated, Version 1)  
DE human STS SHGC-1306 clone pg-299.  
KW primer; sequence tagged site; STS sequence.  
OS Homo sapiens (human)  
OC Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;  
OC Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominoidea.  
RN [1]  
RP 1-391  
RA Myers R.M.;  
RT ;  
RL Unpublished.

CC Contact: Richard M. Myers Stanford Human Genome Center (SHGC)  
CC Stanford University School of Medicine Department of Genetics,  
CC M-344, Stanford, CA 94305, USA Tel: 4157259687 Fax: 4157259689  
CC Email: myers@shgc.stanford.edu Primer A: GATGCTGTGTGATGCTACAGTTC  
CC Primer B: TCAGCTGCCACCTAACTTCTC STS size: 140 PCR Profile:  
CC Initial incubation: 94 degrees C for 90 seconds Denaturation: 94  
CC degrees C for 15 seconds Annealing: 62 degrees C for 23 seconds  
CC Polymerization: 72 degrees C for 30 seconds PCR Cycles: 30 Thermal  
CC Cycler: Perkin Elmer 9600 Protocol: Template: 25 ng Primer: each 1  
CC uM dNTPs: each 200 uM Taq Polymerase: 0.05 units/ul Total Vol: 10  
CC ul Buffer: MgCl2: 2.5 mM KCl: 50 mM Tris-HCl: 20 mM pH: 8.3  
CC Chromosome 4. NCBI gi: 1214118  
FH Key Location/Qualifiers  
FH 1..391  
FT source  
FT /organism="Homo sapiens"  
FT /note="human"  
FT STS  
FT 132..271  
FT /map="4"  
FT  
FT primer\_bind  
FT 132..154  
FT /map="4"  
FT primer\_bind  
FT complement(249..271)  
FT /map="4"  
SQ Sequence 391 BP; 108 A; 78 C; 88 G; 94 T; 23 other;  
  
Query Match 71.4%; Score 15; DB 174; Length 391;  
Best Local Similarity 100.0%; Pred. No. 4.79e-03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
DB 199 tagattgtagtcagc 213  
||||||| |||||  
CP 15 TAGATTGATGCAGC 1  
  
RESULT 7  
LOCUS G16692 391 bp DNA STS 05-MAR-1996  
DEFINITION human STS SHGC-1306 clone pg-299.  
ACCESSION G16692  
NID g1214118  
KEYWORDS  
SOURCE STS sequence; primer; sequence tagged site.  
human Plasmid clones, generated from a lymphoblastoid cell line  
from a human male. Localized to human chromosome 4 by analysis on  
the NIGMS Human/Rodent Somatic Cell Hybrid Panel #1, Coriell  
Institute for Medical Research, Camden, NJ 08103.  
  
ORGANISM Homo sapiens  
Eukaryota; Eukaryotes; Metazoa; Chordata;  
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;  
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;  
Catarrhini; Hominoidea; Homo.  
REFERENCE 1 (bases 1 to 391)  
AUTHORS Myers, R.M.  
JOURNAL Unpublished (1996)  
COMMENT  
  
Contact: Richard M. Myers  
Stanford Human Genome Center (SHGC)  
Stanford University School of Medicine  
Department of Genetics, M-344, Stanford, CA 94305, USA  
Tel: 4157259687  
Fax: 4157259689  
Email: myers@shgc.stanford.edu  
  
Primer A: GATGCTGTGTGATGCTACAGTTC  
Primer B: TCAGCTGCCACCTAACTTCTC  
STS size: 140

## PCR Profile:

Initial incubation: 94 degrees C for 90 seconds

Denaturation: 94 degrees C for 15 seconds

Annealing: 62 degrees C for 23 seconds

Polymerization: 72 degrees C for 30 seconds

PCR Cycles: 30

Thermal Cycler: Perkin Elmer 9600

## Protocol:

Template: 25 ng

Primer: each 1 uM

dNTPs: each 200 uM

Taq Polymerase: 0.05 units/ul

Total Vol: 10 ul

## Buffer:

MgCl<sub>2</sub>: 2.5 mM

KCl: 50 mM

Tris-HCl: 20 mM

pH: 8.3

## Chromosome 4.

Location/Qualifiers

1..391

/organism="Homo sapiens"

/note="human"

/map="4"

132..271

/map="4"

132..154

/map="4"

complement(249..271)

/map="4"

BASE COUNT 108 a 78 c 88 g 94 t 23 others

## Query Match

Best Local Similarity 71.4%; Score 15; DB 134; Length 391;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 199 tagattgacgacg 213

Cp 15 TAGATTGGATCGACG 1

## RESULT 8

LOCUS R55382 449 bp mRNA EST 22-MAY-1995

DEFINITION yj77b04.r1 Homo sapiens cDNA clone 154735 5'.

ACCESSION R55382

NID 9824677

KEYWORDS EST.

SOURCE human clone=154735 library=Soares breast 2NHBst vector=pfT73D

(Pharmacia) with a modified polylinker host=DHI0B (ampicillin

resistant) primer=M13Rpi Rsite1=Not I Rsite2=Eco RI Adult female.

1st strand cDNA was primed with a Not I - oligo(dT) primer [5'

TGTTACCAATCTGAAGTGGAGCGGCCCTTTTTTTTTTTT 3',

double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia),

digested with Not I and cloned into the Not I and Eco RI sites of a

modified pT73 vector (Pharmacia). Library went through one round

of normalization to a Cot = 230. Library constructed by Bento

Soares and M.Fatima Bonaldo.

Homo sapiens

ORGANISM Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;

Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;

Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;

Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE 1 (bases 1 to 449)

## AUTHORS

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,

Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,

Parsons,J., Rifkin,L., Rohlfling,T., Soares,M., Tan,F.,

Trevaaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and

Wilson,R.

TITLE The WashU-Merck EST Project

JOURNAL Unpublished (1995)

## COMMENT

Contact: Wilson RK

WashU-Merck EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence stops: 155

Source: IMAGE Consortium, LLNL

This clone is available royalty-free through LINL ; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

## FEATURES

source

1..449

/organism="Homo sapiens"

/clone="154735"

/note="human"

BASE COUNT 124 a 87 c 108 g 124 t 6 others

## ORIGIN

Query Match 71.4%; Score 15; DB 87; Length 449;

Best Local Similarity 85.7%; Pred. No. 4.79e-03;

Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 169 agactctacattgggtgcacg 189

Cp 21 AGATTCTAGATTGGATCGACG 1

## RESULT 9

LOCUS H36087 563 bp mRNA EST 25-JUL-1995

DEFINITION 14609 Arabidopsis thaliana cDNA clone 173397.

ACCESSION H36087

NID 9905586

KEYWORDS EST.

## SOURCE

thale cress clone=173397 library=Lambda-PRL2 strain=var columbia

vector=Lambda Zip-Lox primer=T7 dye primer Rsite1=Sal Rsite2=Not

Lambda PRL2 is a cDNA library derived from equal quantities of 4

pools of mRNA. The mRNA sources were 1) 7 day germinated etiolated

seedlings; 2) tissue culture grown roots; 3) staged plants half

with 24 hour light cycle, half on 16 hr light, 8 hour dark-

rosettes; 4) same plants as 3 but aerial tissue (stems, flowers

and siliques). The vector is BRL's Lambda Zip-Lox. The cDNA

inserts were directionally cloned with Sal-Not arms using oligo dT

primed cDNA.

Arabidopsis thaliana

ORGANISM Eucaryotae; Embryophyta; Magnoliophyta; Magnoliopsida; Capparales;

Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 563)

## AUTHORS

Newman,T., de Bruijn,F.J., Green,P., Keegstra,K., Kende,H.,

McIntosh,L., Ohlrogge,J., Raikhel,N., Somerville,S., Thomasow,M.,

Retzel,E. and Somerville,C.

Genes galore: a summary of methods for accessing results from

large-scale partial sequencing of anonymous Arabidopsis cDNA clones

Plant Physiol. 106, 1241-1255 (1994)

Mar 19 08:16

US-08-612-929-17.rst

11

## COMMENT

Contact: Thomas Newman  
MSU-DOE Plant Research Laboratory  
Michigan State University  
MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E.  
Lansing, MI  
Tel: 517-353-0854  
Fax: 517-353-9168  
Email: 22313tcn@ibm.ci.msu.edu.

## FEATURES

source  
1..563  
/organism="Arabidopsis thaliana"  
/clone="173097"  
/strain="var columbia"  
/note="thale cress"

BASE COUNT 126 a 95 c 145 g 175 t 22 others  
ORIGIN

Query Match 71.4%; Score 15; DB 17; Length 563;  
Best Local Similarity 89.5%; Pred. No. 4.79e-03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 353 agaattcatattggatgca 371  
||||| ||||| ||||| ||||| |||||  
Cp 21 AGATTCTAGATTGGATGCA 3

## RESULT 10

LOCUS N38958 598 bp mRNA EST 19-JAN-1996  
DEFINITION YV21B03.e1 Homo sapiens cDNA clone 243341 3'.

ACCESSION N38958

NID g1162165

KEYWORDS EST.

SOURCE human clone=243341 primer=m13 -40 forward library=Soares fetal liver spleen 1NPLS vector=p7T3D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) Rsite1=Pac I Rsite2=Eco RI Liver and spleen from a 20 week-post conception male fetus. 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5' AACTGGAAGAATTAATTAAGATCTTTTCTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified p7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo.

## ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomi; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominiidae; Homo.

## REFERENCE 1 (bases 1 to 598)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfs, T., Soares, M., Tan, F., Trevaekis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.

TITLE The WashU-Merck EST Project

JOURNAL Unpublished (1995)

## COMMENT

Contact: Wilson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810

Mar 19 08:16

US-08-612-929-17.rst

12

Email: est@watson.wustl.edu  
High quality sequence stops: 465  
Source: IMAGE Consortium, LNL  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.

## FEATURES

Location/Qualifiers  
source  
1..598  
/organism="Homo sapiens"  
/clone="243341"  
/note="human"

mRNA  
BASE COUNT 174 a 113 c 122 g 184 t 5 others  
ORIGIN

Query Match 71.4%; Score 15; DB 58; Length 598;  
Best Local Similarity 89.5%; Pred. No. 4.79e-03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 545 agactctaggttgatgca 563  
||||| ||||| ||||| ||||| |||||  
Cp 21 AGATTCTAGATTGGATGCA 3

## RESULT 11

LOCUS HSC10A042 195 bp RNA EST 21-SEP-1995  
DEFINITION H. sapiens partial cDNA sequence; clone c-10a04.

ACCESSION Z41644

NID g566018

KEYWORDS partial cDNA sequence; transcribed sequence fragment.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

## REFERENCE 1 (bases 1 to 195)

Genexpress.  
Direct Submission  
Submitted (24-OCT-1994) Genethon, B.P. 60, 91002 Evry Cedex France  
and Genetique Moleculaire et Biologie du developpement, CNRS UPR420  
B.P. 8, 94801 Villejuif Cedex France.E-mail: genexpress@genethon.fr

## REFERENCE 2 (bases 1 to 195)

Genexpress.

TITLE The Genexpress cDNA program

JOURNAL Unpublished

## REFERENCE 3 (bases 1 to 195)

Auf-ray, C., Behar, G., Bois, F., Bouchier, C., da Silva, C., Devignes, M.D., Duprat, S., Houlgatte, R., Jumeau, M.N., Lamy, B., Lorenzo, F., Mitchell, H., Mariage-Samson, R., Pletu, G., Poulliot, Y., Sebastiani-Kabaktchis, C. and Tessier, A.

IMAGE: molecular integration of the analysis of the human genome and its expression

C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)

95277534

Clone library from B.Soaress, Psychiatry Dept. Columbia University  
USA;

Cloning method: total mRNA was oligo-(dT) primed and directionally  
cloned 5' -> 3' into the HindIII -> NotI sites of the lafmid BA  
vector;

Sequencing method: single read, full automatic;

Primer: (-21)M13 universal;

cDNA sequence complementary to mRNA (3' end)

Stretch removed: 20 T removed at sequence 5' end

Normalization method: Bento Soares, P.N.A.S in press;

Genexpress\_library\_idt: C;

Mar 19 08:16

US-08-612-929-17.rst

13

Genexpresse\_sequence\_id: a2c-10a04;

No significant homology found with :  
genbank release 81 swissprot release 28.

## FEATURES

source  
1..195  
/organism="Homo sapiens"  
/isolate="muscular atrophy patient"  
/dev stage="3 months old"  
/tissue type="total brain"  
/clone lib="normalized infant brain cDNA"  
/sex="Female"

BASE COUNT 57 a 32 c 48 g 56 t 2 others  
ORIGIN

Query Match 66.7%; Score 14; DB 41; Length 195;  
Best Local Similarity 93.8%; Pred. No. 1.03e-01;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 50 ctgcattcaatctaga 65  
||||| |||||||  
Qy 2 CTGCATCAATCTAGA 17

## RESULT 12

ID DM123F11S standard; DNA; STS; 248 BP.

AC 232433;

DT 11-APR-1994 (Rel. 39, Created)

DT 17-APR-1996 (Rel. 47, Last updated, Version 4)

DE D. melanogaster STS determined from European Mapping Project  
DE cosmid.

KW sequence tagged site.

OS Drosophila melanogaster (fruit fly)

OC Eukaryota; Animalia; Metazoa; Arthropoda; Insecta;

OC Pterygota; Neoptera; Holometabola; Diptera; Brachycera;

OC Cyclorhapha; Schizophora; Drosophiloidea; Drosophilidae.

RN [1]

RP 1-248

RA European Drosophila Mapping Consortium;

RL Submitted (08-APR-1994) to the EMBL/GenBank/DBJ databases.

RL Michael Ashburner, Department of Genetics, Downing St., Cambridge

RL CB2 3EH, England

RN [2]

RC Updated comments

RA European Drosophila Mapping Consortium;

RT

RL Submitted (15-APR-1996) to the EMBL/GenBank/DBJ databases.

RL Michael Ashburner, Department of Genetics, Downing St., Cambridge

RL CB2 3EH, England

RN [3]

RP 1-248

RX MEDLINE; 95309678.

RA Madueno E., Papagiannakis G., Rimmington G.A., Saunders R.D.C.,

RA Savakis C., Siden-Kiamos I., Skavdis G., Spanos L., Trenear J.,

RA Adam P., Ashburner M., Benos P., Bolshakov V.N., Coulson D.,

RA Glover D.M., Herrmann S., Kafatos F.C., Louis C., Majerus T.,

RA Modolell J.;

RT "A physical map of the X chromosome of Drosophila melanogaster:

RT Cosmid contigs and sequence tagged sites.\*;

RL Genetics 139:1631-1647(1995).

CC STS name = Dm123F11S

CC clone name = 123F11

CC STS from promoter = SP6

Mar 19 08:16

US-08-612-929-17.rst

14

CC vector class = cosmid, Lorient 6  
CC origin\_of\_clone = Oregon-R  
CC in situ site primary = 2B1-10  
CC STS dbSTS AC = 4219  
CC BIAST program = BIASTN  
CC database\_searched = EMBL  
CC database\_version = 45.0 and updates till date\_of\_search  
CC date\_of\_search = 08-01-1996  
CC BIAST program = BIASTX  
CC database\_searched = SWISSPROT  
CC database\_version = 32.0  
CC date\_of\_search = 15-12-1995  
FH Key Location/Qualifiers  
FH  
FT source 1..248  
FT /organism="Drosophila melanogaster"  
FT /strain="Oregon-R"  
FT /clone="123F11"  
SQ Sequence 248 BP; 59 A; 52 C; 51 G; 81 T; 5 other;

Query Match 66.7%; Score 14; DB 173; Length 248;  
Best Local Similarity 93.8%; Pred. No. 1.03e-01;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 126 agattctagatttgat 141  
||||| |||||||  
Cp 21 AGATTCTAGATTGAT 6

## RESULT 13

LOCUS DM123F11S 248 bp DNA STS 17-APR-1996  
DEFINITION D. melanogaster STS determined from European Mapping Project  
cosmid.

ACCESSION Z32433

NID 9471188

KEYWORDS sequence tagged site.

SOURCE fruit fly.

ORGANISM

Drosophila melanogaster  
Eukaryota; mitochondrial eukaryotes; Metazoa; Arthropoda;  
Tracheata; Insecta; Pterygota; Diptera; Brachycera; Muscomorpha;  
Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 248)

AUTHORS European Drosophila Mapping Consortium.

TITLE Direct Submission

JOURNAL Submitted (08-APR-1994) Michael Ashburner, Department of Genetics,

Downing St., Cambridge CB2 3EH, England

REFERENCE 2 (bases 1 to 248)

AUTHORS European Drosophila Mapping Consortium.

TITLE Direct Submission

JOURNAL Submitted (15-APR-1996) Michael Ashburner, Department of Genetics,

Downing St., Cambridge CB2 3EH, England

REMARK Updated comments

REFERENCE 3 (bases 1 to 248)

Madueno E., Papagiannakis G., Rimmington G.A., Saunders R.D.C.,  
Savakis C., Siden-Kiamos I., Skavdis G., Spanos L., Trenear J.,  
Adam P., Ashburner M., Benos P., Bolshakov V.N., Coulson D.,  
Glover D.M., Herrmann S., Kafatos F.C., Louis C., Majerus T. and  
Modolell J.

TITLE A physical map of the X chromosome of Drosophila melanogaster:

cosmid contigs and sequence tagged sites

JOURNAL Genetics 139 (4), 1631-1647 (1995)

MEDLINE 95309678

COMMENT STS name = Dm123F11S

clone\_name = 123F11

STS from promoter = SP6  
vector\_class = cosmid, Loris 6  
origin\_of\_clone = Oregon-R  
in\_situ\_site\_primary = 2B1-10  
STS dbSTS AC = 4219  
BLAST\_program = BLASTN  
database\_searched = EMBL  
database\_version = 45.0 and updates till date\_of\_search  
date\_of\_search = 08-01-1996  
BLAST\_program = BLASTX  
database\_searched = SWISSPROT  
database\_version = 32.0  
date\_of\_search = 15-12-1995.

NCBI gi: 471188  
FEATURES  
source  
1..248  
/organism="Drosophila melanogaster"  
/strain="Oregon-R"  
/clone="123F11"

BASE COUNT 59 a 52 c 51 g 81 t 5 others  
ORIGIN

Query Match 66.7%; Score 14; DB 156; Length 248;  
Best Local Similarity 93.8%; Pred. No. 1.03e-01;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 126 agattctagattgat 141  
|||||  
Cp 21 AGATTCTAGATTGGAT 6

RESULT 14  
LOCUS DM123F11S 248 bp DNA STS 24-OCT-1995  
DEFINITION D. melanogaster STS determined from European Mapping Project  
cosmid.  
ACCESSION 232433  
NID 9471188  
KEYWORDS sequence tagged site.  
SOURCE fruit fly.  
ORGANISM Drosophila melanogaster  
Eukaryotes; mitochondrial eukaryotes; Metazoa; Arthropoda;  
Tracheata; Insecta; Pterygota; Diptera; Brachycera; Cyclorhapha;  
Drosophilidae; Drosophila; Sophophora; melanogaster group;  
melanogaster subgroup.  
REFERENCE 1 (bases 1 to 248)  
AUTHORS European Drosophila Mapping Consortium.  
TITLE Direct Submission  
JOURNAL Submitted (08-APR-1994) to the EMBL/GenBank/DBJ databases. Michael Ashburner, Department of Genetics, Downing St., Cambridge CB2 3EH, England  
REFERENCE 2 (bases 1 to 248)  
AUTHORS Madueno, E., Papagiannakis, G., Rimmington, G.A., Saunders, R.D.C., Savakis, C., Siden-Kiamos, I., Skavdis, G., Spanos, L., Treneer, J., Adam, P., Ashburner, M., Benos, P., Bolshakov, V.N., Coulson, D., Glover, D.M., Herrmann, S., Kafatos, F.C., Louis, C., Majerus, T. and Modelle, J.  
TITLE A physical map of the X chromosome of *Drosophila melanogaster*: cosmid contigs and sequence tagged sites  
JOURNAL Genetics 139 (4), 1631-1647 (1995)  
MEDLINE 95309678  
COMMENT STS name = Dm123F11S  
clone\_name = 123F11  
STS\_from\_promoter = SP6

vector\_class = cosmid, Loris 6  
origin\_of\_clone = Oregon-R  
in\_situ\_site\_primary = 2B1-10  
in\_situ\_site\_secondary = 0  
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BLAST\_program = BLASTN  
database\_searched = EMBL  
database\_version = 37.0  
parameters\_of\_search = default; only HSP scores >200 are reported  
date\_of\_update = 02 April 1994  
AC number of hit =  
probability\_of\_hit =  
HSP\_score\_of\_hit =.

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Location/Qualifiers  
BASE COUNT 59 a 52 c 51 g 81 t 5 others  
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Query Match 66.7%; Score 14; DB 129; Length 248;  
Best Local Similarity 93.8%; Pred. No. 1.03e-01;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 126 agattctagattgat 141  
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Cp 21 AGATTCTAGATTGGAT 6

RESULT 15  
LOCUS H64221 260 bp mRNA EST 16-OCT-1995  
DEFINITION RRAMCA026SK Brugia malayi cDNA clone RRAMCA026 5' similar to ZKS46.14 gene product.  
ACCESSION H64221  
NID g1019982  
KEYWORDS EST.  
SOURCE clone=RRAMCA026 primer=pBluescript SK library=Brugia malayi adult male cDNA (SAM94NL-BmM) strain=FRS Labs vector=lambda UniZap XR host=XLI-Blue MRF' Reitel=EcoR I Rsite2=Xho I lymphatic filarial nematode parasite of humans. mRNA was prepared from adult males of Brugia malayi isolated from jirds and converted to double stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNase I. The library had 4.6 x 10E6 independent recombinants and average insert size was 800 base pairs. The library was constructed by Noelle Ling. The library is available from Dr. S.A. Williams, email swilliams@smith.smith.edu.

ORGANISM Brugia malayi  
Eukaryotes; mitochondrial eukaryotes; Metazoa/Eumycota group; Metazoa; Eumetazoa; Bilateria; Pseudocoelomata; Nematoda; Secernentea; Spirurida; Spirurida; Spirurina; Filarioidea; Onchocercidae; Onchocercinae; Brugia.

REFERENCE 1 (bases 1 to 260)  
AUTHORS Williams, S.A.  
TITLE Genes expressed in adult males of *Brugia malayi*  
JOURNAL Unpublished (1995)  
COMMENT

Contact: Steven A. Williams  
Molecular Parasitology  
Smith College Department of Biological Sciences  
Department of Biological Sciences, Clark Science Center, Smith College, Northampton, MA, 01063, USA  
Tel: 4135853826  
Fax: 4135853786  
Email: swilliams@smith.smith.edu.

Mar 19 08:16

US-08-612-929-17.Jst

17

FEATURES Location/Qualifiers

source

1..260

/organism="Brugia malayi"

/clone="RRAMCA026"

/strain="TRS Labs"

<1..>260

mRNA BASE COUNT 103 a 35 c 62 g 60 t

ORIGIN

Query Match

66.7%; Score 14; DB 26; Length 260;

Best Local Similarity 100.0%; Pred. No. 1.03e-01;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 244 ttctagattggatg 257

|||||

Cp 18 TTCTAGATTGGATG 5

Search completed: Wed Mar 19 08:18:47 1997

Job time : 65 secs.

Mar 19 08:15

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WAVES  
\*\*\*\*\*  
(TM)  
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MPPerch\_nm n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed Mar 19 08:17:07 1997; MasPar time 10.33 Seconds  
177.345 Million cell updates/sec  
Tabular output not generated.

Title: >US-08-612-929-17  
Description: (1-21) from US08612929.seq  
Perfect Score: 21  
N.A. Sequence: 1 CCGTCATCCATCTAGACTCT 21  
Comp: CCGCTAGCTTAGCTTACG

Scoring table: TABLE default  
Gap 10

Nmatch STD : Dbase 0; Query 0

Searched: 113505 seqs, 43611913 bases x 2

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: n-gensseq25  
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13  
14:part14 15:part15 16:part16 17:part17 18:part18  
19:part19 20:part20 21:part21 22:part22

Statistics: Mean 5.314; Variance 3.041; scale 1.747

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Match	Length	ID	Description	Pred. No.
c	1	21	100.0	51	14	Q83510 IL-4 CDR2 gene fragme	4.15e-03
	2	21	100.0	55	14	Q83509 IL-4 CDR2 gene fragme	4.15e-03
	3	21	100.0	333	11	Q65554 Mouse anti-HIV mu5.5	4.15e-03
	4	21	100.0	333	12	Q70376 Chimeric anti HIV ant	4.15e-03
	5	21	100.0	333	11	Q65558 Mouse-human chimeric	4.15e-03
	6	21	100.0	333	12	Q70372 Anti HIV antibody lig	4.15e-03
	7	21	100.0	334	1	N90492 Gene fragment of immu	4.15e-03
	8	21	100.0	393	6	Q36609 Anti-CD4 antibody WT	4.15e-03

Mar 19 08:15

US-08-612-929-17.mg

2

9 21 100.0 393 14 Q73986 Humanized antibody 3B 4.15e-03  
10 21 100.0 393 14 Q83520 Humanized antibody 3B 4.15e-03  
11 21 100.0 396 14 Q83490 Mouse MAb 3B9 Light c 4.15e-03  
12 21 100.0 733 4 Q25658 Mouse 0.5beta anti-HI 4.15e-03  
13 21 100.0 780 1 N90458 A V chi region gene. 4.15e-03  
14 21 100.0 900 1 Q04039 Anti-Leu 3a Light cha 6.13e-02  
15 19 90.5 397 1 Q04041 Anti-Leu 3a Light cha 6.13e-02  
c 16 17 81.0 31 17 T08708 Human antibody light 8.33e-01  
17 17 81.0 91 9 Q51746 Oligonucleotide probe 8.33e-01  
18 17 81.0 333 17 T06051 Murine NM-01 variable 8.33e-01  
19 17 81.0 333 14 Q82818 Murine 206 antibody v 8.33e-01  
20 17 81.0 333 11 Q63908 Light chain variable 8.33e-01  
21 17 81.0 333 12 Q71286 Light chain variable 8.33e-01  
22 17 81.0 334 11 Q73749 Light chain variable 8.33e-01  
23 17 81.0 334 9 Q55002 Murine anti-CD18 Ab 6 8.33e-01  
24 17 81.0 334 9 Q49617 Light chain variable 8.33e-01  
25 17 81.0 336 2 Q12684 Murine 1B4 light chai 8.33e-01  
26 17 81.0 336 16 Q74148 Human thyroid stimula 8.33e-01  
27 17 81.0 336 15 Q97506 Light chain variable 8.33e-01  
28 17 81.0 336 16 Q96285 Human IgE receptor-bi 8.33e-01  
29 17 81.0 336 2 Q10379 Chimeric MAB 9.2.27 1 8.33e-01  
30 17 81.0 336 16 Q98534 V1 coding sequence fr 8.33e-01  
31 17 81.0 336 16 Q96283 Human IgE receptor-bi 8.33e-01  
32 17 81.0 363 6 Q37472 Sequence encoding the 8.33e-01  
33 17 81.0 393 5 Q30757 p64-k4. 8.33e-01  
34 17 81.0 393 5 Q30757 pl2-k2. 8.33e-01  
35 17 81.0 393 6 Q34575 Antibody 4A2 light ch 8.33e-01  
36 17 81.0 399 16 Q92501 Mouse antibody FB3-2 8.33e-01  
37 17 81.0 632 10 Q56690 Genomic sequence of t 8.33e-01  
38 17 81.0 632 10 Q56691 Anti-EGFR single chai 8.33e-01  
39 17 81.0 717 18 T04019 Mouse antibody F4-7 1 8.33e-01  
40 17 81.0 723 16 Q92503 Anti-CS MAB N19/8 scF 8.33e-01  
41 17 81.0 783 17 T08490 Encodes kappa Light c 8.33e-01  
42 17 81.0 1014 2 Q10834 Rei light chain varia 2.96e+00  
43 16 76.2 39 2 Q12689 Rei light chain varia 2.96e+00  
c 44 16 76.2 41 2 Q12688

ALIGNMENTS

RESULT 1  
ID Q83510 standard; DNA; 51 BP.  
AC Q83510;  
DT 20-SEP-1995 (first entry)  
DE IL-4 CDR2 gene fragment.  
KW Humanized antibody; antibody engineering; monoclonal antibody;  
KW MAb; interleukin-4; IL-4; allergy; heavy chain; CDR;  
KW complementarity determining region; se.  
OS Synthetic.  
PN W09507301-A.  
PD 16-MAR-1995.  
PF 07-SEP-1994; U10308.  
PR 07-SEP-1993; US-117366.  
PR 14-OCT-1993; US-136783.  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
PI (SMIK ) SMITHKLINE BEECHAM PLC.  
PI Gross MS, Holmes SD, Sylvester DR;  
PT WPI; 95-123387/16.  
PT Chimeric and humanized IL-4 monoclonal antibodies (mAbs), derived  
PT from high affinity mAbs - useful in treatment of IL-4-mediated  
PT and IgE-mediated allergic conditions  
PS Example 3; Page 28; 97pp; English.  
CC A humanized antibody was designed to contain mouse CDRs (from

CC anti-IL-4 Mab 3B9 Mab) within a human antibody framework. A  
CC synthetic heavy chain was made using the oligonucleotides given  
CC in Q83498-502 and amplified by PCR using the primers given in  
CC Q83503-04. The construct was ligated into vector pCD, along  
CC with a signal sequence (Q83494) and an IgG1 human constant  
CC region. The CDR gene regions of a pre-existing light chain  
CC framework were replaced with synthetic IL-4 CDR genes constructed  
CC from oligonucleotides given in Q83505-08 (CDR1), Q83509-10 (CDR2),  
CC and Q83511-12 (CDR3). The synthetic VL (Q73986) was ligated into  
CC the vector. The anti-IL4 engineered antibody was expressed in  
CC COS and CHO cells.  
SQ Sequence 51 BP; 14 A; 12 C; 14 G; 11 T;

Query Match 100.0%; Score 21; DB 14; Length 51;

Best Local Similarity 100.0%; Pred. No. 4.15e-03;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 4 agattctagattggtgcagc 24

|||||

Cp 21 AGATTCTAGATTGGATGCAGC 1

## RESULT 2

ID Q83509 standard; DNA; 55 BP.

AC Q83509;

DT 20-SEP-1995 (first entry)

DE IL-4 CDR2 gene fragment.

KW Humanized antibody; antibody engineering; monoclonal antibody;

KW Mab; interleukin-4; IL-4; allergy; heavy chain; CDR;

KW complementarity determining region; ss.

OS Synthetic.

PN W09507301-A.

PD 16-MAR-1995.

PF 07-SEP-1994; U10308.

PR 07-SEP-1993; US-117366.

PR 14-OCT-1993; US-136783.

PA (SMIK ) SMITHKLINE BEECHAM CORP.

PA (SMIK ) SMITHKLINE BEECHAM PLC.

PI Gross MS, Holmes SD, Sylvester DR;

DR WPI; 95-123387/16.

PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived

PT from high affinity mAbs - useful in treatment of IL-4-mediated

PT and IgE-mediated allergic conditions

PS Example 3; Page 28; 9/pp; English.

CC A humanized antibody was designed to contain mouse CDRs (from

CC anti-IL-4 Mab 3B9 Mab) within a human antibody framework. A

CC synthetic heavy chain was made using the oligonucleotides given

CC in Q83498-502 and amplified by PCR using the primers given in

CC Q83503-04. The construct was ligated into vector pCD, along

CC with a signal sequence (Q83494) and an IgG1 human constant

CC region. The CDR gene regions of a pre-existing light chain

CC framework were replaced with synthetic IL-4 CDR genes constructed

CC from oligonucleotides given in Q83505-08 (CDR1), Q83509-10 (CDR2),

CC and Q83511-12 (CDR3). The synthetic VL (Q73986) was ligated into

CC the vector. The anti-IL4 engineered antibody was expressed in

CC COS and CHO cells.

SQ Sequence 55 BP; 12 A; 15 C; 13 G; 15 T;

Query Match 100.0%; Score 21; DB 14; Length 55;

Best Local Similarity 100.0%; Pred. No. 4.15e-03;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 28 gctgcattccattctagaatct 48

|||||

Qy 1 GCTGCATCCAATCTAGAAATCT 21

## RESULT 3

ID Q65554 standard; cDNA; 333 BP.

AC Q65554;

DT 27-JAN-1995 (first entry)

DE Mouse anti-HIV mu5.5 light chain variable region cDNA.

KW Immunoglobulin; light chain; anti-HIV antibody; neutralisation;

KW human immunodeficiency virus; variable region; VL chain; murine; ds.

OS Mus musculus.

FH Key Location/Qualifiers

FT misc\_feature 70..114

FT /tag= a

FT /note= "encodes CDR1"

FT misc\_feature 160..180

FT /tag= b

FT /note= "encodes CDR2"

FT misc\_feature 277..303

FT /tag= c

FT /note= "encodes CDR3"

PN J06125783-A.

PD 10-MAY-1994.

PF 28-DEC-1991; 359808.

PR 28-DEC-1991; JP-359808.

PA (KAGA-) 2H KAGAKU KESSEI-RYOHO KENKYUSHO.

DR WPI; 94-187942/23.

DR P-PSDB; R55123.

PT Mouse-human chimeric anti-HIV antibody heavy and light chains -

PT and recombinant antibody consisting of the H- and L-chains,

PT useful in AIDS therapy

PS Example 3; Fig 4; 22pp; Japanese.

CC Murine monoclonal antibodies mu 39.1 and mu 5.5 both neutralise HIV.

CC The heavy and light chain variable regions from these antibodies

CC were sequenced (Q65551-Q65554). The murine anti-HIV CDRs were

CC introduced into human framework regions to construct chimeric

CC antibodies (Q65555-Q65558).

SQ Sequence 333 BP; 88 A; 83 C; 86 G; 76 T;

Query Match 100.0%; Score 21; DB 11; Length 333;

Best Local Similarity 100.0%; Pred. No. 4.15e-03;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 160 gctgcattccattctagaatct 180

|||||

Qy 1 GCTGCATCCAATCTAGAAATCT 21

## RESULT 4

ID Q70376 standard; cDNA to mRNA; 333 BP.

AC Q70376;

DT 13-MAR-1995 (first entry)

DE Chimeric anti HIV antibody light chain variable region.

KW Antibody; heavy chain; light chain; human immunodeficiency virus;

KW HIV; acquired immune deficiency syndrome; AIDS; treatment;

KW prophylaxis; Mus musculus; Homo sapiens; ss.

OS Chimeric Homo sapiens

OS Chimeric Mus musculus.

FH Key Location/Qualifiers

FT CDS 1..333

FT /tag= a

FT /product= Antibody light chain variable region.

PN W09415969-A.

PD 21-JUL-1994.



Mar 19 08:15

US-08-612-929-17.rng

5

PF 14-JAN-1993; J00039.  
 PR 14-JAN-1993; AU-032671.  
 PR 14-JAN-1993; WO-J00039.  
 PA (KAGA ) CHERO SERO THERAPEUTIC RES INST.  
 PI Eda Y, Kimachi K, Maeda H, Osatomi K, Shiosaki K;  
 PI Tokiyoshi S;  
 DR WPI; 94-249145/30.  
 DR P-PSDB; R60306.  
 PT Recombinant chimeric anti HIV antibody - useful for the treatment  
 PT and prevention of HIV  
 PS Claim 14; Figure 12; 51pp; Japanese.  
 CC The recombinant antibody light chain has neutralising activity  
 CC against HIV. Chimeric antibodies comprising both mouse and human  
 CC sequences are useful in the treatment/prevention of AIDS caused by  
 CC HIV. This sequence is derived from the mu5.5 anti HIV monoclonal  
 CC antibody producing cell.  
 SQ Sequence 333 BP; 95 A; 90 C; 88 G; 60 T;

Query Match 100.0%; Score 21; DB 12; Length 333;  
 Best Local Similarity 100.0%; Pred. No. 4.15e-03;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 160 gctgcattcaatctagaatct 180  
 |||||  
 QY 1 GCTGCATCCAATCTAGAATCT 21

# RESULT 5

ID Q65558 standard; cDNA; 333 BP.  
 AC Q65558;  
 DT 30-JAN-1995 (first entry)  
 DE Mouse-human chimeric anti-HIV mu5.5-derived light chain V region.  
 KW Immunoglobulin; heavy chain; anti-HIV antibody; neutralisation;  
 KW human immunodeficiency virus; variable region; VL chain; murine;  
 KW chimeric; humanised; ds.  
 OS Chimeric Mus musculus.  
 OS Chimeric Homo sapiens.  
 FH Key Location/Qualifiers  
 FT misc feature 70..114  
 FT /\*tag= a  
 FT /\*note= "encodes murine CDR1"  
 FT misc feature 160..180  
 FT /\*tag= b  
 FT /\*note= "encodes murine CDR2"  
 FT misc feature 277..303  
 FT /\*tag= c  
 FT /\*note= "encodes murine CDR3"  
 PN J06125783-A.  
 PD 10-MAY-1994.  
 PF 28-DEC-1991; 359808.  
 PR 28-DEC-1991; JP-359808.  
 PA (KAGA-) 2H KAGAKU KESSEI-RYOHO KENKYUSHO.  
 DR WPI; 94-187942/23.  
 DR P-PSDB; R55127.  
 PT Mouse-human chimeric anti-HIV antibody heavy and light chains -  
 PT and recombinant antibody consisting of the H- and L-chains,  
 PT useful in AIDS therapy  
 PS Claim 5; Fig 12; 22pp; Japanese.  
 CC Murine monoclonal antibodies mu 39.1 and mu 5.5 both neutralise HIV.  
 CC The heavy and light chain variable regions from these antibodies  
 CC were sequenced (Q65551-Q65554). The murine anti-HIV CDRs were  
 CC introduced into human framework regions to construct chimeric  
 CC antibodies (Q65555-Q65558).  
 SQ Sequence 333 BP; 95 A; 90 C; 88 G; 60 T;

Mar 19 08:15

US-08-612-929-17.rng

6

Query Match 100.0%; Score 21; DB 11; Length 333;  
 Best Local Similarity 100.0%; Pred. No. 4.15e-03;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 160 gctgcattcaatctagaatct 180  
 |||||  
 QY 1 GCTGCATCCAATCTAGAATCT 21

# RESULT 6

ID Q70372 standard; cDNA to mRNA; 333 BP.  
 AC Q70372;  
 DT 09-MAR-1995 (first entry)  
 DE Anti HIV antibody light chain variable region.  
 KW Antibody; heavy chain; light chain; human immunodeficiency virus;  
 KW HIV; acquired immune deficiency syndrome; AIDS; treatment;  
 KW prophylaxis; Mus musculus; Homo sapiens; ss.  
 OS Mus musculus.  
 FH Key Location/Qualifiers  
 FT CDS 1..333  
 FT /\*tag= a  
 FT /\*product= Antibody light chain variable region.  
 PN W09415969-A.  
 PD 21-JUL-1994.  
 PF 14-JAN-1993; J00039.  
 PR 14-JAN-1993; AU-032671.  
 PR 14-JAN-1993; WO-J00039.  
 PA (KAGA ) CHERO SERO THERAPEUTIC RES INST.  
 PI Eda Y, Kimachi K, Maeda H, Osatomi K, Shiosaki K;  
 PI Tokiyoshi S;  
 DR WPI; 94-249145/30.  
 DR P-PSDB; R60302.  
 PT Recombinant chimeric anti HIV antibody - useful for the treatment  
 PT and prevention of HIV  
 PS Claim 15; Figure 4; 51pp; Japanese.  
 CC The recombinant antibody light chain has neutralising activity  
 CC against HIV. Chimeric antibodies comprising both mouse and human  
 CC sequences are useful in the treatment/prevention of AIDS caused by  
 CC HIV. This sequence is obtained from the mu5.5 anti HIV monoclonal  
 CC antibody producing cell.  
 SQ Sequence 333 BP; 88 A; 83 C; 86 G; 76 T;

Query Match 100.0%; Score 21; DB 12; Length 333;  
 Best Local Similarity 100.0%; Pred. No. 4.15e-03;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 160 gctgcattcaatctagaatct 180  
 |||||  
 QY 1 GCTGCATCCAATCTAGAATCT 21

# RESULT 7

ID N90492 standard; DNA; 334 BP.  
 AC N90492;  
 DT 20-OCT-1989 (first entry)  
 DE Gene fragment of immunoglobulin L chain variable region.  
 KW Gene fragment; immunoglobulin; L chain variable region; HIV.  
 OS Mus musculus  
 FH Key Location/Qualifiers  
 FT CDS 1..333  
 FT /\*tag= a  
 PN EP-327000-A.  
 PD 09-AUG-1989.

PF 30-JAN-1989; 101583.  
 PR 30-JAN-1988; JP-20255.  
 PR 08-JUL-1988; JP-171385.  
 PA (KAGA) The Chemo-Sero-Therapeutic Research Institute.  
 PI Maeda H, Eda Y, Kimachi K, Tokiyoshi S, Mateushita S, Hattori T,  
 PI Takatsuki K;  
 DR WPI; 89-229050/32.  
 PT Chimeric anti-human immune virus antibodies - contg. mouse variable  
 PT regions and human constant regions for diagnosis, treatment and  
 PT prevention of AIDS  
 PS Claim 6; page 15; 33pp; English.  
 CC The gene fragment encodes an L chain variable region from an  
 CC immunoglobulin with anti-HIV neutralising activity. It is used, with an  
 CC H chain variable region gene fragment (see N90491), to produce a chimeric  
 CC anti-HIV antibody with mouse variable regions and human constant regions.  
 CC The antibody retains its original specificity, but have much lower  
 CC antigenicity to humans. See also p90541, N90493 and N90495.  
 SQ Sequence 334 BP; 91 A; 83 C; 81 G; 79 T;

Query Match 100.0%; Score 21; DB 1; Length 334;  
 Best Local Similarity 100.0%; Pred. No. 4.15e-03;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 160 gctgcattcaatctagaatct 180  
 |||||  
 QY 1 GCTGCATCCAATCTAGAAATCT 21

RESULT 8  
 ID Q36609 standard; DNA; 393 BP.  
 AC Q36609;  
 DT 02-JUN-1993 (first entry)  
 DE Anti-CD4 antibody MT 3.10 light chain variable region.  
 KW immunosuppression; tissue transplantation; graft; L chain; V region;  
 KW T-helper cell inhibition; transplant rejection; MAb;  
 KW interleukin-2 receptor; ss.  
 FH Key Location/Qualifiers  
 FT sig\_peptide 1..60  
 FT /tag= a  
 FT mat\_peptide 61..393  
 FT /tag= b  
 FT /note= "J1 region begins at position 361"  
 PN DE4143214-A.  
 PD 28-JAN-1993.  
 PF 30-DEC-1991; 143214.  
 PR 25-JUL-1991; DE-124759.  
 PR 30-DEC-1991; DE-143214.  
 PA (BOEF) BOEHRINGER MANNHEIM GMBH.  
 PI Kaluza B, Rietmuller G, Scheuer W, Weidle U;  
 DR WPI; 93-037582/05.  
 DR P-PSDB; R32123.  
 PT Synergistic antibody compsn. for use as immunosuppressant -  
 PT comprises monoclonal anti-CD4 antibodies and monoclonal anti-IL2R  
 PT alpha- or anti-IL2R beta antibodies  
 PS Claim 5; Page 11; 18pp; German.  
 CC This sequence encodes the light chain variable region of a preferred  
 CC anti-CD4 monoclonal antibody for use in the claimed synergistic  
 CC composition. MAB MT 3.10 is deposited as clone 3.101/sB10 (ECACC  
 CC 90090702). The anti-CD4 antibody is used with at least one anti-IL2R  
 CC alpha or beta antibody. Individually the antibodies are strongly  
 CC inhibiting and when used together their immunosuppressive properties  
 CC are improved; they synergistically inhibit T-helper cell  
 CC proliferation to effectively inhibit transplant rejection at low  
 CC doses without significantly reducing the general immune response.

CC See Q36607-Q36616.  
 SQ Sequence 393 BP; 100 A; 105 C; 98 G; 90 T;

Query Match 100.0%; Score 21; DB 6; Length 393;  
 Best Local Similarity 100.0%; Pred. No. 4.15e-03;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 220 gctgcattcaatctagaatct 240  
 |||||  
 QY 1 GCTGCATCCAATCTAGAAATCT 21

RESULT 9  
 ID Q73986 standard; cDNA; 393 BP.  
 AC Q73986;  
 DT 20-SEP-1995 (first entry)  
 DE Humanized antibody 3B9 light chain.  
 KW Humanized antibody; antibody engineering; monoclonal antibody;  
 KW MAb; interleukin-4; IL-4; allergy; ds.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT CDS 1..393  
 FT /tag= a  
 FT sig\_peptide 1..60  
 FT /tag= b  
 FT mat\_peptide 61..393  
 FT /tag= c  
 PN W09507301-A.  
 PD 16-MAR-1995.  
 PE 07-SEP-1994; US-117366.  
 PR 07-SEP-1993; US-117366.  
 PR 14-OCT-1993; US-136783.  
 PA (SMIK) SMITHKLINE BEECHAM CORP.  
 PA (SMIK) SMITHKLINE BEECHAM PLC.  
 PI Gross MS, Holmes SD, Sylvester DR;  
 DR WPI; 95-123387/16.  
 DR P-PSDB; R75355.  
 PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived  
 PT from high affinity mAbs - useful in treatment of IL-4-mediated  
 PT and IgE-mediated allergic conditions  
 PS Disclosure: Fig. 5; 97pp; English.  
 CC A humanized antibody light chain variable region and signal  
 CC sequence is given in R75355. The signal sequence is also  
 CC provided in R70194. The sequences of the first 2 CDRs  
 CC are identical to mouse anti-human IL-4 MAb 3B9 light chain  
 CC CDRs (given in R70195-96), but the third (R70201) differs  
 CC by a single amino acid from the native mouse CDR (R70197).  
 SQ Sequence 393 BP; 97 A; 96 C; 108 G; 92 T;

Query Match 100.0%; Score 21; DB 14; Length 393;  
 Best Local Similarity 100.0%; Pred. No. 4.15e-03;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 217 gctgcattcaatctagaatct 237  
 |||||  
 QY 1 GCTGCATCCAATCTAGAAATCT 21

RESULT 10  
 ID Q83520 standard; cDNA; 393 BP.  
 AC Q83520;  
 DT 20-SEP-1995 (first entry)  
 DE Humanized antibody 3B9 light chain.  
 KW Humanized antibody; antibody engineering; monoclonal antibody;

Mar 19 08:15

US-08-612-929-17.mg

9

KW MAb; interleukin-4; IL-4; allergy; ds.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT CDS 1..393  
FT /tag= a  
PN W09507301-A.  
PD 16-MAR-1995.  
PF 07-SEP-1994; U10308.  
PR 07-SEP-1993; US-117366.  
PR 14-OCT-1993; US-136783.  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
PA (SMIK ) SMITHKLINE BEECHAM PLC.  
PI Gross MS, Holmes SD, Sylvester DR;  
DR WPI; 95-123387/16.  
DR P-PSDB; R70202.  
PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived from high affinity mAbs - useful in treatment of IL-4-mediated PT and IgE-mediated allergic conditions  
PS Disclosure; Page 71-72; 97pp; English.  
CC A humanized antibody light chain variable region and signal sequence is given in R75355. The signal sequence is also provided in R70194. The sequences of the 3 CDRs are identical to mouse anti-human IL-4 MAb 3B9 light chain CC CDRs (given in R70195-97).  
SQ Sequence 393 BP; 97 A; 98 C; 105 G; 93 T;

Query Match 100.0%; Score 21; DB 14; Length 393;  
Best Local Similarity 100.0%; Pred. No. 4.15e-03;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 217 gctgcacccaatcagaatct 237  
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QY 1 GCTGCATCCAATCTAGAACTCT 21

RESULT 11  
ID Q83490 standard; cDNA; 396 BP.  
AC Q83490;  
DT 20-SEP-1995 (first entry)  
DE Mouse MAb 3B9 light chain.  
KW Chimeric antibody; humanized antibody; antibody engineering;  
KW monoclonal antibody; MAb; interleukin-4; IL-4; allergy; ds.  
OS Mus sp.  
FH Key Location/Qualifiers  
FT CDS 1..396  
FT /tag= a  
FT sig\_peptide 1..60  
FT /tag= b  
FT mat\_peptide 61..396  
FT /tag= c  
PN W09507301-A.  
PD 16-MAR-1995.  
PF 07-SEP-1994; U10308.  
PR 07-SEP-1993; US-117366.  
PR 14-OCT-1993; US-136783.  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
PA (SMIK ) SMITHKLINE BEECHAM PLC.  
PI Gross MS, Holmes SD, Sylvester DR;  
DR WPI; 95-123387/16.  
DR P-PSDB; R70189.  
PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived from high affinity mAbs - useful in treatment of IL-4-mediated PT and IgE-mediated allergic conditions  
PS Disclosure; Fig.1; 97pp; English.

Mar 19 08:15

US-08-612-929-17.mg

10

CC Spleen cells from mice immunised with human IL-4 were used to prepare CC hybridomas, which were screened for anti-IL-4 MAb secretion. Only CC clone 3B9 was positive. cDNA clones of the 3B9 light and heavy CC chains were cloned into pGEM7f+ and transformed into E. coli CC DH5-alpha. The clones were sequenced (Q83490-91), and used for CC antibody engineering.  
SQ Sequence 396 BP; 99 A; 103 C; 103 G; 91 T;

Query Match 100.0%; Score 21; DB 14; Length 396;  
Best Local Similarity 100.0%; Pred. No. 4.15e-03;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 220 gctgcacccaatcagaatct 240  
|||||  
QY 1 GCTGCATCCAATCTAGAACTCT 21

RESULT 12  
ID Q25658 standard; DNA; 733 BP.  
AC Q25658;  
DT 08-DEC-1992 (first entry)  
DE Mouse 0.5beta anti-HIV antibody Light chain.  
KW Heavy; Light; CDR; HIV; AIDS; FR; framework region; ds.  
OS Synthetic.  
FH Key Location/Qualifiers  
FT primer\_bind complement (77..106)  
FT /tag= a  
FT /note= "binding site for the primer  
FT represented Q30550"  
FT primer\_bind 709..730  
FT /tag= b  
FT /note= "binding site for the primer  
FT represented Q30551"  
PN J04141095-A.  
PD 14-MAY-1992.  
PF 02-OCT-1990; 266091.  
PR 02-OCT-1990; JP-266091.  
PA (KAGA ) KAGAKU OYOBI KESSEI RYOHO.  
DR WPI; 92-212765/26.  
PT New recombinant modified anti-HIV antibodies - comprise human x PT mouse modified antibody H and L chains  
PS Disclosure; Fig 4; 15pp; Japanese.  
CC Recombinant modified anti-HIV antibodies comprise framework regions CC derived from human antibody and CDRs derived from mouse monoclonal CC antibody 0.5beta. The anti-HIV modified antibody can be used for CC the prophylaxis and treatment of AIDS.  
SQ Sequence 733 BP; 194 A; 162 C; 161 G; 216 T;

Query Match 100.0%; Score 21; DB 4; Length 733;  
Best Local Similarity 100.0%; Pred. No. 4.15e-03;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 541 gctgcacccaatcagaatct 561  
|||||  
QY 1 GCTGCATCCAATCTAGAACTCT 21

RESULT 13  
ID N90495 standard; DNA; 780 BP.  
AC N90495;  
DT 24-OCT-1989 (first entry)  
DE A V chi region gene.  
KW V chi region gene; immunoglobulin; L chain variable region; HIV.  
OS Mus musculus.

FH Key Location/Qualifiers  
FT exon 119..167  
FT /\*tag= a 398..742  
FT exon /\*tag= b  
PN EP-327000-A.  
PD 09-AUG-1989. 101583.  
PR 30-JAN-1988; JP-20255.  
PR 08-JUL-1988; JP-171385.  
PA (KAGA ) The Chemo-Sero-Therapeutic Research Institute.  
PI Maeda H, Eda Y, Kimachi K, Tokiyoshi S, Mateushita S, Hattori T,  
PI Takatsuki K;  
DR WPI; 89-229050/32.  
DR P-PSDB; P90543.  
PT Chimeric anti-human immune virus antibodies - contg. mouse variable  
PT regions and human constant regions for diagnosis, treatment and  
PT prevention of AIDS  
PS Disclosure; Fig 7; 33pp; English.  
CC The sequence is a chi region gene, encoding an L chain variable region  
CC (see P90543). See also N90491-3.  
SQ Sequence 780 BP; 205 A; 172 C; 171 G; 232 T;

Query Match 100.0%; Score 21; DB 1; Length 780;  
Best Local Similarity 100.0%; Pred. No. 4.15e-03;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 568 gctgcattcccaatctagaatct 588  
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QY 1 GCTGCATCCAATCTAGAAATCT 21

RESULT 14  
ID Q04039 standard; DNA; 900 BP.  
AC Q04039;  
DT 06-SEP-1990 (first entry)  
DE Anti-leu 3a light chain variable region gene, 206 Vx.  
KW HIV; AIDS; anti-leu3A; vaccine; ds.  
OS Mus musculus.  
FH Key Location/Qualifiers  
FT exon 259..307  
FT /\*tag= a  
FT intron 308..537  
FT /\*tag= b  
FT exon 538..882  
FT /\*tag= c  
PN EP-365209-A.  
PD 25-APR-1990.  
PE 11-OCT-1989; 010415.  
PR 17-OCT-1988; US-260558.  
PA (BECT) Becton Dickinson Co.  
PI Hinton R, Oi VT;  
DR WPI; 90-126329/17.  
DR P-PSDB; R04132.  
PT New chimeric variants of murine antibody anti-leucine -  
PT contg. human antibody regions, and DNA encoding sequences.  
PS Claim 1; Fig 2; 12pp; English.  
CC Variants of murine monoclonal anti-CD4 antibody, anti-leu3A can be  
CC used to form chimeric mouse-variable, human-constant region Abs  
CC suggested as being useful as a vaccine to HIV.  
SQ Sequence 900 BP; 261 A; 206 C; 187 G; 246 T;

Query Match 100.0%; Score 21; DB 1; Length 900;  
Best Local Similarity 100.0%; Pred. No. 4.15e-03;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 708 gctgcattcccaatctagaatct 728  
|||||  
QY 1 GCTGCATCCAATCTAGAAATCT 21

RESULT 15  
ID Q04041 standard; DNA; 397 BP.  
AC Q04041;  
DT 06-SEP-1990 (first entry)  
DE Anti-leu 3a light chain variable region gene, KOL/206 V1.  
KW HIV; AIDS; anti-leu3A; vaccine; ds.  
OS Mus musculus.  
FH Key Location/Qualifiers  
FT exon 43..387  
FT /\*tag= a  
PN EP-365209-A.  
PD 25-APR-1990.  
PE 11-OCT-1989; 010415.  
PR 17-OCT-1988; US-260558.  
PA (BECT) Becton Dickinson Co.  
PI Hinton R, Oi VT;  
DR WPI; 90-126329/17.  
DR P-PSDB; R04134.  
PT New chimeric variants of murine antibody anti-leucine -  
PT contg. human antibody regions, and DNA encoding sequences.  
PS Claim 4; Fig 4; 12pp; English.  
CC Variants of murine monoclonal anti-CD4 antibody, anti-leu3A can be  
CC used to form chimeric mouse-variable, human-constant region Abs  
CC suggested as being useful as a vaccine to HIV.  
SQ Sequence 397 BP; 105 A; 99 C; 84 G; 109 T;

Query Match 90.5%; Score 19; DB 1; Length 397;  
Best Local Similarity 95.2%; Pred. No. 6.13e-02;  
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 210 gctgcattcccaatctagaatct 230  
|||||  
QY 1 GCTGCATCCAATCTAGAAATCT 21

Search completed: Wed Mar 19 08:17:22 1997  
Job time : 15 secs.

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WVPPREH (TM)

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MPsrch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed Mar 19 15:54:13 1997; MafPar time 51.42 Seconds  
Tabular output not generated. 336.386 Million cell updates/sec

Title: >US-08-612-929-17  
Description: (1-21) from US08612929.seq  
Perfect Score: 21  
N.A. Sequence: 1 GCTGCATCCAACTAGAACTCT 21  
Comp: CGACGTAGCTTAGACTTAGA

Scoring table: TABLE default  
Gap 10

Nmatch STD : Dbase 0; Query 0

Searched: 279077 seqs, 411808665 bases x 2

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: emb1-new5  
1: BCT 2: FUN 3: INV1 4: INV2 5: ORG 6: MAM 7: VRT 8: PLN 9: PRI  
10: PRO1 11: PRO2 12: ROD 13: SYN 14: UNC 15: VIR

Database: genbank94  
16: BCT1 17: BCT2 18: BCT3 19: BCT4 20: BCT5 21: BCT6 22: BCT7  
23: BCT8 24: BCT9 25: INV1 26: INV2 27: INV3 28: INV4 29: INV5  
30: INV6 31: INV7 32: MAM1 33: MAM2 34: MAM3 35: VRT1 36: VRT2  
37: VRT3 38: PAT1 39: PAT2 40: PAT3 41: PHG 42: PLN1 43: PLN2  
44: PLN3 45: PLN4 46: PLN5 47: PLN6 48: PLN7 49: PLN8 50: PRI1  
51: PRI2 52: PRI3 53: PRI4 54: PRI5 55: PRI6 56: PRI7 57: PRI8  
58: PRI9 59: PRI10 60: PRI11 61: PRI12 62: PRI13 63: ROD1  
64: ROD2 65: ROD3 66: ROD4 67: ROD5 68: ROD6 69: ROD7 70: ROD8  
71: STR 72: SYN 73: UNA 74: VRL1 75: VRL2 76: VRL3 77: VRL4  
78: VRL5 79: VRL6 80: VRL7 81: VRL8

Database: genbank-new5  
82: BCT 83: INV1 84: INV2 85: MAM 86: VRT 87: PAT 88: PHG

Database: u-emb146\_94  
89: PLN 90: PRI 91: ROD 92: STR 93: SYN 94: UNA 95: VRL  
96: part1

Statistics: Mean 6.819; Variance 2.532; scale 2.693

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	21	100.0	195 66	MUSIGKAAAC	Mouse Igk chain mRNA,	5.82e-04
2	21	100.0	195 66	MUSIGKAAAB	Mouse Igk chain mRNA,	5.82e-04
3	21	100.0	228 65	MMU18577	Mus musculus immunogl	5.82e-04
4	21	100.0	238 65	MMU18563	Mus musculus immunogl	5.82e-04
5	21	100.0	255 64	MMIGKVRD	M.musculus immunoglob	5.82e-04
6	21	100.0	262 64	MMIGKVRP	M.musculus immunoglob	5.82e-04
7	21	100.0	264 64	MMIGKVRP	M.musculus immunoglob	5.82e-04
8	21	100.0	266 64	MMIGKVRP	M.musculus immunoglob	5.82e-04
9	21	100.0	270 64	MMIGKVRG	M.musculus immunoglob	5.82e-04
10	21	100.0	270 64	MMIGKVRP	M.musculus immunoglob	5.82e-04
11	21	100.0	270 64	MMIGKVRB	M.musculus immunoglob	5.82e-04
12	21	100.0	279 66	MUSIGKAAA	Mouse Igk chain mRNA,	5.82e-04
13	21	100.0	286 65	MMU29628	Mus musculus anti-DNA	5.82e-04
14	21	100.0	292 65	MMU18599	Mus musculus immunogl	5.82e-04
15	21	100.0	297 65	MMU29629	Mus musculus anti-DNA	5.82e-04
16	21	100.0	313 70	S74550	Ig V kappa -rheumatoi	5.82e-04
17	21	100.0	317 67	MUSIGVACR	Mus musculus Ig rearr	5.82e-04
18	21	100.0	318 66	MUSIGVKB	Mouse immunoglobulin	5.82e-04
19	21	100.0	333 70	S42888	Ig V kappa -immunogl	5.82e-04
20	21	100.0	333 67	MUSIGLSB	Mouse Igl chain H2L2	5.82e-04
21	21	100.0	336 64	MMIGLC40	M.musculus mRNA for I	5.82e-04
22	21	100.0	336 67	MUSIGVAP	Mus musculus Ig rearr	5.82e-04
23	21	100.0	336 64	MMIGLC413	M.musculus mRNA for I	5.82e-04
24	21	100.0	336 64	MMIGLC310	M.musculus mRNA for I	5.82e-04
25	21	100.0	350 66	MUSIGKABC	Mouse Ig kappa chain	5.82e-04
26	21	100.0	353 66	MUSIGKABBE	Mouse Ig kappa chain	5.82e-04
27	21	100.0	354 67	MUSL71IGKV	Mouse hybridoma Ig re	5.82e-04
28	21	100.0	360 67	MUSIGKAF	Mouse Ig active kappa	5.82e-04
29	21	100.0	363 67	MUSL93IGKV	Mouse hybridoma Ig re	5.82e-04
30	21	100.0	363 67	MUSL2021GK	Mouse hybridoma Ig re	5.82e-04
31	21	100.0	393 70	S50265	Ig VL=anti-CD4 mAb M-	5.82e-04
32	21	100.0	900 40	I08223	Sequence 1 from paten	5.82e-04
33	19	90.5	245 64	MMIGKVRH	M.musculus immunoglob	2.34e-02
34	19	90.5	333 64	MMU07207	Mus musculus clone 31	2.34e-02
35	19	90.5	333 70	S54207	V kappa 21=immunoglob	2.34e-02
36	19	90.5	333 65	MMVL1E10	Mouse mRNA for kappa-	2.34e-02
37	19	90.5	351 66	MUSIGKABBH	Mouse Ig kappa chain	2.34e-02
38	19	90.5	353 66	MUSIGKABBG	Mouse Ig kappa chain	2.34e-02
39	19	90.5	353 66	MUSIGKABBD	Mouse Ig kappa chain	2.34e-02
40	19	90.5	363 67	MUSL341GKV	Mouse hybridoma Ig re	2.34e-02
41	19	90.5	397 40	I08225	Sequence 5 from paten	2.34e-02
42	19	90.5	671 67	MUSIGKVS	Mouse Ig germline kap	2.34e-02
43	17	81.0	276 91	MMU26472	Mus musculus nucleoso	7.83e-01
44	17	81.0	333 63	MMALDICH	M.musculus mRNA for a	7.83e-01
45	17	81.0	2707 89	SCTNR053C	S.cerevisiae chromoso	7.83e-01

## ALIGNMENTS

RESULT 1  
LOCUS MUSIGKAAAC 195 bp mRNA  
DEFINITION Mouse Igk chain mRNA, VJ1 region.  
ACCESSION M57980  
NID gi196406  
KEYWORDS J-region; V-region; anti-cytochrome c antibody;  
immunoglobulin kappa-chain; immunoglobulin light chain.  
SOURCE Mouse (BALB/c) secondary B cell hybridoma 2B5 mRNA, clone 2B5.F8.  
ORGANISM Mus musculus

Mar 19 15:53

US-08-612-929-17.rge

3

Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.

REFERENCE 1 (bases 1 to 195)  
AUTHORS Goshorn, S.C., Retzel, E. and Jemmerson, R.  
TITLE Common structural features among monoclonal antibodies binding the same antigenic region of cytochrome c  
JOURNAL J. Biol. Chem. 266 (4), 2134-2142 (1991)  
MEDLINE 91115823

FEATURES  
source  
1..195  
/organism="Mus musculus"  
/clone="2B5.F8"  
/strain="BALB/c"  
/sub\_species="domesticus"  
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/sequenced\_mol="cDNA to mRNA"  
/tissue\_type="hybridoma"  
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19..39  
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/gene="IgM"  
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/gene="IgM"  
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V\_region

CDS

misc\_feature

misc\_feature

J\_segment

BASE COUNT 52 a 50 c 51 g 42 t  
ORIGIN Chromosome 6.

Query Match 100.0%; Score 21; DB 66; Length 195;  
Best Local Similarity 100.0%; Pred. No. 5.82e-04;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 19 gctgcaccaatctagaatct 39  
|||||  
Qy 1 GCTGCATCCAACTAGAACT 21

RESULT 2

LOCUS MUSICKAAB 195 bp mRNA  
DEFINITION Mouse Igk chain mRNA, VJ5 region.  
ACCESSION M57979  
NID g196404  
KEYWORDS J-region; V-region; anti-cytochrome c antibody;  
immunoglobulin kappa-chain; immunoglobulin light chain.  
SOURCE Mouse (BALB/c) secondary B cell hybridoma 7d4 mRNA, clone 7d4.H4.  
ORGANISM Mus musculus

Mar 19 15:53

US-08-612-929-17.rge

4

Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.

REFERENCE 1 (bases 1 to 195)  
AUTHORS Goshorn, S.C., Retzel, E. and Jemmerson, R.  
TITLE Common structural features among monoclonal antibodies binding the same antigenic region of cytochrome c  
JOURNAL J. Biol. Chem. 266 (4), 2134-2142 (1991)  
MEDLINE 91115823

FEATURES  
source  
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/clone="7d4.H4"  
/strain="BALB/c"  
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/cell\_type="secondary B cell"  
/sequenced\_mol="cDNA to mRNA"  
/tissue\_type="hybridoma"  
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/map="chromosome 6"  
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/product="Ig kappa chain"  
/db\_xref="PID:g196405"  
/translation="PKLLIYAASNLESGIPARFGSGSGTDFTLNHPVEEDAATYY  
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19..39  
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136..162  
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/note="J5"

V\_region

CDS

misc\_feature

misc\_feature

J\_segment

BASE COUNT 47 a 54 c 50 g 44 t  
ORIGIN Chromosome 6.

Query Match 100.0%; Score 21; DB 66; Length 195;  
Best Local Similarity 100.0%; Pred. No. 5.82e-04;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 19 gctgcaccaatctagaatct 39  
|||||  
Qy 1 GCTGCATCCAACTAGAACT 21

RESULT 3

LOCUS MW018577 228 bp mRNA  
DEFINITION Mus musculus immunoglobulin kappa light chain, variable region mRNA, clone BALB/c-51, partial cds.  
ACCESSION U18577  
NID g619707  
KEYWORDS .  
SOURCE mouse.  
ORGANISM Mus musculus

Eukaryotae; mitochondrial eukaryotes; eukaryote crown group; Metazoa/Eumycota group; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia; Sciurognathi; Myomorphae; Muridae; Mus. 1 (bases 1 to 228)

REFERENCE  
AUTHORS Roark, J.H., Kuntz, C.L., Nguyen, K.A., Caton, A.J. and Erikson, J.  
TITLE Breakdown of B cell tolerance in a mouse model of systemic lupus erythematosus

J. Exp. Med. 181 (3), 1157-1167 (1995)  
MEDLINE 95173583

REFERENCE 2 (bases 1 to 228)

AUTHORS Roark, J.H.

Direct Submission

JOURNAL Submitted (14-DEC-1994) Jessica H. Roark, Wistar Institute, 3601

Spruce St., Philadelphia, PA 19104, USA

FEATURES Location/Qualifiers

source

1..228  
/strain="BALB/c"  
/organism="Mus musculus"  
/cell\_type="splenic B cell hybridoma"  
/tissue\_type="spleen"  
/dev\_stage="adult"  
<1..>228

CDS

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/db\_xref="PID:g619708"

/translation="YGDGSGYNNWYQKQPCKLLIYAASNLGSGIPARFSGSGTD  
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BASE COUNT 61 a 57 c 57 g 53 t

ORIGIN

Query Match 100.0%; Score 21; DB 65; Length 228;

Best Local Similarity 100.0%; Pred. No. 5.82e-04;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 70 gctgcacccaatcagaatct 90

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Qy 1 GCTGCATCCAATCTAGAATCT 21

RESULT 4

LOCUS MMU18563 238 bp mRNA ROD 21-JUN-1995

DEFINITION Mus musculus immunoglobulin kappa light chain, variable region mRNA, clone BALB/c-11, partial cds.

ACCESSION U18563

NID 9619679

KEYWORDS mouse.

SOURCE Mus musculus

ORGANISM

Eukaryotae; mitochondrial eukaryotes; eukaryote crown group; Metazoa/Eumycota group; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia; Sciurognathi; Myomorphae; Muridae; Mus. 1 (bases 1 to 238)

REFERENCE  
AUTHORS Roark, J.H., Kuntz, C.L., Nguyen, K.A., Caton, A.J. and Erikson, J.  
TITLE Breakdown of B cell tolerance in a mouse model of systemic lupus erythematosus

J. Exp. Med. 181 (3), 1157-1167 (1995)

MEDLINE 95173583

REFERENCE 2 (bases 1 to 238)

AUTHORS Roark, J.H.

TITLE Direct Submission

JOURNAL Submitted (14-DEC-1994) Jessica H. Roark, Wistar Institute, 3601  
Spruce St., Philadelphia, PA 19104, USA

FEATURES Location/Qualifiers

source

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/strain="BALB/c"  
/organism="Mus musculus"  
/cell\_type="splenic B cell hybridoma"  
/tissue\_type="spleen"  
/dev\_stage="adult"  
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CDS

/codon\_start=1  
/product="Immunoglobulin kappa light chain, variable region"  
/db\_xref="PID:g619680"

/translation="SYVDGSGYNNWYQKQPCKLLIYAASNLGSGIPARFSGSGS  
GTDFTLNHPVEEDAAATYCCQSDNPPTFGSGT"

BASE COUNT 63 a 56 c 61 g 58 t

ORIGIN

Query Match 100.0%; Score 21; DB 65; Length 238;

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Db 79 gctgcacccaatcagaatct 99

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Qy 1 GCTGCATCCAATCTAGAATCT 21

RESULT 5

LOCUS MMICKVRD 255 bp RNA ROD 13-OCT-1993

DEFINITION M.musculus immunoglobulin kappa light chain (DBA/1) gene, v region.  
ACCESSION Z25448

NID 9407836

KEYWORDS Igk gene; immunoglobulin; light chain; variable region.

SOURCE house mouse.

ORGANISM

Mus musculus  
Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia; Sciurognathi; Myomorphae; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 255)

AUTHORS Mo, J.A., Bona, C.A. and Holmdahl, R.

TITLE Variable region gene selection of immunoglobulin G expressing B cells with specificity for a defined epitope on type II collagen

JOURNAL Eur. J. Immunol. (1993) In press

REFERENCE 2 (bases 1 to 255)

AUTHORS Mo, J.A.

TITLE Direct Submission

JOURNAL Submitted (02-AUG-1993) to the EMBL/GenBank/DBJ databases. John A Mo, Department of Medical and Physiological, Department of, Medical and Physiological Chemistry, Huseargatan 3, Uppsala, 75123, Sweden

REFERENCE 3 (bases 1 to 255)

AUTHORS Mo, J.A., Bona, C.A. and Holmdahl, R.

TITLE Variable region gene selection of immunoglobulin G-expressing B cells with specificity for a defined epitope on type II collagen

JOURNAL Eur. J. Immunol. 23 (10), 2503-2510 (1993)

MEDLINE 94009207

FEATURES Location/Qualifiers

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Db 118 gctgcatccaatctagaatct 138  
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Qy 1 CCTGCATCCAATCTAGAACT 21

RESULT 6  
LOCUS MMIGKCVRE 262 bp RNA ROD 13-OCT-1993  
DEFINITION M.musculus immunoglobulin kappa light chain (DBA/1) gene, v region.  
ACCESSION Z75450  
NID g407838  
KEYWORDS IgK gene; immunoglobulin; light chain; variable region.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryote; mitochondrial eukaryotes; Metazoa/Eumycota group;  
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;  
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;  
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;  
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 262)  
AUTHORS Mo, J.A., Bona, C.A. and Holmdahl, R.  
TITLE Variable region gene selection of immunoglobulin G expressing B cells with specificity for a defined epitope on type II collagen  
JOURNAL Eur. J. Immunol. (1993) In press  
REFERENCE 2 (bases 1 to 262)  
AUTHORS Mo, J.A.

TITLE Direct Submission  
JOURNAL Submitted (02-AUG-1993) to the EMBL/GenBank/DBJ databases. John A Mo, Department of Medical and Physiological, Department of, Medical and Physiological Chemistry, Husargatan 3, Uppsala, 75123, Sweden  
REFERENCE 3 (bases 1 to 262)  
AUTHORS Mo, J.A., Bona, C.A. and Holmdahl, R.

TITLE Variable region gene selection of immunoglobulin G-expressing B cells with specificity for a defined epitope on type II collagen  
JOURNAL Eur. J. Immunol. 23 (10), 2503-2510 (1993)  
MEDLINE 94009207

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Query Match 100.0%; Score 21; DB 64; Length 262;  
Best Local Similarity 100.0%; Pred. No. 5.82e-04;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 125 gctgcatccaatctagaatct 145  
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Qy 1 CCTGCATCCAATCTAGAACT 21

RESULT 7  
LOCUS MMIGKCVRI 264 bp RNA ROD 13-OCT-1993  
DEFINITION M.musculus immunoglobulin kappa light chain (DBA/1) gene, v region.  
ACCESSION Z75458  
NID g407844  
KEYWORDS IgK gene; immunoglobulin; light chain; variable region.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryote; mitochondrial eukaryotes; Metazoa/Eumycota group;  
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;  
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;  
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;  
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 264)  
AUTHORS Mo, J.A., Bona, C.A. and Holmdahl, R.  
TITLE Variable region gene selection of immunoglobulin G expressing B cells with specificity for a defined epitope on type II collagen  
JOURNAL Eur. J. Immunol. (1993) In press  
REFERENCE 2 (bases 1 to 264)  
AUTHORS Mo, J.A.

TITLE Direct Submission  
JOURNAL Submitted (02-AUG-1993) to the EMBL/GenBank/DBJ databases. John A Mo, Department of Medical and Physiological, Department of, Medical and Physiological Chemistry, Husargatan 3, Uppsala, 75123, Sweden  
REFERENCE 3 (bases 1 to 264)  
AUTHORS Mo, J.A., Bona, C.A. and Holmdahl, R.

TITLE Variable region gene selection of immunoglobulin G-expressing B cells with specificity for a defined epitope on type II collagen  
JOURNAL Eur. J. Immunol. 23 (10), 2503-2510 (1993)  
MEDLINE 94009207

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Query Match      100.0%; Score 21; DB 64; Length 264;
Best Local Similarity 100.0%; Pred. No. 5.82e-04;
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Db 127 gctgcattcccaatctagaatct 147
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RESULT 8
LOCUS      MMICKVRC      266 bp      RNA      ROD      13-OCT-1993
DEFINITION M.musculus immunoglobulin kappa light chain (DBA/1) gene, v region.
ACCESSION      Z25446
NID      g407834
KEYWORDS      Igk gene; immunoglobulin; light chain; variable region.
SOURCE      house mouse.
ORGANISM      Mus musculus
Eukaryotes; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.
REFERENCE      1 (bases 1 to 266)
AUTHORS      Mo, J.A., Bona, C.A. and Holmdahl, R.
TITLE      Variable region gene selection of immunoglobulin G expressing B
cells with specificity for a defined epitope on type II collagen
JOURNAL      Eur. J. Immunol. (1993) In press
REFERENCE      2 (bases 1 to 266)
AUTHORS      Mo, J.A.
TITLE      Direct Submission
JOURNAL      Submitted (02-AUG-1993) to the EMBL/GenBank/DBJ databases. John A
Mo, Department of Medical and Physiological, Department of, Medical
and Physiological Chemistry, Husargatan 3, Uppsala, 75123, Sweden
REFERENCE      3 (bases 1 to 266)
AUTHORS      Mo, J.A., Bona, C.A. and Holmdahl, R.
TITLE      Variable region gene selection of immunoglobulin G-expressing B
cells with specificity for a defined epitope on type II collagen
JOURNAL      Eur. J. Immunol. 23 (10), 2503-2510 (1993)
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      3  1 GGTGCATCCCAATCTAGAACTCT 21

Query Match      100.0%; Score 21; DB 64; Length 266;
Best Local Similarity 100.0%; Pred. No. 5.82e-04;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 129 gctgcattcccaatctagaatct 149
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      2  1 GGTGCATCCCAATCTAGAACTCT 21

RESULT 9
LOCUS      MMICKVRC      270 bp      RNA      ROD      13-OCT-1993
DEFINITION M.musculus immunoglobulin kappa light chain (DBA/1) gene, v region.
ACCESSION      Z25454
NID      g407842
KEYWORDS      Igk gene; immunoglobulin; light chain; variable region.
SOURCE      house mouse.
ORGANISM      Mus musculus
Eukaryotes; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.
REFERENCE      1 (bases 1 to 270)
AUTHORS      Mo, J.A., Bona, C.A. and Holmdahl, R.
TITLE      Variable region gene selection of immunoglobulin G expressing B
cells with specificity for a defined epitope on type II collagen
JOURNAL      Eur. J. Immunol. (1993) In press
REFERENCE      2 (bases 1 to 270)
AUTHORS      Mo, J.A.
TITLE      Direct Submission
JOURNAL      Submitted (02-AUG-1993) to the EMBL/GenBank/DBJ databases. John A
Mo, Department of Medical and Physiological, Department of, Medical
and Physiological Chemistry, Husargatan 3, Uppsala, 75123, Sweden
REFERENCE      3 (bases 1 to 270)
AUTHORS      Mo, J.A., Bona, C.A. and Holmdahl, R.
TITLE      Variable region gene selection of immunoglobulin G-expressing B
cells with specificity for a defined epitope on type II collagen
JOURNAL      Eur. J. Immunol. 23 (10), 2503-2510 (1993)
MEDLINE      94009207
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ORIGIN
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Query Match 100.0%; Score 21; DB 64; Length 270;  
Best Local Similarity 100.0%; Pred. No. 5.82e-04;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 133 gctgcatccaatctagaatct 153  
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Qy 1 GCTGCATCCAACTAGAACT 21

RESULT 10  
LOCUS MMIGKCVRF 270 bp RNA 13-OCT-1993  
DEFINITION M.musculus immunoglobulin kappa light chain (DBA/1) gene, v region.  
ACCESSION Z25452  
NID g407840  
KEYWORDS Igk gene; immunoglobulin; light chain; variable region.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;  
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;  
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata;  
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;  
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 270)

AUTHORS Mo, J.A., Bona, C.A. and Holmdahl, R.

TITLE Variable region gene selection of immunoglobulin G expressing B

cells with specificity for a defined epitope on type II collagen

REFERENCE 2 (bases 1 to 270)

AUTHORS Mo, J.A.

TITLE Direct Submission

JOURNAL Submitted (02-AUG-1993) to the EMBL/GenBank/DBJ databases. John A

Mo, Department of Medical and Physiological, Department of, Medical

and Physiological Chemistry, Husargatan 3, Uppsala, 75123, Sweden

REFERENCE 3 (bases 1 to 270)

AUTHORS Mo, J.A., Bona, C.A. and Holmdahl, R.

TITLE Variable region gene selection of immunoglobulin G-expressing B

cells with specificity for a defined epitope on type II collagen

REFERENCE 4 (bases 1 to 270)

AUTHORS Mo, J.A.

TITLE Direct Submission

JOURNAL Submitted (02-AUG-1993) to the EMBL/GenBank/DBJ databases. John A

Mo, Department of Medical and Physiological, Department of, Medical

and Physiological Chemistry, Husargatan 3, Uppsala, 75123, Sweden

REFERENCE 5 (bases 1 to 270)

AUTHORS Mo, J.A., Bona, C.A. and Holmdahl, R.

TITLE Variable region gene selection of immunoglobulin G-expressing B

cells with specificity for a defined epitope on type II collagen

REFERENCE 6 (bases 1 to 270)

AUTHORS Mo, J.A.

TITLE Direct Submission

JOURNAL Submitted (02-AUG-1993) to the EMBL/GenBank/DBJ databases. John A

Mo, Department of Medical and Physiological, Department of, Medical

and Physiological Chemistry, Husargatan 3, Uppsala, 75123, Sweden

REFERENCE 7 (bases 1 to 270)

AUTHORS Mo, J.A., Bona, C.A. and Holmdahl, R.

TITLE Variable region gene selection of immunoglobulin G-expressing B

cells with specificity for a defined epitope on type II collagen

REFERENCE 8 (bases 1 to 270)

AUTHORS Mo, J.A.

TITLE Direct Submission

JOURNAL Submitted (02-AUG-1993) to the EMBL/GenBank/DBJ databases. John A

Mo, Department of Medical and Physiological, Department of, Medical

and Physiological Chemistry, Husargatan 3, Uppsala, 75123, Sweden

REFERENCE 9 (bases 1 to 270)

AUTHORS Mo, J.A., Bona, C.A. and Holmdahl, R.

TITLE Variable region gene selection of immunoglobulin G-expressing B

cells with specificity for a defined epitope on type II collagen

REFERENCE 10 (bases 1 to 270)

AUTHORS Mo, J.A.

TITLE Direct Submission

JOURNAL Submitted (02-AUG-1993) to the EMBL/GenBank/DBJ databases. John A

Db 133 gctgcatccaatctagaatct 153  
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Qy 1 GCTGCATCCAACTAGAACT 21

RESULT 11  
LOCUS MMIGKCVRF 270 bp RNA 13-OCT-1993  
DEFINITION M.musculus immunoglobulin kappa light chain (DBA/1) gene, v region.  
ACCESSION Z25444  
NID g407832  
KEYWORDS Igk gene; immunoglobulin; light chain; variable region.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;  
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;  
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata;  
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;  
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 270)

AUTHORS Mo, J.A., Bona, C.A. and Holmdahl, R.

TITLE Variable region gene selection of immunoglobulin G expressing B

cells with specificity for a defined epitope on type II collagen

REFERENCE 2 (bases 1 to 270)

AUTHORS Mo, J.A.

TITLE Direct Submission

JOURNAL Submitted (02-AUG-1993) to the EMBL/GenBank/DBJ databases. John A

Mo, Department of Medical and Physiological, Department of, Medical

and Physiological Chemistry, Husargatan 3, Uppsala, 75123, Sweden

REFERENCE 3 (bases 1 to 270)

AUTHORS Mo, J.A., Bona, C.A. and Holmdahl, R.

TITLE Variable region gene selection of immunoglobulin G-expressing B

cells with specificity for a defined epitope on type II collagen

REFERENCE 4 (bases 1 to 270)

AUTHORS Mo, J.A.

TITLE Direct Submission

JOURNAL Submitted (02-AUG-1993) to the EMBL/GenBank/DBJ databases. John A

Mo, Department of Medical and Physiological, Department of, Medical

and Physiological Chemistry, Husargatan 3, Uppsala, 75123, Sweden

REFERENCE 5 (bases 1 to 270)

AUTHORS Mo, J.A.

TITLE Direct Submission

JOURNAL Submitted (02-AUG-1993) to the EMBL/GenBank/DBJ databases. John A

Mo, Department of Medical and Physiological, Department of, Medical

and Physiological Chemistry, Husargatan 3, Uppsala, 75123, Sweden

REFERENCE 6 (bases 1 to 270)

AUTHORS Mo, J.A.

TITLE Direct Submission

JOURNAL Submitted (02-AUG-1993) to the EMBL/GenBank/DBJ databases. John A

Mo, Department of Medical and Physiological, Department of, Medical

and Physiological Chemistry, Husargatan 3, Uppsala, 75123, Sweden

REFERENCE 7 (bases 1 to 270)

AUTHORS Mo, J.A.

TITLE Direct Submission

JOURNAL Submitted (02-AUG-1993) to the EMBL/GenBank/DBJ databases. John A

Mo, Department of Medical and Physiological, Department of, Medical

and Physiological Chemistry, Husargatan 3, Uppsala, 75123, Sweden

REFERENCE 8 (bases 1 to 270)

AUTHORS Mo, J.A.

TITLE Direct Submission

JOURNAL Submitted (02-AUG-1993) to the EMBL/GenBank/DBJ databases. John A

Mo, Department of Medical and Physiological, Department of, Medical

and Physiological Chemistry, Husargatan 3, Uppsala, 75123, Sweden

REFERENCE 9 (bases 1 to 270)

AUTHORS Mo, J.A.

TITLE Direct Submission

JOURNAL Submitted (02-AUG-1993) to the EMBL/GenBank/DBJ databases. John A

Mo, Department of Medical and Physiological, Department of, Medical

and Physiological Chemistry, Husargatan 3, Uppsala, 75123, Sweden

REFERENCE 10 (bases 1 to 270)

AUTHORS Mo, J.A.

TITLE Direct Submission

JOURNAL Submitted (02-AUG-1993) to the EMBL/GenBank/DBJ databases. John A

Mar 19 15:53

US-08-612-929-17.rge

13

RESULT 12  
LOCUS MUSICKAAAA 279 bp mRNA ROD 07-MAR-1995  
DEFINITION Mouse IgK chain mRNA, VJ5 region.  
ACCESSION M57978  
NID g196402  
KEYWORDS J-region; V-region; anti-cytochrome c antibody;  
immunoglobulin kappa-chain; immunoglobulin light chain.  
SOURCE Mouse (BALB/c) secondary B cell hybridoma 1G3 mRNA, clone 1G3.E3.  
ORGANISM Mus musculus  
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;  
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.  
REFERENCE 1 (bases 1 to 279)  
AUTHORS Goshorn,S.C., Retzel,E. and Jemerson,R.  
TITLE Common structural features among monoclonal antibodies binding the  
same antigenic region of cytochrome c  
JOURNAL J. Biol. Chem. 266 (4), 2134-2142 (1991)  
MEDLINE 91115823  
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source Location/Qualifiers  
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Mar 19 15:53

US-08-612-929-17.rge

14

Db 103 gctgcattcaatctagaatct 123  
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Qy 1 GCTGCATCCAATCTAGATCT 21  
RESULT 13  
LOCUS MMU29628 286 bp mRNA ROD 08-DEC-1995  
DEFINITION Mus musculus anti-DNA antibody Ig kappa chain mRNA, V-J region,  
hybridoma 52.60, partial cds.  
ACCESSION U29628  
NID g896124  
KEYWORDS house mouse.  
SOURCE Mus musculus  
ORGANISM Eukaryota; mitochondrial eukaryotes; Metazoa; Chordata;  
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;  
Murinae; Mus.  
REFERENCE 1 (bases 1 to 286)  
AUTHORS Ibrahim,S.M., Weigert,M., Basu,C., Erikson,J. and Radic,M.Z.  
TITLE Light chain contribution to specificity in anti-DNA antibodies  
JOURNAL J. Immunol. 155 (6), 3223-3233 (1995)  
MEDLINE 95403997  
REFERENCE 2 (bases 1 to 286)  
AUTHORS Ibrahim,S.M., Weigert,M., Basu,C., Erikson,J. and Radic,M.Z.  
TITLE Direct Submission  
JOURNAL Submitted (21-JUN-1995) Saleh M. Ibrahim, Molecular Biology,  
Princeton University, Princeton, NJ 08544, USA  
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Query Match 100.0%; Score 21; DB 65; Length 286;  
Best Local Similarity 100.0%; Pred. No. 5.82e-04;  
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DEFINITION Mus musculus immunoglobulin kappa light chain variable region mRNA,  
clone BALB/c-9, partial cds.  
ACCESSION U18599  
NID g623397  
KEYWORDS .  
SOURCE mouse.  
ORGANISM Mus musculus  
Eukaryota; mitochondrial eukaryotes; eukaryote crown group;  
Metazoa/Eumycota group; Metazoa; Eumetazoa; Bilateria; Coelomata;  
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;

REFERENCE 1 (bases 1 to 292)  
AUTHORS Roark, J.H., Kuntz, C.L., Nguyen, K.A., Caton, A.J. and Erikson, J.  
TITLE Breakdown of B cell tolerance in a mouse model of systemic lupus erythematosus  
JOURNAL J. Exp. Med. 181 (3), 1157-1167 (1995)  
MEDLINE 95173583  
REFERENCE 2 (bases 1 to 292)  
AUTHORS Roark, J.H.  
TITLE Direct Submission  
JOURNAL Submitted (14-DEC-1994) Jessica H. Roark, Wistar Institute, 3601 Spruce St., Philadelphia, PA 19104, USA

FEATURES  
source

1..292  
Location/Qualifiers  
/strain="BALB/c"  
/organism="Mus musculus"  
/clone="BALB/c-9"  
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BASE COUNT  
ORIGIN

Query Match 100.0%; Score 21; DB 65; Length 292;  
Best Local Similarity 100.0%; Pred. No. 5.82e-04;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 133 gctgcaccaatctagaatct 153  
|||||  
Qy 1 GCTGCATCCAATCTAGAACT 21

## RESULT 15

LOCUS MMU29629 297 bp mRNA ROD 08-DEC-1995  
DEFINITION Mus musculus anti-DNA antibody Ig kappa chain mRNA, V-J region, hybridoma 52.468, partial cds.  
ACCESSION U29629  
NID g896126  
KEYWORDS house mouse.  
SOURCE Mus musculus  
ORGANISM Mus musculus

Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 297)  
AUTHORS Ibrahim, S.M., Weigert, M., Basu, C., Erikson, J. and Radic, M.Z.  
TITLE Light chain contribution to specificity in anti-DNA antibodies  
JOURNAL J. Immunol. 155 (6), 3223-3233 (1995)  
MEDLINE 95403997

REFERENCE 2 (bases 1 to 297)  
AUTHORS Ibrahim, S.M., Weigert, M., Basu, C., Erikson, J. and Radic, M.Z.  
TITLE Direct Submission  
JOURNAL Submitted (21-JUN-1995) Saleh M. Ibrahim, Molecular Biology, Princeton University, Princeton, NJ 08544, USA

FEATURES  
source

1..297  
Location/Qualifiers

/organism="Mus musculus"  
/strain="BALB/c"  
/isolate="hybridoma 52.468"  
/chromosome="6"  
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/note="V-J region"  
/codon\_start=1  
/product="Ig kappa chain"  
/db\_xref="PID:g896127"  
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BASE COUNT 78 a 77 c 72 g 70 t  
ORIGIN

Query Match 100.0%; Score 21; DB 65; Length 297;  
Best Local Similarity 100.0%; Pred. No. 5.82e-04;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 160 gctgcaccaatctagaatct 180  
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Qy 1 GCTGCATCCAATCTAGAACT 21

## RESULT 16

LOCUS S74550 313 bp mRNA ROD 12-MAY-1995  
DEFINITION Ig V kappa r-rheumatoid factor RF3-5A (clone I) [mice, MRL/lpr, spleen, B cell hybridoma, mRNA Partial Mutant, 313 nt].

ACCESSION S74550  
NID g806981

KEYWORDS mice spleen MRL/lpr B cell hybridoma.  
SOURCE Mus sp  
ORGANISM Mus sp

REFERENCE 1 (bases 1 to 313)

AUTHORS Shan, H., Shlomchik, M.J., Marshak-Rothstein, A., Pisetsky, D.S., Litwin, S. and Weigert, M.G.  
TITLE The mechanism of autoantibody production in an autoimmune MRL/lpr mouse  
JOURNAL J. Immunol. 153 (11), 5104-5120 (1994)  
MEDLINE 95052677  
REMARK GenBank staff at the National Library of Medicine created this entry [NCBI gibseq 158647] from the original journal article. This sequence comes from Fig. 2B.

FEATURES  
source

Location/Qualifiers  
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/organism="Mus sp."  
/note="mice"  
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/partial  
/genes="Ig V<kappa>"  
/notes="IgA autoantibody kappa chain variable region; anti-IgG2a-specific. Method: conceptual translation supplied by author. This sequence comes from Fig. 2B."  
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/db\_xref="PID:g806982"  
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BASE COUNT 82 a 75 c 79 g 77 t  
ORIGIN

Query Match 100.0%; Score 21; DB 70; Length 313;  
Best Local Similarity 100.0%; Pred. No. 5.82e-04;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 133 gctgcacccaatctagaatct 153  
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 Qy 1 GCTGCATCCCAATCTAGAATCT 21

RESULT 17  
 LOCUS MUSIGVACR 317 bp mRNA ROD 08-MAR-1993  
 DEFINITION Mus musculus Ig rearranged anti-Sm hybridoma mRNA V-region  
 sequence.  
 ACCESSION L09042  
 NID g198040  
 KEYWORDS V-region; immunoglobulin V region; processed gene.  
 SOURCE Mus musculus (strain mrl/mp-lpr/lpr) adult spleen mRNA.  
 ORGANISM Mus musculus  
 Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;  
 Eutheria; Rodentia; Myomorpha; Muridae; Murinae.  
 REFERENCE 1 (bases 1 to 317)  
 AUTHORS Bloom, D.D., Davignon, J.-L., Retter, M.W., Shlomchik, M.J.,  
 Pisetsky, D.S., Cohen, P.L., Eisenberg, R.A. and Clarke, S.H.  
 TITLE V region gene analysis of anti-sm hybridomas from mrl/mp-lpr/lpr  
 mice  
 JOURNAL J. Immunol. 150, 1591-1610 (1993)  
 MEDLINE 93163585  
 FEATURES Location/Qualifiers  
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 1..317  
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 /cell\_line="anti-Sm hybridoma 3C2K"  
 /cell\_type="B-cell"  
 /dev\_stage="adult"  
 /sequenced\_mol="mRNA"  
 /tissue\_type="spleen"

BASE COUNT 81 a 80 c 79 g 74 t 3 others  
 ORIGIN

Query Match 100.0%; Score 21; DB 67; Length 317;  
 Best Local Similarity 100.0%; Pred. No. 5.82e-04;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 143 gctgcacccaatctagaatct 163  
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 Qy 1 GCTGCATCCCAATCTAGAATCT 21

RESULT 18  
 LOCUS MUSIGVKB 318 bp mRNA ROD 29-OCT-1994  
 DEFINITION Mouse immunoglobulin kappa light chain variable region anti-DNA  
 antibody (VX21E family) mRNA.  
 ACCESSION L14734  
 NID g793392  
 KEYWORDS V-region; anti-DNA antibody; immunoglobulin light chain;  
 immunoglobulin-kappa.  
 SOURCE Mus musculus (strain BALB/c, sub\_species domesticus) female somatic  
 variant spleen cDNA to mRNA.

ORGANISM Mus musculus  
 Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;  
 Eutheria; Rodentia; Myomorpha; Muridae; Murinae.  
 REFERENCE 1 (bases 1 to 318)  
 AUTHORS Tillman, D.M., Jou, N.T., Hill, R.J. and Marion, T.N.  
 TITLE Both IgM and IgG anti-DNA antibodies are the products of clonally  
 selective B cell stimulation in (NZB x NZW)F1 mice  
 JOURNAL J. Exp. Med. 176 (3), 761-779 (1992)

MEDLINE 92381444  
 REFERENCE 2 (bases 1 to 318)  
 AUTHORS Krishnan, M.R. and Marion, T.N.  
 TITLE Structural similarity of antibody variable regions from immune and  
 auto-immune anti-DNA antibodies  
 JOURNAL J. Immunol. (1993) In press  
 FEATURES Location/Qualifiers  
 source  
 1..318  
 /organism="Mus musculus"  
 /strain="BALB/c"  
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 /cell\_type="hybridoma"  
 /dev\_stage="somatic variant"  
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 /sex="female"  
 /tissue\_type="spleen"

V\_region  
 BASE COUNT 85 a 77 c 79 g 72 t 5 others  
 ORIGIN

Query Match 100.0%; Score 21; DB 66; Length 318;  
 Best Local Similarity 100.0%; Pred. No. 5.82e-04;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 145 gctgcacccaatctagaatct 165  
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 Qy 1 GCTGCATCCCAATCTAGAATCT 21

RESULT 19  
 LOCUS S42888 333 bp DNA ROD 09-NOV-1992  
 DEFINITION Ig V kappa =immunoglobulin V kappa region [mice, hybridoma 54'CB1,  
 Genomic, nt].  
 ACCESSION S42888  
 NID g254222  
 KEYWORDS mice hybridoma 54'CB1.  
 SOURCE Mus sp.  
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 333)  
 AUTHORS Matsushita, S., Maeda, H., Kimachi, K., Eda, Y., Maeda, Y., Murakami, T.,  
 Tokiyoshi, S. and Takatsuki, K.  
 TITLE Characterization of a mouse/human chimeric monoclonal antibody (C  
 beta 1) to a principal neutralizing domain of the human  
 immunodeficiency virus type 1 envelope protein  
 AIDS Res. Hum. Retroviruses 8 (6), 1107-1115 (1992)  
 JOURNAL  
 MEDLINE 92368728  
 REMARK GenBank staff at the National Library of Medicine created this  
 entry [NCBI gisseq 111883] from the original journal article.  
 This sequence comes from Fig. 2.

FEATURES Location/Qualifiers  
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 /note="Description: immunoglobulin V kappa region,  
 antibody C beta 1; This sequence comes from Fig. 2.  
 antibody C beta 1"  
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 /product="immunoglobulin V kappa region"

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GSGTKLEIK"  
BASE COUNT 91 a 82 c 81 g 79 t  
ORIGIN  
Query Match 100.0%; Score 21; DB 70; Length 333;  
Best Local Similarity 100.0%; Pred. No. 5.82e-04;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 160 gctgcacccaatctagaatct 180  
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Qy 1 GCTGCATCCAATCTAGAATCT 21  
RESULT 20  
LOCUS MUSIGLSB 333 bp DNA ROD 01-NOV-1991  
DEFINITION Mouse IgL chain H2L2 V-region, partial cds.  
ACCESSION M80406  
NID gi97577  
KEYWORDS V-region; immunoglobulin light chain.  
SOURCE Mus musculus (strain BALB/c, sub\_species domesticus) (library: lambda-gt11) DNA.  
ORGANISM Mus musculus  
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;  
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.  
REFERENCE 1 (bases 1 to 333)  
AUTHORS Matsushita,S., Maeda,H., Kimachi,K., Eda,Y., Maeda,Y., Hattori,T., Tokiyoshi,S. and Takatsuki,K.  
TITLE Characterization of a mouse/human chimeric monoclonal antibody (C-beta-1) to a principal neutralizing domain of the human immunodeficiency virus type I envelope protein  
JOURNAL Unpublished (1991)  
FEATURES Location/Qualifiers  
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/issue\_lib="lambda-gt11"  
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GSGTKLEIK"  
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/note="CDR1"  
misc\_feature 115..159  
/gene="0.5 beta-VL"  
/note="FR2"  
misc\_feature 160..180  
/gene="0.5 beta-VL"  
/note="CDR2"

misc\_feature 181..276  
/gene="0.5 beta-VL"  
/note="FR3"  
misc\_feature 277..303  
/gene="0.5 beta-VL"  
/note="CDR3"  
misc\_feature 304..333  
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/note="FR4"  
BASE COUNT 91 a 82 c 81 g 79 t  
ORIGIN  
Query Match 100.0%; Score 21; DB 67; Length 333;  
Best Local Similarity 100.0%; Pred. No. 5.82e-04;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 160 gctgcacccaatctagaatct 180  
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Qy 1 GCTGCATCCAATCTAGAATCT 21  
RESULT 21  
LOCUS MMIGLC404 336 bp RNA ROD 07-MAY-1992  
DEFINITION M.musculus mRNA for IG light chain VJ region (M-T404).  
ACCESSION X65092  
NID g52292  
KEYWORDS ig light chain; VJ domain.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; mitochondrial eukaryotes; Metazoa/Eumycota group;  
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;  
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;  
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;  
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 336)  
AUTHORS Weissenhorn,W.  
TITLE Direct Submission  
JOURNAL Submitted (10-MAR-1992) to the EMBL/GenBank/DBJ databases. W.  
Weissenhorn, Institut fuer Immunologie, Goethestrasse 31, W-8000 Muenchen 2, FRG  
REFERENCE 2 (bases 1 to 336)  
AUTHORS Weissenhorn,W., Riethmueller,G., Weiss,E.M. and Rieber,E.P.  
TITLE Structural characterization of CD4 mAb  
JOURNAL Unpublished  
FEATURES Location/Qualifiers  
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GGGCKLEIKR"  
BASE COUNT 89 a 90 c 81 g 76 t  
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Query Match 100.0%; Score 21; DB 64; Length 336;  
Best Local Similarity 100.0%; Pred. No. 5.82e-04;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 160 gctgcatccaatctagaatct 180
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Qy 1 GCTGCATCCAACTAGAACT 21

RESULT 22
LOCUS MUSIGVACP 336 bp mRNA ROD 08-MAR-1993
DEFINITION Mus musculus Ig rearranged anti-Sm hybridoma mRNA V-region
sequence.
ACCESSION L09040
NID g198038
KEYWORDS V-region; immunoglobulin V region; processed gene.
SOURCE Mus musculus (strain mrl/mp-lpr/lpr) adult spleen mRNA.
ORGANISM Mus musculus
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE 1 (bases 1 to 336)
AUTHORS Bloom,D.D., Davignon,J.-L., Retter,M.W., Shlomchik,M.J.,
Pisetsky,D.S., Cohen,P.L., Eisenberg,R.A. and Clarke,S.H.
TITLE V region gene analysis of anti-sm hybridomas from mrl/mp-lpr/lpr
mice
JOURNAL J. Immunol. 150, 1591-1610 (1993)
MEDLINE 93163585
FEATURES
source
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 5.82e-04;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 160 gctgcatccaatctagaatct 180
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Qy 1 GCTGCATCCAACTAGAACT 21

RESULT 23
LOCUS MMIGLC413 336 bp RNA ROD 07-MAY-1992
DEFINITION M.musculus mRNA for IG light chain VJ region (M-T413).
ACCESSION X65093
NID g52298
KEYWORDS Ig light chain; VJ domain.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 336)
AUTHORS Weissenhorn,W.
TITLE Direct Submission
JOURNAL Submitted (10-MAR-1992) to the EMBL/GenBank/DBJ databases. W.
Weissenhorn, Institut fuer Immunologie, Goethestrasse 31, W-8000
Muenchen 2, FRG

Db 160 gctgcatccaatctagaatct 180
|||||
Qy 1 GCTGCATCCAACTAGAACT 21

RESULT 24
LOCUS MMIGLC310 336 bp RNA ROD 07-MAY-1992
DEFINITION M.musculus mRNA for IG light chain VJ region (M-T310).
ACCESSION X65091
NID g52288
KEYWORDS Ig light chain; VJ domain.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 336)
AUTHORS Weissenhorn,W.
TITLE Direct Submission
JOURNAL Submitted (10-MAR-1992) to the EMBL/GenBank/DBJ databases. W.
Weissenhorn, Institut fuer Immunologie, Goethestrasse 31, W-8000
Muenchen 2, FRG

Db 160 gctgcatccaatctagaatct 180
|||||
Qy 1 GCTGCATCCAACTAGAACT 21

RESULT 25
LOCUS MMIGLC310 336 bp RNA ROD 07-MAY-1992
DEFINITION M.musculus mRNA for IG light chain VJ region (M-T310).
ACCESSION X65091
NID g52288
KEYWORDS Ig light chain; VJ domain.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 336)
AUTHORS Weissenhorn,W.
TITLE Direct Submission
JOURNAL Submitted (10-MAR-1992) to the EMBL/GenBank/DBJ databases. W.
Weissenhorn, Institut fuer Immunologie, Goethestrasse 31, W-8000
Muenchen 2, FRG
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REFERENCE 2 (bases 1 to 336)
AUTHORS Weissenhorn,W., Riethmuller,G., Weiss,E.M. and Rieber,E.P.
TITLE Structural characterization of CD4 mAb
JOURNAL Unpublished
FEATURES
source
Location/Qualifiers
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/strain="Balb/c"
/cell_type="B-cell"
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/product="alpha CD4 mAb immunoglobulin light chain VJ
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/db_xref="PID:g52299"
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GRPKLLIYAASNLSESGIPARFSGSGTFTLNHPVEEDAAITYCQOSTQDPTF
GGGTLKLEIKR"
BASE COUNT 88 a 87 c 84 g 77 t
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Query Match 100.0%; Score 21; DB 64; Length 336;
Best Local Similarity 100.0%; Pred. No. 5.82e-04;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 160 gctgcatccaatctagaatct 180
|||||
Qy 1 GCTGCATCCAACTAGAACT 21

RESULT 24
LOCUS MMIGLC310 336 bp RNA ROD 07-MAY-1992
DEFINITION M.musculus mRNA for IG light chain VJ region (M-T310).
ACCESSION X65091
NID g52288
KEYWORDS Ig light chain; VJ domain.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 336)
AUTHORS Weissenhorn,W.
TITLE Direct Submission
JOURNAL Submitted (10-MAR-1992) to the EMBL/GenBank/DBJ databases. W.
Weissenhorn, Institut fuer Immunologie, Goethestrasse 31, W-8000
Muenchen 2, FRG

Db 160 gctgcatccaatctagaatct 180
|||||
Qy 1 GCTGCATCCAACTAGAACT 21

RESULT 25
LOCUS MMIGLC310 336 bp RNA ROD 07-MAY-1992
DEFINITION M.musculus mRNA for IG light chain VJ region (M-T310).
ACCESSION X65091
NID g52288
KEYWORDS Ig light chain; VJ domain.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 336)
AUTHORS Weissenhorn,W.
TITLE Direct Submission
JOURNAL Submitted (10-MAR-1992) to the EMBL/GenBank/DBJ databases. W.
Weissenhorn, Institut fuer Immunologie, Goethestrasse 31, W-8000
Muenchen 2, FRG

Db 160 gctgcatccaatctagaatct 180
|||||
Qy 1 GCTGCATCCAACTAGAACT 21

RESULT 26
LOCUS MMIGLC310 336 bp RNA ROD 07-MAY-1992
DEFINITION M.musculus mRNA for IG light chain VJ region (M-T310).
ACCESSION X65091
NID g52288
KEYWORDS Ig light chain; VJ domain.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 336)
AUTHORS Weissenhorn,W.
TITLE Direct Submission
JOURNAL Submitted (10-MAR-1992) to the EMBL/GenBank/DBJ databases. W.
Weissenhorn, Institut fuer Immunologie, Goethestrasse 31, W-8000
Muenchen 2, FRG
```

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Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS Mouse Ig kappa chain mRNA, V-J region from hybridoma MOR8.2.1,  
DEFINITION partial cds.  
ACCESSION M92401  
NID g196481  
KEYWORDS J-region; V-region; immunoglobulin light chain;  
immunoglobulin-kappa; morphine specific antibody; processed gene.  
SOURCE Mus musculus (strain BALB/c, sub\_species domesticus) B-lymphocyte  
cDNA to mRNA.

ORGANISM Mus musculus  
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;  
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.  
REFERENCE 1 (bases 1 to 350)  
AUTHORS Sawada,J., Yamazaki,T. and Terao,T.  
TITLE Molecular and biochemical analyses of combining sites of monoclonal  
anti-morphine antibodies  
JOURNAL Mol. Immunol. 30 (1), 77-86 (1993)  
MEDLINE 93109376  
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ORIGIN chromosome 6.

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Best Local Similarity 100.0%; Pred. No. 5.82e-04;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 160 gctgcaccaatctagaatct 180  
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LOCUS Mouse Ig kappa chain mRNA, V-J region from hybridoma MOR35.4.12,  
DEFINITION partial cds.  
ACCESSION M92403  
NID g196485  
KEYWORDS J-region; V-region; immunoglobulin light chain;  
immunoglobulin-kappa; morphine specific antibody; processed gene.  
SOURCE Mus musculus (strain BALB/c, sub\_species domesticus) B-lymphocyte  
cDNA to mRNA.

ORGANISM Mus musculus  
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;  
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.  
REFERENCE 1 (bases 1 to 353)  
AUTHORS Sawada,J., Yamazaki,T. and Terao,T.  
TITLE Molecular and biochemical analyses of combining sites of monoclonal  
anti-morphine antibodies  
JOURNAL Mol. Immunol. 30 (1), 77-86 (1993)  
MEDLINE 93109376  
FEATURES Location/Qualifiers  
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## V\_region

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## CDS

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RESULT 27 MUSL71IGKV 354 bp mRNA ROD 29-OCT-1994  
LOCUS Mouse hybridoma Ig rearranged kappa-chain mRNA V-region, partial  
DEFINITION



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cds.
ACCESSION M97875
NID g198677
KEYWORDS V-region; immunoglobulin light chain; immunoglobulin-kappa;
processed gene.
SOURCE Mus musculus (strain BALB/c, sub_species domesticus) SP20-BALB/c
fusion hybridoma cDNA to mRNA.
ORGANISM Mus musculus
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE 1 (bases 1 to 354)
AUTHORS Lohman,K.L., Buck,D.W., Carrillo,M.A. and Kennedy,R.C.
TITLE Characterization of murine monoclonal anti-CD4; epitope
recognition, idiootope expression, and variable gene sequence
JOURNAL Unpublished (1992)
FEATURES
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            DEFINITION Mouse Ig active kappa chain mRNA V-region (V-D-J).
            ACCESSION M61046
            NID g196679
            KEYWORDS anti-CD4; immunoglobulin light chain; monoclonal antibody.
            SOURCE Mouse, cDNA to mRNA.
            ORGANISM Mus musculus
            Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
            Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
            REFERENCE 1 (bases 1 to 360)
            AUTHORS Attanasio,R., Dilley,D., Buck,D.W., Maino,V.C., Lohman,K.L.,
            Kanda,P. and Kennedy,R.C.
            TITLE Structural characterization of a cross-reactive idiootype sharedby
            monoclonal antibodies specific for the human CD4 molecule
            JOURNAL J. Biol. Chem. 266, 14611-14619 (1991)
            MEDLINE 91317827
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    DEFINITION Mouse hybridoma Ig rearranged kappa-chain mRNA V-region, partial
    cds.
    ACCESSION M97879
    NID g198681
    KEYWORDS V-region; immunoglobulin light chain; immunoglobulin-kappa;
    processed gene.
    SOURCE Mus musculus (strain BALB/c, sub_species domesticus) SP20-BALB/c
    fusion hybridoma cDNA to mRNA.
    ORGANISM Mus musculus
    Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
    Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
    REFERENCE 1 (bases 1 to 363)
    AUTHORS Lohman,K.L., Buck,D.W., Carrillo,M.A. and Kennedy,R.C.
    TITLE Characterization of murine monoclonal anti-CD4; epitope
    recognition, idiootope expression, and variable gene sequence
    JOURNAL Unpublished (1992)
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                Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DEFINITION Mouse hybridoma Ig rearranged kappa-chain mRNA V-region, partial cde.

ACCESSION M97869

NID g198667

KEYWORDS V-region; immunoglobulin light chain; immunoglobulin-kappa; processed gene.

SOURCE Mus musculus (strain BALB/c, sub\_species domesticus) SP20-BALB/c fusion hybridoma cDNA to mRNA.

ORGANISM Mus musculus

Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.

REFERENCE 1 (bases 1 to 363)

AUTHORS Lohman,K.L., Buck,D.W., Carrillo,M.A. and Kennedy,R.C.

TITLE Characterization of murine monoclonal anti-CD4; epitope recognition, idiotope expression, and variable gene sequence

JOURNAL Unpublished (1992)

FEATURES

Location/Qualifiers

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Best Local Similarity 100.0%; Pred. No. 5.82e-04;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 160 gctgcattccaatctagaatct 180

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Qy 1 GCTGCATCCAATCTAGATCT 21

RESULT 31

LOCUS S50265 393 bp mRNA ROD 02-APR-1993

DEFINITION Ig VL=anti-CD4 mAb M-T310 variable region light chain (JL, chimeric antibody) [mice, hybridoma cells, mRNA Partial, 393 nt].

ACCESSION S50265

NID g260765

KEYWORDS mice hybridoma cells.

SOURCE Mus sp.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 393)

AUTHORS Weissenhorn,W., Scheuer,W., Kaluza,B., Schwirzke,M., Reiter,C., Flieger,D., Lenz,H., Weiss,E.H., Rieber,E.P., Riettmuller,G. et.al.

TITLE Combinatorial functions of two chimeric antibodies directed to human CD4 and one directed to the alpha-chain of the human interleukin-2 receptor

JOURNAL Gene 121 (2), 271-278 (1992)

MEDLINE 93077041

REMARK GenBank staff at the National Library of Medicine created this entry [NCBI glibsq 119503] from the original Journal article. This sequence comes from Fig. 1c.

FEATURES

Location/Qualifiers

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CDS

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BASE COUNT 100 a 105 c 98 g 90 t

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 5.82e-04;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 32

LOCUS I08223 900 bp PAT 14-NOV-1994

DEFINITION Sequence 1 from patent EP 0365209.

ACCESSION I08223

NID g589062

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 900)

AUTHORS Hinton,R. and Ol,V.T.

TITLE Anti-leu 3A amino acid sequence

JOURNAL Patent: EP 0365209-A2 1 25-APR-1990;

FEATURES

Location/Qualifiers

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Search completed: Wed Mar 19 15:55:24 1997

Job time : 71 secs.

Mar 19 08:20

US-08-612-929-19.rst

1

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WVVSQELH

(TM)

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Release 2.1D John F. Collins, Biocomputing Research Unit.  
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MPsrch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed Mar 19 08:21:00 1997; MaePar time 59.78 Seconds  
199.194 Million cell updates/sec

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Description: (1-27) from US08612929.seq  
Perfect Score: 27  
N.A. Sequence: 1 CACGACACTATGAGCATCCCGACGC 27  
Comp: GTCCGTTCACTACTCTAGGAGCTGC

Scoring table: TABLE default  
Gap 10

Mismatch STD : Dbase 0; Query 0

Searched: 630489 seqs, 220513910 bases x 2

Post-processing: Minimum Match 0\$  
Listing first 45 summaries

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Mar 19 08:20

US-08-612-929-19.rst

2

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Statistics: Mean 6.936; Variance 1.332; scale 5.209

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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c	6	15	55.6	305	168	HSW04100	T1792.WVAT4 bloodstre	4.99e-02
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c	9	15	55.6	329	149	W12396	ma67g11.rl Soares mou	4.99e-02
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c	12	15	55.6	361	108	T26512	AB284F11R Homo sapien	4.99e-02
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c	17	15	55.6	372	155	HSPD04181	H.sapiens mitochondri	4.99e-02
c	18	15	55.6	372	46	HSPD04181	H.sapiens mitochondri	4.99e-02
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c	22	15	55.6	423	168	HSPD03830	H.sapiens mitochondri	4.99e-02
c	23	15	55.6	423	46	HSPD03830	H.sapiens mitochondri	4.99e-02
c	24	15	55.6	423	155	HSPD03830	H.sapiens mitochondri	4.99e-02
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Mar 19:08:20

US-08-612-929-19:rst

3

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c 45 14 51.9 560 47 HUM093A03B Human fetal brain cDN 8.55e-01

## ALIGNMENTS

RESULT 1  
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DEFINITION yd45q03.r1 Homo sapiens cDNA clone 111220 5'.  
ACCESSION T84399  
NID g712687  
KEYWORDS EST.  
SOURCE human clone=111220 library=Soares fetal liver spleen lNfLS vector=PT73D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) primer=M13RP1 Rsite1=Pac I Rsite2=Eco RI Liver and spleen from a 20 week-post conception male fetus. 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5' AACTGGAAGATTAATTAAGATCTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM Homo sapiens  
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 314)  
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.

TITLE The WashU-Merck EST Project  
JOURNAL Unpublished (1995)  
COMMENT

Contact: Wilson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence stops: 207

Source: IMAGE Consortium, LNL

This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES  
source  
Location/Qualifiers  
1..314

/organism="Homo sapiens"

/clone="111220"

/note="human"

BASE COUNT 90 a 55 c 74 g 91 t 4 others  
ORIGIN

Query Match 63.0%; Score 17; DB 124; Length 314;  
Best Local Similarity 87.0%; Pred. No. 1.11e-04;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 282 ggtggatctacttacttgctg 304

|| ||| ||||| ||||| |||||

Cp 23 GGAGGATCCTCATCTTTGCTG 1

RESULT 2

Mar 19:08:20

US-08-612-929-19:rst

4

LOCUS H77752 408 bp mRNA EST 09-NOV-1995  
DEFINITION yu23q11.r1 Homo sapiens cDNA clone 234692 5'.  
ACCESSION H77752  
NID g1055841  
KEYWORDS EST.  
SOURCE human clone=234692 primer=M13RP1 library=Soares fetal liver spleen lNfLS vector=PT73D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) Rsite1=Pac I Rsite2=Eco RI Liver and spleen from a 20 week-post conception male fetus. 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5' AACTGGAAGATTAATTAAGATCTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM Homo sapiens  
Eucaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 408)

AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.

TITLE The WashU-Merck EST Project

JOURNAL Unpublished (1995)

COMMENT

Contact: Wilson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence stops: 281

Source: IMAGE Consortium, LNL

This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES  
source  
Location/Qualifiers  
1..408

/organism="Homo sapiens"

/clone="234692"

/note="human"

<1..>408

BASE COUNT 116 a 50 c 85 g 154 t 3 others  
ORIGIN

Query Match 59.3%; Score 16; DB 30; Length 408;  
Best Local Similarity 94.4%; Pred. No. 2.51e-03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 155 ggaggatctctcataatt 172

||||| ||||| ||||| ||

Cp 23 GGAGGATCCTCATCTT 6

RESULT 3

LOCUS T98290 482 bp mRNA EST 31-MAR-1995  
DEFINITION ye59g06.s1 Homo sapiens cDNA clone 122074 3' similar to contains Alu repetitive element;.

ACCESSION T98290

NID 9748027

**KEYWORDS** EST. human clone=12074 library=Soares fetal liver spleen lNFLS vector=pT73D (Pharmacia) with a modified polylinker host=DHI0B (ampicillin resistant) primer=-2ml3 Reitel=Pac I Reitel=Eco RI Liver and spleen from a 20 week-post conception male fetus. 1st strand cDNA was primed with a Pac I - oligo (dT) primer [5' AACTGGACGATTAATTAAGATCTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM      Homo sapiens  
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;  
Eutheria; Primates; Chordata; Carnivora; Hominidae; Homo.  
1 (bases 1 to 482)  
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
Holman, M., Hultman, K., Kucaba, T., Le, M., Lennon, G., Marz, M.,  
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,  
Trevas, E., Waterston, R., Williamson, A., Wohlmann, P. and  
Wilson, R.

**TITLE** The WashU-Merck EST Project  
**JOURNAL** Unpublished (1995)

Contact: Wilson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: [est@watson.wustl.edu](mailto:est@watson.wustl.edu)  
High quality sequence stops: 288  
Source: IMAGE Consortium, LNL.  
This clone is available royalty-free through LNL ; contact the  
IMAGE Consortium ([info@image.lnl.gov](mailto:info@image.lnl.gov)) for further information.

```
FEATURES
  source
    Location/Qualifiers
      1..482
        /organism="Homo sapiens"
        /clone="122074"
        /note="human"
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BASE COUNT	119 a	89 c	142 g	123 t	9 others
ORIGIN					
Query Match		59.3%	Score 16;	DB 128;	Length 482;
Best Local Similarity		90.0%	Pred. No. 2.5le-03;		
Matches	18;	Conservative	0;	Mismatches 2;	Indels 0;
Gaps	0;				

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Db 166 caacacagtaatgaggatcc 185
      ||| ||||| |||||
Ov 1 CAGCAAGTAAATGAGGATCC 20

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RESULT	4				
LOCUS	N49151	215 bp	mRNA	EST	
DEFINITION	yy84b12.r1 Homo sapiens cDNA clone 280223 5'.				14-FEB-1996
ACCESSION	N49151				
KEYWORDS	g1190317				
	NID				
	EST.				

SOURCE

human clone=280223 primer=7f library=Soares multiple sclerosis 2NBHSP vector=pt773D (Pharmacia) with a modified polylinker V. TYPE: phagemid host=DH10B (ampicillin resistant) Retel=Not I ReiteZ=Eco RI 46 year old male. lat strand cDNA was primed with a Not I - oligo(dT) primer [5'-TGTTACCAATCTCAAGTGGGCGGCGCGGCTTTTTTTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters

(Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from 4 multiple sclerosis lesions from one patient was kindly provided by Dr. Kevin G. Becker (NINDS/NIH).

ORGANISM

Homo sapiens

Eukaryotae: Metazoa: Eumetazoa: Bilateria: Coelomata; Eukaryotae: Metazoa: Eumetazoa: Bilateria: Coelomata; Deuterostomia: Chordata: Vertebrata; Gnathostomata: Osteichthyes; Sarcopterygii: Choanata: Tetrapoda: Amniota: Mammalia: Theria; Eutheria: Archonta: Primates: Catarrhini: Hominoidea: Homo.

REFERENCE  
1 (bases 1 to 215)  
HILLIER, D., CLARK, N., DUBUQUE, T., ELLISTON, K., HAWKINS, M.,  
HOLMAN, M., HULTMAN, M., KUCABA, T., LE, M., LENNON, G., MARA, M.,  
PARSONS, J., RIFKIN, L., ROHLFING, T., SOARES, M., TAN, F.,  
TREVADEKIS, E., WATERSTON, R., WILLIAMSON, A., WOHLDMANN, P. and  
WILSON, R.

**TITLE** The WashU-Merck EST Project  
**JOURNAL** Unpublished (1995)  
**COMMENT**

Contact: Wilson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810

Email: [est@watson.wustl.edu](mailto:est@watson.wustl.edu)  
 High quality sequence stops: 193  
 Source: IMAGE Consortium, L1NL  
 This clone is available royalty-free through L1NL ; contact the  
 IMAGE Consortium ([info@image.l1nl.gov](mailto:info@image.l1nl.gov)) for further information.

```

FEATURES
  source
    Location/Qualifiers
      1..215
        /organism="Homo sapiens"
        /clone="280223"
        /note="human"

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Accession	U00096	U00097	U00098	U00099	U00100	U00101	U00102	U00103	U00104	U00105	U00106	U00107	U00108	U00109	U00110	U00111	U00112	U00113	U00114	U00115	U00116	U00117	U00118	U00119	U00120	U00121	U00122	U00123	U00124	U00125	U00126	U00127	U00128	U00129	U00130	U00131	U00132	U00133	U00134	U00135	U00136	U00137	U00138	U00139	U00140	U00141	U00142	U00143	U00144	U00145	U00146	U00147	U00148	U00149	U00150	U00151	U00152	U00153	U00154	U00155	U00156	U00157	U00158	U00159	U00160	U00161	U00162	U00163	U00164	U00165	U00166	U00167	U00168	U00169	U00170	U00171	U00172	U00173	U00174	U00175	U00176	U00177	U00178	U00179	U00180	U00181	U00182	U00183	U00184	U00185	U00186	U00187	U00188	U00189	U00190	U00191	U00192	U00193	U00194	U00195	U00196	U00197	U00198	U00199	U00200	U00201	U00202	U00203	U00204	U00205	U00206	U00207	U00208	U00209	U00210	U00211	U00212	U00213	U00214	U00215	U00216	U00217	U00218	U00219	U00220	U00221	U00222	U00223	U00224	U00225	U00226	U00227	U00228	U00229	U00230	U00231	U00232	U00233	U00234	U00235	U00236	U00237	U00238	U00239	U00240	U00241	U00242	U00243	U00244	U00245	U00246	U00247	U00248	U00249	U00250	U00251	U00252	U00253	U00254	U00255	U00256	U00257	U00258	U00259	U00260	U00261	U00262	U00263	U00264	U00265	U00266	U00267	U00268	U00269	U00270	U00271	U00272	U00273	U00274	U00275	U00276	U00277	U00278	U00279	U00280	U00281	U00282	U00283	U00284	U00285	U00286	U00287	U00288	U00289	U00290	U00291	U00292	U00293	U00294	U00295	U00296	U00297	U00298	U00299	U00300	U00301	U00302	U00303	U00304	U00305	U00306	U00307	U00308	U00309	U00310	U00311	U00312	U00313	U00314	U00315	U00316	U00317	U00318	U00319	U00320	U00321	U00322	U00323	U00324	U00325	U00326	U00327	U00328	U00329	U00330	U00331	U00332	U00333	U00334	U00335	U00336	U00337	U00338	U00339	U00340	U00341	U00342	U00343	U00344	U00345	U00346	U00347	U00348	U00349	U00350	U00351	U00352	U00353	U00354	U00355	U00356	U00357	U00358	U00359	U00360	U00361	U00362	U00363	U00364	U00365	U00366	U00367	U00368	U00369	U00370	U00371	U00372	U00373	U00374	U00375	U00376	U00377	U00378	U00379	U00380	U00381	U00382	U00383	U00384	U00385	U00386	U00387	U00388	U00389	U00390	U00391	U00392	U00393	U00394	U00395	U00396	U00397	U00398	U00399	U00400	U00401	U00402	U00403	U00404	U00405	U00406	U00407	U00408	U00409	U00410	U00411	U00412	U00413	U00414	U00415	U00416	U00417	U00418	U00419	U00420	U00421	U00422	U00423	U00424	U00425	U00426	U00427	U00428	U00429	U00430	U00431	U00432	U00433	U00434	U00435
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```

b 151 agtatctctcattgcctgtgtg 171
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p 21 AGGATCCTCATTACTTTGTG 1
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

RESULT	5	236 bp	mRNA	EST	14-FEB-1996
LOCUS	N48736				
DEFINITION	yy55d11.r1 Homo sapiens cDNA clone 277461 5'.				
ACCESSION	N48736				
IID	gi1189902				
KEYWORDS	EST.				

SOURCE

human clones-277461 primer=T7 library=Soares multiple sclerosis 2NbJMSIP vector=p7T73D (Pharmacia) with a modified polyLinker V type; phagemid host=DH10B (ampicillin resistant) Raitel=Not I Raitel2=Eco RI 46 year old male. 1st strand cDNA was primed with a Not I- oligo(dT) primer [5'-TGTTACCAATCGAATGGCGCGCGATTTTTTTTTTTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified p7T7 vector (Pharmacia). Library went

through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from 4 multiple sclerosis lesions from one patient was kindly provided by Dr. Kevin G. Becker (NINDS/NIH).

## ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Homidae; Homo. 1 (bases 1 to 236)

## REFERENCE

## AUTHORS

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevas, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.

The WashU-Merck EST Project

Unpublished (1995)

## TITLE

## JOURNAL

## COMMENT

Contact: Wilson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.edu  
High quality sequence stops: 193  
Source: IMAGE Consortium, LNL

This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

## FEATURES

source

1..236  
/organism="Homo sapiens"  
/clone="277461"  
/note="human"  
<1..>236

mRNA

BASE COUNT

ORIGIN

51 a 44 c 50 g 87 t 4 others

Query Match 55.6%; Score 15; DB 61; Length 236;  
Best Local Similarity 85.7%; Pred. No. 4.99e-02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 168 agtactctcattgcttgctg 188

Cp 21 AGGATCCTCATTACTTTCTG 1

## RESULT

ID HSW04100 standard; RNA; EST; 305 BP.

AC W04100;

DT 30-APR-1996 (Rel. 47, Created)

DT 30-APR-1996 (Rel. 47, Last updated, Version 1)

DE T1792 W04100 bloodstream form of serodeme WRATat1.1 Trypanosoma

DE brucei rhodesiense cDNA 5'.

RW EST.

OS Trypanosoma brucei rhodesiense

OC Eukaryota; Animalia; Protozoa; Sarcostigophora; Mastigophora;

OC Zoomastigophora; Kinetoplastida; Trypanosomatina; Trypanosomatidae.

RN [1]

RP 1-305

RA Majiwa P.A.O.;

RT "Facile identification of genes of the Trypanosoma by single pass

RT cDNA sequence determination";

RL Unpublished.

Contact: Majiwa PAO Molecular Biology Unit International Livestock Research Institute P.O. Box 30709, Nairobi, Kenya Tel: 254-2 630743  
CC Fax: 254-2 631499 Email: p.majiwa@cnet.com Seq primer: T3 primer.  
CC NCBI gi: 1275942

## FH Key

Location/Qualifiers

FH source 1..305

FT /organism="Trypanosoma brucei rhodesiense"

FT /note="Vector: Lambda ZAP II (Stratagene); Site 1: EcoRI;

FT Site 2: XhoI; The mRNA was purified from a cloned

FT population of bloodstream trypanosomes reexpressing the

FT W04100 metacyclic variant surface glycoprotein (VSG). A

FT unidirectional oligo dT-primed EcoRI/XhoI cDNA library was

FT constructed in Lambda ZAP II (Stratagene)."

FT /clone\_lib="W04100 bloodstream form of serodeme WRATat1.1"

FT mRNA <1..>305

SQ Sequence 305 BP; 74 A; 71 C; 88 G; 72 T; 0 other;

Query Match 55.6%; Score 15; DB 168; Length 305;  
Best Local Similarity 80.0%; Pred. No. 4.99e-02;  
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Db 182 agcaaatcaatgagggctcctac 206

Qy 2 ACCAAAGTATGAGGATCTCCGAC 26

## RESULT

LOCUS

DEFINITION T1792 W04100 bloodstream form of serodeme WRATat1.1 Trypanosoma

brucei rhodesiense cDNA 5'.

ACCESSION W04100

NID g1275942

KEYWORDS EST.

SOURCE Trypanosoma brucei rhodesiense.

Trypanosoma brucei rhodesiense

Eukaryota; mitochondrial eukaryotes; Euglenozoa; Kinetoplastida;

Trypanosomatidae; Trypanosoma.

REFERENCE 1 (bases 1 to 305)

AUTHORS Majiwa, P.A.O.

TITLE Facile identification of genes of the Trypanosoma by single pass

cDNA sequence determination

Unpublished (1996)

JOURNAL

COMMENT

Contact: Majiwa PAO  
Molecular Biology Unit  
International Livestock Research Institute  
P.O. Box 30709, Nairobi, Kenya  
Tel: 254-2 630743  
Fax: 254-2 631499  
Email: p.majiwa@cnet.com  
Seq primer: T3 primer.

NCBI gi: 1275942

Location/Qualifiers

source

1..305

/organism="Trypanosoma brucei rhodesiense"

/note="Vector: Lambda ZAP II (Stratagene); Site 1: EcoRI;

Site 2: XhoI; The mRNA was purified from a cloned

FT population of bloodstream trypanosomes reexpressing the

FT W04100 metacyclic variant surface glycoprotein (VSG). A

FT unidirectional oligo dT-primed EcoRI/XhoI cDNA library was

FT constructed in Lambda ZAP II (Stratagene)."

FT /clone\_lib="W04100 bloodstream form of serodeme WRATat1.1"



RESULT 11

L-452, Biology and Biotechnology Research Program,  
Livermore National Laboratory, Livermore, CA 94550



Mar 19 08:20

US-08-612-929-19.rst

13

Tel: 5104225711  
Fax: 5104233608  
Email: greg@medel.llnl.gov.  
Location/Qualifiers

FEATURES

source  
1..361  
/organism="Homo sapiens"  
/clone="LLAB284F11"  
/note="human"  
<1..>361

mRNA

BASE COUNT 101 a 124 c 39 g 94 t 3 others  
ORIGIN

Query Match 55.6%; Score 15; DB 108; Length 361;  
Best Local Similarity 89.5%; Pred. No. 4.99e-02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 286 gatctcattactattctg 304

Cp 19 GATCCTCATTACTTTGCTG 1  
|||||

RESULT 13

LOCUS T26512 361 bp mRNA EST 15-APR-1996  
DEFINITION AB284F11R Homo sapiens cDNA clone LLAB284F11 5'.

ACCESSION T26512

NTID g773829

KEYWORDS EST.

SOURCE human clone=LLAB284F11 primer=M13 Reverse library=Infant brain,  
LLNL array of Dr. M. Soares INTB vector=tafmid BA Rsite1=HindIII  
Rsite2=NotI Normalized infant brain cDNA library made by Dr. M.  
Soares (Columbia University), oligo-dT primed and directionally  
cloned between HindIII (5') and NotI (3') sites.

ORGANISM

Homo sapiens  
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;  
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;  
Sarcopterygii; Choonata; Tetrapoda; Amniota; Mammalia; Theria;  
Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 361)

AUTHORS Ghiso,N.S., Eveleth,G.G., Lieuallen,K. and Lennon,G.G.

TITLE Chromosomal assignment of 20 cDNAs using flow-sorted spot-blot  
stamps

JOURNAL Genomics 28 (3), 570-572 (1995)

MEDLINE 96039272

COMMENT

Contact: Greg G. Lennon  
Human Genome Center, L-452  
Lawrence Livermore National Laboratory  
Livermore CA 94550  
Tel: 510 422 8361  
Fax: 510 422 2282  
Email: info@limage.llnl.gov.

FEATURES

source

1..361  
/organism="Homo sapiens"  
/clone="LLAB284F11"  
/note="human"  
<1..>361

mRNA

BASE COUNT 101 a 124 c 39 g 94 t 3 others  
ORIGIN

Query Match 55.6%; Score 15; DB 143; Length 361;  
Best Local Similarity 89.5%; Pred. No. 4.99e-02;

Mar 19 08:20

US-08-612-929-19.rst

14

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 286 gatctcattactattctg 304

Cp 19 GATCCTCATTACTTTGCTG 1  
|||||

RESULT 14

LOCUS HSPD03654 368 bp DNA EST 22-DEC-1995  
DEFINITION H.sapiens mitochondrial EST sequence (004-X2-28) from skeletal  
muscle.

ACCESSION F19057

NTID g1135472

KEYWORDS EST.

SOURCE human.

ORGANISM

Homo sapiens  
Eukaryotae; Mitochondrial eukaryotes; Metazoa; Chordata;  
Vertebrata; Euthera; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 368)  
AUTHORS Lanfranchi,G., Muraro,T., Caldara,F., Pacchioni,B., Pallavicini,A.,  
Pandolfo,D., Toppo,S., Trevisan,S., Scarso and Valle,G.

TITLE Identification of 4,370 expressed sequence tags (ESTs) from a  
3'-end specific cDNA library of human skeletal muscle by DNA  
sequencing and filter hybridisation

JOURNAL Genome Res. (1996) in press

REFERENCE 2 (bases 1 to 368)

AUTHORS Valle,G.

TITLE Direct Submission

JOURNAL Submitted (19-DEC-1995) CRIBI Biotechnology Centre, University of  
Padua, Via Trieste 75, 35121 Padua, Italy  
COMMENT ABI Chromatograms and other information are available on WWW at  
http://eos.bio.unipd.it

Vector: pcDNAII (Invitrogen)

V type: Plasmid

RE\_1: EcoRI

RE\_2: NotI

PRIMER: PC2R

DESCR: The cDNA was constructed using a biotin-NotI-oligo(dT)  
primer,

sonicated and size selected (450-550 BP). The biotinylated 3'-ends  
were affinity purified, directionally cloned and sequenced (5' ->  
3').

FEATURES

source

Location/Qualifiers

1..368

/organism="Homo sapiens"

/note="caucasian"

/tissue type="pectoral muscle (after mastectomy)"

/clone\_lib="HM1"

/sex="female"

BASE COUNT 108 a 123 c 39 g 89 t 9 others

ORIGIN

Query Match 55.6%; Score 15; DB 46; Length 368;  
Best Local Similarity 88.9%; Pred. No. 4.99e-02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 24 atctcattactatnctg 41

Cp 18 ATCCTCATTACTTTGCTG 1  
|||||

RESULT 15

ID HSPD03654 standard; DNA; EST; 368 BP.

AC F19057;

Mar 19 08:20

US-08-612-920-19.rst

15

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DT 22-DEC-1995 (Rel. 46, Created)
DE 06-MAY-1996 (Rel. 47, Last updated, Version 2)
DE H.sapiens mitochondrial EST sequence (004-X2-28) from skeletal
DE muscle.
KW EST.
OS Homo sapiens (human)
OC Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
OC Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominoidea.
RN [1]
RP 1-368
RA Lanfranchi G., Muraro T., Caldara F., Pacchioni B.,
RA Pallavicini A., Pandolfo D., Toppo S., Trevisan S.,
RA Scarso and Valle G.;
RT "Identification of 4,370 expressed sequence tags (ESTs) from a
RT 3'-end specific cDNA library of human skeletal muscle by DNA
RT sequencing and filter hybridisation";
RL Genome Res. 1:35-42 (1996).
RV [2]
RP 1-368
RA Valle G.;
RT ;
RL Submitted (19-DEC-1995) to the EMBL/GenBank/DBJ databases.
RL CRIBI Biotechnology Centre, University of Padua, Via Trieste 75,
RL 35121 Padua, Italy.
CC ABI Chromatograms and other information are available on WWW at
CC http://eos.bio.unipd.it
CC Vector: pcDNAII (Invitrogen)
CC V_type: Plasmid
CC RE_1: EcoRI
CC RE_2: NotI
CC PRIMER: PC2R
CC DESC: The cDNA was constructed using a biotin-NotI-oligo(dT)
CC primer,
CC sonicated and size selected (450-550 BP). The biotinylated 3'-ends
CC were affinity purified, directionally cloned and sequenced (5' ->
CC 3').
FH Key
FH Location/Qualifiers
FT source
FT 1..368
FT /organism="Homo sapiens"
FT /tissue_type="pectoral muscle (after mastectomy)"
FT /clone_lib="HM1"
FT /note="caucasian"
FT /sex="female"
SQ Sequence 368 BP; 108 A; 123 C; 39 G; 89 T; 9 other;

Query Match 55.6%; Score 15; DB 168; Length 368;
Best Local Similarity 88.9%; Pred. No. 4.99e-02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 24 atccctactactatnctg 41
|||||
Cp 18 ATCCTCAATTAATTCGTC 1
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Search completed: Wed Mar 19 08:22:09 1997  
Job time : 69 secs.

\*\*\*\*\*

WQ5REH (TM)

\*\*\*\*\*

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Distribution rights by IntelliGenetics, Inc.

MParch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed Mar 19 08:20:26 1997; MasPar time 10.83 Seconds  
217.531 Million cell updates/sec

Tabular output not generated.

Title: &gt;US-08-612-929-19

Description: (1-27) from US08612929.seq

Perfect Score: 27

N.A. Sequence: 1 CAGCAAGTAATGAGGATCTCGGACG 27

Comp: GTCGTTTCATTACTCTAGGAGCTCC

Scoring table: TABLE default

Gap 10

Nmatch STD : Dbase 0; Query 0

Searched: 113505 seqs, 43611913 bases x 2

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: n-geneseq25

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13  
14:part14 15:part15 16:part16 17:part17 18:part18  
19:part19 20:part20 21:part21 22:part22

Statistics: Mean 5.665; Variance 3.162; scale 1.792

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	27	100.0	393 14	Q83520	Humanized antibody 3B	1.39e-06
2	27	100.0	396 14	Q83490	Mouse MAb 3B9 light c	1.39e-06
3	25	92.6	51 14	Q83511	IL-4 CDR3 gene fragme	2.52e-05
4	25	92.6	53 14	Q83512	IL-4 CDR3 gene fragme	2.52e-05
5	25	92.6	99 9	Q55014	Humanized Ab 60.3 VL	2.52e-05
6	25	92.6	334 9	Q55002	Murine anti-CD18 Ab 6	2.52e-05
7	25	92.6	334 9	Q55000	Humanised anti-CD18 A	2.52e-05
8	25	92.6	393 5	Q30757	p64-k4.	2.52e-05

9	25	92.6	393 6	Q36609	Anti-CD4 antibody MT	2.52e-05
10	25	92.6	393 14	Q73986	Humanized antibody 3B	2.52e-05
11	23	85.2	336 2	Q12684	Murine 1B4 light chai	4.32e-04
12	23	85.2	645 13	Q80292	Monoclonal antibody 2	4.32e-04
13	22	81.5	87 9	Q55013	Humanised Ab 60.3 VL	1.75e-03
14	22	81.5	91 9	Q51746	Oligonucleotide probe	1.75e-03
15	22	81.5	900 1	Q04039	Anti-Leu 3a light cha	1.75e-03
16	21	77.8	91 9	Q51746	Oligonucleotide probe	6.93e-03
17	21	77.8	309 9	Q55915	Light chain region of	6.93e-03
18	21	77.8	333 11	Q65554	Mouse anti-HIV mu5.5	6.93e-03
19	21	77.8	333 9	Q55917	Humanised light chain	6.93e-03
20	21	77.8	333 12	Q70372	Anti HIV antibody lig	6.93e-03
21	21	77.8	451 1	Q04694	Light chain variable	6.93e-03
22	20	74.1	41 2	Q12690	Rei light chain varia	2.70e-02
23	20	74.1	45 2	Q12691	Rei light chain varia	2.70e-02
24	20	74.1	334 1	N90492	Gene fragment of immu	2.70e-02
25	20	74.1	396 7	Q42987	Mouse 4C10 anti-idiot	2.70e-02
26	20	74.1	733 4	Q25658	Mouse 0.5beta anti-HI	2.70e-02
27	20	74.1	780 1	N90495	A V chi region gene.	2.70e-02
28	19	70.4	333 12	Q70376	Chimeric anti HIV ant	1.03e-01
29	19	70.4	333 11	Q55558	Mouse-human chimeric	1.03e-01
30	19	70.4	333 14	Q82818	Murine NM-01 variable	1.03e-01
31	19	70.4	334 11	Q73749	Light chain variable	1.03e-01
32	19	70.4	336 2	Q10379	Chimeric MAb 9.2.27 1	1.03e-01
33	19	70.4	363 10	Q56688	Sequence of the monoc	1.03e-01
34	18	66.7	336 16	Q96283	Human IgE receptor-bi	3.84e-01
35	18	66.7	336 16	Q96285	Human IgE receptor-bi	3.84e-01
36	18	66.7	363 6	Q37472	Sequence encoding the	3.84e-01
37	18	66.7	363 10	Q56686	Sequence of the monoc	3.84e-01
38	18	66.7	1014 2	Q10834	Encodes kappa light c	3.84e-01
39	17	63.0	118 4	Q26784	Oligomer ma8 used to	1.39e+00
40	17	63.0	204 1	N81164	Base substituted E.co	1.39e+00
41	17	63.0	333 11	Q63908	Light chain variable	1.39e+00
42	17	63.0	339 18	T04013	Anti-EGFR antibody 1i	1.39e+00
43	17	63.0	339 18	T04015	Anti-EGFR antibody 1i	1.39e+00
44	17	63.0	632 10	Q56691	Genomic sequence of t	1.39e+00
45	17	63.0	2015 5	Q30455	Sequence of ACP (acyl	1.39e+00

## ALIGNMENTS

RESULT 1  
ID Q83520 standard; cDNA; 393 BP.  
AC Q83520;  
DT 20-SEP-1995 (first entry)  
DE Humanized antibody 3B9 light chain.  
KW Humanized antibody; antibody engineering; monoclonal antibody;  
KW MAb; interleukin-4; IL-4; allergy; ds.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT CDS 1..393  
FT /\*tag= a  
PN WO9507301-A.  
PD 16-MAR-1995.  
PF 07-SEP-1994; U10308.  
PR 07-SEP-1993; US-117366.  
PR 14-OCT-1993; US-136783.  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
PA (SMIK ) SMITHKLINE BEECHAM PLC.  
PI Gross MS, Holmes SD, Sylvester DR;  
DR WPI; 95-123387/16.  
DR P-PSDB; R70202.  
PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived  
PT from high affinity mAbs - useful in treatment of IL-4-mediated

PT and IgE-mediated allergic conditions  
PS Disclosure; Page 71-72; 97pp; English.  
CC A humanized antibody light chain variable region and signal  
CC sequence is given in R75355. The signal sequence is also  
CC provided in R70194. The sequences of the 3 CDRs  
CC are identical to mouse anti-human IL-4 Mab 3B9 light chain  
CC CDRs (given in R70195-97).  
SQ Sequence 393 BP; 97 A; 98 C; 105 G; 93 T;

Query Match 100.0%; Score 27; DB 14; Length 393;  
Best Local Similarity 100.0%; Pred. No. 1.39e-06;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 334 cagcaagaatgagatcctccgacg 360  
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Qy 1 CAGCAAGTAATGAGATCCTCCGACG 27

RESULT 2  
ID Q83490 standard; cDNA; 396 BP.  
AC Q83490;  
DT 20-SEP-1995 (first entry)  
DE Mouse Mab 3B9 light chain.  
KW Chimeric antibody; humanized antibody; antibody engineering;  
KW monoclonal antibody; Mab; interleukin-4; IL-4; allergy; ds.  
OS Mus sp.

FT	Key	Location/Qualifiers
FT CDS	1..396	
FT /tag= a		
FT sig_peptide	1..60	
FT /tag= b		
FT mat_peptide	61..396	
FT /tag= c		
PN W09507301-A.		
PD 16-MAR-1995.		
PF 07-SEP-1994; U10308.		
PR 07-SEP-1993; US-117366.		
PR 14-OCT-1993; US-136783.		
PA (SMIK ) SMITHKLINE BEECHAM CORP.		
PA (SMIK ) SMITHKLINE BEECHAM PLC.		
PI Gross MS, Holmes SD, Sylvester DR;		
DR P-PSDB; R70189.		
PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived		
PT from high affinity mAbs - useful in treatment of IL-4-mediated		
PT and IgE-mediated allergic conditions		
PS Disclosure; Fig.1; 97pp; English.		
CC Spleen cells from mice immunized with human IL-4 were used to prepare		
CC hybridomas, which were screened for anti-IL-4 Mab secretion. Only		
CC clone 3B9 was positive. cDNA clones of the 3B9 light and heavy		
CC chains were cloned into pGEM7f+ and transformed into E. coli		
CC DH5-alpha. The clones were sequenced (Q83490-91), and used for		
CC antibody engineering.		
SQ Sequence 396 BP; 99 A; 103 C; 103 G; 91 T;		

Query Match 100.0%; Score 27; DB 14; Length 396;  
Best Local Similarity 100.0%; Pred. No. 1.39e-06;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 337 cagcaagaatgagatcctccgacg 363  
|||||  
Qy 1 CAGCAAGTAATGAGATCCTCCGACG 27

RESULT 3  
ID Q83511 standard; DNA; 51 BP.  
AC Q83511;  
DT 20-SEP-1995 (first entry)  
DE IL-4 CDR3 gene fragment.  
KW Humanized antibody; antibody engineering; monoclonal antibody;  
KW Mab; interleukin-4; IL-4; allergy; heavy chain; CDR;  
KW complementarity determining region; ss.  
OS Synthetic.  
PN W09507301-A.  
PD 16-MAR-1995.  
PF 07-SEP-1994; U10308.  
PR 07-SEP-1993; US-117366.  
PR 14-OCT-1993; US-136783.  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
PA (SMIK ) SMITHKLINE BEECHAM PLC.  
PI Gross MS, Holmes SD, Sylvester DR;

DR WPI; 95-123387/16.  
PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived  
PT from high affinity mAbs - useful in treatment of IL-4-mediated  
PT and IgE-mediated allergic conditions  
PS Example 3; Page 28; 97pp; English.  
CC A humanized antibody was designed to contain mouse CDRs (from  
CC anti-IL-4 Mab 3B9 Mab) within a human antibody framework. A  
CC synthetic heavy chain was made using the oligonucleotides given  
CC in Q83498-502 and amplified by PCR using the primers given in  
CC Q83503-04. The construct was ligated into vector pCD, along  
CC with a signal sequence (Q83494) and an IgG1 human constant  
CC region. The CDR gene regions of a pre-existing light chain  
CC framework were replaced with synthetic IL-4 CDR genes constructed  
CC from oligonucleotides given in Q83505-08 (CDR1), Q83509-10 (CDR2),  
CC and Q83511-12 (CDR3). The synthetic VL (Q73986) was ligated into  
CC the vector. The anti-IL4 engineered antibody was expressed in  
CC COS and CHO cells.

SQ Sequence 51 BP; 14 A; 11 C; 16 G; 10 T;  
Query Match 92.6%; Score 25; DB 14; Length 51;  
Best Local Similarity 100.0%; Pred. No. 2.52e-05;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 11 cagcaagaatgagatcctccga 35  
|||||  
Qy 1 CAGCAAGTAATGAGATCCTCCGA 25

RESULT 4  
ID Q83512 standard; DNA; 53 BP.  
AC Q83512;  
DT 20-SEP-1995 (first entry)  
DE IL-4 CDR3 gene fragment.  
KW Humanized antibody; antibody engineering; monoclonal antibody;  
KW Mab; interleukin-4; IL-4; allergy; heavy chain; CDR;  
KW complementarity determining region; ss.  
OS Synthetic.  
PN W09507301-A.  
PD 16-MAR-1995.  
PF 07-SEP-1994; U10308.  
PR 07-SEP-1993; US-117366.  
PR 14-OCT-1993; US-136783.  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
PA (SMIK ) SMITHKLINE BEECHAM PLC.  
PI Gross MS, Holmes SD, Sylvester DR;

DR WPI; 95-123387/16.  
PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived

Mar 19 08:18

US-08-612-929-19 mg

5

PT from high affinity mabs - useful in treatment of IL-4-mediated  
PT and IgE-mediated allergic conditions  
PS Example 3; Page 28; 97pp; English.  
CC A humanized antibody was designed to contain mouse CDRs (from  
CC anti-IL-4 Mab 3B9 Mab) within a human antibody framework. A  
CC synthetic heavy chain was made using the oligonucleotides given  
CC in Q83498-502 and amplified by PCR using the primers given in  
CC Q83503-04. The construct was ligated into vector pCD, along  
CC with a signal sequence (Q83494) and an IgG1 human constant  
CC region. The CDR gene regions of a pre-existing light chain  
CC framework were replaced with synthetic IL-4 CDR genes constructed  
CC from oligonucleotides given in Q83505-08 (CDR1), Q83509-10 (CDR2),  
CC and Q83511-12 (CDR3). The synthetic VL (Q73986) was ligated into  
CC the vector. The anti-IL4 engineered antibody was expressed in  
CC COS and CHO cells.  
SQ Sequence 53 BP; 9 A; 17 C; 12 G; 15 T;  
  
Query Match 92.6%; Score 25; DB 14; Length 53;  
Best Local Similarity 100.0%; Pred. No. 2.52e-05;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Db 21 tcggaggtctcttactttctg 45  
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Cp 25 TCGGAGATCCTCATTACTTCTG 1  
  
RESULT 5  
ID Q55014 standard; DNA; 99 BP.  
AC Q55014;  
DT 06-JUL-1994 (first entry)  
DE Humanised Ab 60.3 VL oligonucleotide.  
KW Monoclonal antibody; Mab; heavy chain; light chain;  
KW constant region; variable region; amplification; primer;  
KW polymerase chain reaction; PCR; chimera; Ig;  
KW immunoglobulin; humanised antibody; leucocyte; integrin; ss.  
OS Synthetic.  
PN EP-578515-A.  
PD 12-JAN-1994.  
PF 24-MAY-1993; 401328.  
PR 26-MAY-1992; US-888233.  
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
PI Bajorath J, Harris LJ, Heiao K, Ku-Chuan H;  
DR WPI; 94-010334/02.  
PT Humanised monoclonal antibodies prepn. - using comparative model  
PT building, by computer database searching  
PS Disclosure; Fig 3; 68pp; English.  
CC A humanised monoclonal antibody corresponding to the murine anti-CD18  
CC antibody 60.3 was prepared. The variable (V) region sequences from  
CC both the heavy (H) and light (L) chains were determined from cDNA  
CC (amplified by PCR), and spliced onto human constant (C) regions,  
CC resulting in a chimeric 60.3 Ab (IgG1, kappa). The chimeric Ab was  
CC expressed in tissue culture (Aq8.653 mouse myeloma cells, detected  
CC by ELISA), and examined in binding assays. The results from  
CC competition and inhibition assays showed that the chimeric Ab was  
CC as effective as the murine 60.3 Mab. The deduced murine VH and VL  
CC protein sequences were compared to the protein sequence data base,  
CC and two human Ig protein sequences were selected to be used as  
CC templates. A murine 60.3 Fv was modeled according to the deduced  
CC VH and VL protein sequences. Based on the 60.3 Fv model and the two  
CC human template sequences selected from the protein data base, a  
CC humanised Fv was modeled. Construction of the humanised 60.3 was  
CC done by piecing 5 pairs of complementary oligonucleotides together  
CC (spanning the entire V region) to form the VH and VL. These were  
CC then attached onto vectors containing genes for appropriate C regions

Mar 19 08:18

US-08-612-929-19 mg

6

CC to form humanised Ab (IgG1, kappa). The humanised proteins were again  
CC expressed in Aq8.653 cells and binding assays were done. FACS analyses  
CC indicated that the humanised Ab recognised cells expressing CD18.  
CC About a dozen of the humanised 60.3 Ab master wells were transferred  
CC and assayed for Ig.  
SQ Sequence 99 BP; 26 A; 28 C; 19 G; 26 T;  
  
Query Match 92.6%; Score 25; DB 9; Length 99;  
Best Local Similarity 96.3%; Pred. No. 2.52e-05;  
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Db 64 cgtccgaggtctcttactttctg 90  
|||||  
Cp 27 CGTCGGAGATCCTCATTACTTCTG 1  
  
RESULT 6  
ID Q55002 standard; DNA; 334 BP.  
AC Q55002;  
DT 06-JUL-1994 (first entry)  
DE Murine anti-CD18 Ab 60.3 light chain.  
KW Monoclonal antibody; Mab; heavy chain; light chain;  
KW constant region; variable region; amplification; primer;  
KW polymerase chain reaction; PCR; chimera; Ig;  
KW immunoglobulin; humanised antibody; leucocyte; integrin; ss.  
OS Mus sp.  
PN EP-578515-A.  
PD 12-JAN-1994.  
PF 24-MAY-1993; 401328.  
PR 26-MAY-1992; US-888233.  
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
PI Bajorath J, Harris LJ, Heiao K, Ku-Chuan H;  
DR WPI; 94-010334/02.  
DR P-PSDB; R47494.  
PT Humanised monoclonal antibodies prepn. - using comparative model  
PT building, by computer database searching  
PS Disclosure; Page 21; 68pp; English.  
CC A humanised monoclonal antibody corresponding to the murine anti-CD18  
CC antibody 60.3 was prepared. The variable (V) region sequences from  
CC both the heavy (H) and light (L) chains were determined from cDNA  
CC (amplified by PCR), and spliced onto human constant (C) regions,  
CC resulting in a chimeric 60.3 Ab (IgG1, kappa). The chimeric Ab was  
CC expressed in tissue culture (Aq8.653 mouse myeloma cells, detected  
CC by ELISA), and examined in binding assays. The results from  
CC competition and inhibition assays showed that the chimeric Ab was  
CC as effective as the murine 60.3 Mab. The deduced murine VH and VL  
CC protein sequences were compared to the protein sequence data base,  
CC and two human Ig protein sequences were selected to be used as  
CC templates. A murine 60.3 Fv was modeled according to the deduced  
CC VH and VL protein sequences. Based on the 60.3 Fv model and the two  
CC human template sequences selected from the protein data base, a  
CC humanised Fv was modeled. Construction of the humanised 60.3 was  
CC done by piecing 5 pairs of complementary oligonucleotides together  
CC (spanning the entire V region) to form the VH and VL. These were  
CC then attached onto vectors containing genes for appropriate C regions  
CC to form humanised Ab (IgG1, kappa). The humanised proteins were again  
CC expressed in Aq8.653 cells and binding assays were done. FACS analyses  
CC indicated that the humanised Ab recognised cells expressing CD18.  
CC About a dozen of the humanised 60.3 Ab master wells were transferred  
CC and assayed for Ig.  
SQ Sequence 334 BP; 88 A; 85 C; 81 G; 80 T;  
  
Query Match 92.6%; Score 25; DB 9; Length 334;  
Best Local Similarity 96.3%; Pred. No. 2.52e-05;

Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 277 cagcaagaatgaggtatctccgacg 303  
 |||||

Qy 1 CAGCAAGTAATGAGGATCTCCGACG 27

## RESULT 7

ID Q55000 standard; DNA; 334 BP.  
 AC Q55000;  
 DT 06-JUL-1994 (first entry)  
 DE Humanised anti-CD18 Ab 60.3 light chain.  
 KW Monoclonal antibody; Mab; heavy chain; light chain;  
 KW constant region; variable region; amplification; primer;  
 KW polymerase chain reaction; PCR; chimera; Ig;  
 KW immunoglobulin; humanised antibody; leucocyte; integrin; ss.  
 OS Chimeric; Homo sapiens.  
 OS Chimeric; Mus sp.  
 PN EP-578515-A.  
 PD 12-JAN-1994.  
 PF 24-MAY-1993; 401328.  
 PR 26-MAY-1992; US-888233.  
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.  
 PI Bajorath J, Harris LJ, Hsiao K, Ku-Chuan H;  
 DR WPI; 94-010334/02.  
 DR P-PSDB; R47492.  
 PT Humanised monoclonal antibodies prepn. - using comparative model building, by computer database searching  
 PS Disclosure; Page 18-19; 68pp; English.  
 CC A humanised monoclonal antibody corresponding to the murine anti-CD18  
 CC antibody 60.3 was prepared. The variable (V) region sequences from  
 CC both the heavy (H) and light (L) chains were determined from cDNA  
 CC (amplified by PCR), and spliced onto human constant (C) regions,  
 CC resulting in a chimeric 60.3 Ab (IgG1, kappa). The chimeric Ab was  
 CC expressed in tissue culture (A9.653 mouse myeloma cells, detected  
 CC by ELISA), and examined in binding assays. The results from  
 CC competition and inhibition assays showed that the chimeric Ab was  
 CC as effective as the murine 60.3 Mab. The deduced murine VH and VL  
 CC protein sequences were compared to the protein sequence data base,  
 CC and two human Ig protein sequences were selected to be used as  
 CC templates. A murine 60.3 Fv was modeled according to the deduced  
 CC VH and VL protein sequences. Based on the 60.3 Fv model and the two  
 CC human template sequences selected from the protein data base, a  
 CC humanised Fv was modeled. Construction of the humanised 60.3 was  
 CC done by piecing 5 pairs of complementary oligonucleotides together  
 CC (spanning the entire V region) to form the VH and VL. These were  
 CC then attached onto vectors containing genes for appropriate C regions  
 CC to form humanised Ab (IgG1, kappa). The humanised proteins were again  
 CC expressed in A9.653 cells and binding assays were done. FACS analyses  
 CC indicated that the humanised Ab recognised cells expressing CD18.  
 CC About a dozen of the humanised 60.3 Ab master wells were transferred  
 CC and assayed for Ig.  
 SQ Sequence 334 BP; 90 A; 79 C; 80 G; 85 T;

Query Match 92.6%; Score 25; DB 9; Length 334;  
 Best Local Similarity 96.3%; Pred. No. 2.52e-05;  
 Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 277 cagcaagaatgaggtatctccgacg 303

Qy 1 CAGCAAGTAATGAGGATCTCCGACG 27

## RESULT 8

ID Q30757 standard; cDNA; 393 BP.

AC Q30757;  
 DT 30-MAR-1993 (first entry)  
 DE p64-k4.  
 KW Human; antibody; interleukin-6; receptor; IL-6R; light chain; L; H;  
 KW heavy chain; variable region; mouse; monoclonal; hybridoma; AUK64-7;  
 KW plasmid; p64-k4; p64-h2; ss.  
 OS Synthetic.

FH Key Location/Qualifiers  
 FT sig\_peptide 1..60  
 FT /\*tag= a  
 FT mat\_peptide 61..393  
 FT /\*tag= b  
 PN W09219759-A.  
 PD 12-NOV-1992. J00544.  
 PF 24-APR-1992; J00544.  
 PR 25-APR-1991; JP-095476.  
 PR 19-FEB-1992; JP-032084.  
 PA (CHUS) CHUGAI SEIYAKU KK.  
 PI Bendig MM, Jones ST, Saldanha JW, Sato K, Tsuchiya M;  
 DR WPI; 92-398882/48.  
 DR P-PSDB; R29008.  
 PT Reconstituted human antibody to human interleukin-6 receptor -  
 PT has low antigenicity and contains mouse V-region complementarity  
 PT determining regions  
 PS Disclosure; Page 124-125; 207pp; Japanese.  
 CC The sequences given in Q30757-58 were used in example to illustrate  
 CC the production of a human antibody which recognises human  
 CC interleukin-6 receptor (IL-6R). The antibody comprises light (L)  
 CC chain and heavy (H) chain variable regions which were derived from a  
 CC mouse monoclonal antibody produced from the hybridoma AUK64-7 which  
 CC contained the plasmids p64-k4 and p64-h2.  
 SQ Sequence 393 BP; 93 A; 101 C; 100 G; 99 T;

Query Match 92.6%; Score 25; DB 5; Length 393;  
 Best Local Similarity 96.3%; Pred. No. 2.52e-05;  
 Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 337 cagcaagaatgaggtatctccgacg 363

Qy 1 CAGCAAGTAATGAGGATCTCCGACG 27

## RESULT 9

ID Q36609 standard; DNA; 393 BP.  
 AC Q36609;  
 DT 02-JUN-1993 (first entry)  
 DE Anti-CD4 antibody MT 3.10 light chain variable region.  
 KW immunosuppression; tissue transplantation; graft; L chain; V region;  
 KW T-helper cell inhibition; transplant rejection; Mab;  
 KW interleukin-2 receptor; ss.  
 FH Key Location/Qualifiers  
 FT sig\_peptide 1..60  
 FT /\*tag= a  
 FT mat\_peptide 61..393  
 FT /\*tag= b  
 FT /note= "JL region begins at position 361"  
 PN DE4143214-A.  
 PD 28-JAN-1993.  
 PF 30-DEC-1991; 143214.  
 PR 25-JUL-1991; DE-124759.  
 PR 30-DEC-1991; DE-143214.  
 PA (BOEF) BOEHRINGER MANNHEIM GMBH.  
 PI Kaluza B, Riethmüller G, Scheuer W, Weidle U;

WFI; 93-037582/05.  
 P-PSDB; R32123.  
 Synergistic anti-CD4 antibody compsn. for use as immunosuppressant - comprises monoclonal anti-CD4 antibodies and monoclonal anti-IL2R alpha- or anti-IL2R beta antibodies  
 Claim 5; Page 11; 18pp; German.  
 This sequence encodes the light chain variable region of a preferred anti-CD4 monoclonal antibody for use in the claimed synergistic composition. Mab MT 3.10 is deposited as clone 3.101/SB10 (ECACC 90090702). The anti-CD4 antibody is used with at least one anti-IL2R alpha or beta antibody. Individually the antibodies are strongly inhibiting and when used together their immunosuppressive properties are improved; they synergistically inhibit T-helper cell proliferation to effectively inhibit transplant rejection at low doses without significantly reducing the general immune response.  
 See Q36607-Q36616.  
 Sequence 393 BP; 100 A; 105 C; 98 G; 90 T;

```

Query Match      92.6%; Score 25; DB 6; Length 393;
Best Local Similarity 96.3%; Pred.No. 2.52e-05;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
db 337 cagcaagtagtgagatcctccagacg 363
QV 1 CAGCAAGTAATGAGGATCCTCCGAGG 27

```

RESULT	ID	Location/Qualifiers
AC	Q73986 standard; cDNA; 393 BP.	
AC	Q73986;	
DT	20-SEP-1995 (first entry)	
DE	Humanized antibody 389 light chain.	
KW	Humanized antibody; antibody engineering; monoclonal antibody;	
KW	MAb; interleukin-4; IL-4; allergy; ds.	
OS	Homo sapiens.	
FF	Key	Location/Qualifiers
FT	CDS	1..393
FT	/*tag= a	
FT	sig_peptide	1..60
FT	/*tag= b	
FT	mat_peptide	61..393
FT	/*tag= c	
PN	W09507301-A.	
PD	16-MAR-1995.	
PF	07-SEP-1994; US-117366.	
PR	07-SEP-1993; US-117366.	
PR	14-OCT-1993; US-136783.	
PPA	(SMIK ) SMITHKLINE BEECHAM CORP.	
PPA	(SMIK ) SMITHKLINE BEECHAM PLC.	
PI	Gross MS, Holmes SD, Sylvester DR;	
PI	WPI; 95-123387/16.	
DR	P-PSDB; R75355.	
PT	Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived	
PT	from high affinity mAbs - useful in treatment of IL-4-mediated	
PT	and IgE-mediated allergic conditions	
PS	Disclosure; Fig.5; 97pp; English.	
CC	A humanized antibody light chain variable region and signal	
CC	sequence is given in R75355. The signal sequence is also	
CC	provided in R70194. The sequences of the first 2 CDRs	
CC	are identical to mouse anti-human IL-4 MAb 389 light chain	
CC	CDRs (given in R70195-96), but the third (R70201) differs	
CC	by a single amino acid from the native mouse CDR (R70197).	
SQ	Sequence 393 BP; 97 A; 96 C; 108 G; 92 T;	

Query Match	92.6%	Score 25;	DB 14;	Length 393;
Best Local Similarity	100.0%;	Pred. No. 2.52e-05;		
Matches	25;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
Ddb	334	cagcaaaagtaatgaggatcctccga	358	
Qy	1	CAGCAAAAGTAATGAGGATCCTCCGA	25	
RESULT	11			
ID	Q12684	standard; DNA; 336 BP.		
AC	Q12684;			
DT	01-OCT-1991	(first entry)		
DE	Murine 1B4 light chain-2 variable region.			
KW	Monoclonal antibody; complementary determining region; CDR;			
QW	integrin; hybridoma 1B4; protein REI; Gal/Rei; Ig; ss.			

24-JUL-1991.  
PF 17-JAN-1991; 300367.  
PPR 19-JAN-1990; US-467692.  
PR 20-DEC-1990; US-627421.  
PPA (MERI ) MERCK & CO INC.  
PPI Law MF, Mark GE, Schmidt JA, Singer II;  
DR WPI; 91-216985/30.  
DR P-PSDB; RI3089.  
DPT New recombinant immunoglobulin(s) reactive with leukocyte CD18  
DPT antigen - comprise human heavy chain framework and murine  
PPT complementarity regions useful in treatment of inflammation  
PT Disclosure; Fig 25; 77pp; English.  
CC A recombinant human Ig comprises a human heavy chain framework  
CC and murine CDRs (with the heavy chain framework mutated at sites  
CC near the CDRs), a human light chain framework and murine CDRs.  
CC It has a mean IC50 nearly equal to that of the murine monoclonal  
CC antibody from which the CDRs were derived. It is designated  
CC mutated Gal/Rei. The human Ig is capable of binding to a human  
CC CD18 integrin.  
CC The murine CDRs are obcd. from murine hybridoma 1B4  
CC (ATCC HB 10164). The light chain framework is derived from  
CC human myeloma protein REI (EP-239400).  
CC See also Q12682-84 and EP-438310.  
CC Sequence 336 BP; 80 A; 87 C; 85 G; 84 T;  
SQ

```

Query Match      85.2%; Score 23; DB 2; Length 336;
Best Local Similarity 92.6%; Pred. No. 4.32e-04;
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 277 cagcaagaatgaggatcctctcag 303
Ov 1 CAGCAAGCTATGAGGATCCTCGAGC 27

```

RESULT	12	
ID	Q80292	standard; DNA; 645 BP.
AC	Q80292;	
DT	08-JUL-1995	(first entry)
DE	Monoclonal antibody 28C5 light chain.	
KW	CD14 receptor; monoclonal antibody; 28C5; hybridoma;	
KW	antiseptic; therapeutic; ds.	
OS	Homo sapiens.	
FH	Key	Location/Qualifiers
FT	mat_peptide	1..645
FT	/*tag= a	
PN	W09428025-A.	

Mar 19 08:18

US-08-612-929-19.mg

11

PD 08-DEC-1994.  
 PF 27-MAY-1994; U05898.  
 PR 28-MAY-1993; US-070160.  
 PA (SCRI ) SCRIPPS RES INST.  
 PI Leturcq DJ, Mathison JC, Moriarty AM, Tobias PS;  
 PI Ulevitch RJ;  
 DR P-PSDB; R64202.  
 PT Hybridoma cell lines produce MAB which inhibit CD14-mediated cell  
 PT activation - for detecting CD14 in a sample and to inhibit the  
 PT binding of LPS to CD14.  
 PS Disclosure; Fig 3; 91pp; English.  
 CC Anti-human soluble CD14 receptor MAB 28C5 may be used to  
 CC detect CD14 in cell samples, to inhibit binding of LPS to  
 CC CD14 or a LPS/CD14 complex to a cell, to inhibit CD14-mediated  
 CC activation of a cell expressing CD14 receptor, and for sepsis  
 CC therapy.  
 SQ Sequence 645 BP; 180 A; 170 C; 150 G; 145 T;  
  
 Query Match 85.2%; Score 23; DB 13; Length 645;  
 Best Local Similarity 92.6%; Pred. No. 4.32e-04;  
 Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
 Db 268 cagcaagaatgagcgatcgagcg 294  
 QY 1 CAGCAAGTATGAGGATCTCCGACG 27  
 |||||||||||||||||||  
  
 RESULT 13  
 ID Q55013 standard; DNA; 87 BP.  
 AC Q55013;  
 DT 06-JUL-1994 (first entry)  
 DE Humanised Ab 60.3 VL oligonucleotide.  
 KW Monoclonal antibody; MAB; heavy chain; light chain;  
 KW constant region; variable region; amplification; primer;  
 KW polymerase chain reaction; PCR; chimera; Ig;  
 KW immunoglobulin; humanised antibody; leucocyte; integrin; ss.  
 OS Synthetic.  
 PN EP-578515-A.  
 PD 12-JAN-1994.  
 PF 24-MAY-1993; 401328.  
 PR 26-MAY-1992; US-888233.  
 PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
 PI Bajorath J, Harris LJ, Hsiao K, Ku-Chuan H;  
 DR WPI; 94-010334/02.  
 PT Humanised monoclonal antibodies prepn. - using comparative model  
 PT building, by computer database searching  
 PS Disclosure; Fig 3; 68pp; English.  
 CC A humanised monoclonal antibody corresponding to the murine anti-CD18  
 CC antibody 60.3 was prepared. The variable (V) region sequences from  
 CC both the heavy (H) and light (L) chains were determined from cDNA  
 CC (amplified by PCR), and spliced onto human constant (C) regions,  
 CC resulting in a chimeric 60.3 Ab (IgG1, kappa). The chimeric Ab was  
 CC expressed in tissue culture (A98.653 mouse myeloma cells, detected  
 CC by ELISA), and examined in binding assays. The results from  
 CC competition and inhibition assays showed that the chimeric Ab was  
 CC as effective as the murine 60.3 MAB. The deduced murine VH and VL  
 CC protein sequences were compared to the protein sequence data base,  
 CC and two human Ig protein sequences were selected to be used as  
 CC templates. A murine 60.3 Fv was modeled according to the deduced  
 CC VH and VL protein sequences. Based on the 60.3 Fv model and the two  
 CC human template sequences selected from the protein data base, a  
 CC humanised Fv was modeled. Construction of the humanised 60.3 was  
 CC done by piecing 5 pairs of complementary oligonucleotides together

Mar 19 08:18

US-08-612-929-19.mg

12

CC (spanning the entire V region) to form the VH and VL. These were  
 CC then attached onto vectors containing genes for appropriate C regions  
 CC to form humanised Ab (IgG1, kappa). The humanised proteins were again  
 CC expressed in A98.653 cells and binding assays were done. FACS analyses  
 CC indicated that the humanised Ab recognised cells expressing CD18.  
 CC About a dozen of the humanised 60.3 Ab master wells were transferred  
 CC and assayed for Ig.  
 SQ Sequence 87 BP; 23 A; 17 C; 26 G; 21 T;  
  
 Query Match 81.5%; Score 22; DB 9; Length 87;  
 Best Local Similarity 95.8%; Pred. No. 1.75e-03;  
 Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
 Db 1 caaagtaatgagcgatcgagcg 24  
 QY 4 CAAAGTATGAGGATCTCCGACG 27  
 |||||||||||||||||||  
  
 RESULT 14  
 ID Q51746 standard; cDNA; 91 BP.  
 AC Q51746;  
 DT 31-MAY-1994 (first entry)  
 DE Oligonucleotide probe MK14-A  
 KW Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;  
 KW ss.  
 OS Synthetic.  
 PN EP-571911-A.  
 PD 01-DEC-1993.  
 PF 24-MAY-1993; 108325.  
 PR 26-MAY-1992; US-889651.  
 PA (BECT ) BECTON DICKINSON CO.  
 PI Shank DD, Spears PA;  
 DR WPI; 93-37884/48.  
 PT New oligo:nucleotide probes specific for Mycobacteria - used for  
 PT detection and amplification of Mycobacteria nucleic acid in  
 PT samples  
 PS Claim 3; Page 14; 23pp; English.  
 CC Oligonucleotide probe MK14-A consists of nucleotides 5-95 of MK14  
 CC (Q51735). It hybridized to all spp. of mycobacteria tested, but  
 CC cross reacted to a few non-mycobacterial spp. The probe may  
 CC be useful as an initial screen for mycobacterial infection.  
 CC See also Q51735-45 and Q51747-59.  
 SQ Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;  
  
 Query Match 81.5%; Score 22; DB 9; Length 91;  
 Best Local Similarity 0.0%; Pred. No. 1.75e-03;  
 Matches 0; Conservative 22; Mismatches 0; Indels 0; Gaps 0;  
  
 Db 34 hvhsvvvvhhvhhvhhvhhv 55  
 QY 27 CGTCGAGGATCTCTACTT 6  
 |||||||||||||||||||  
  
 RESULT 15  
 ID Q04039 standard; DNA; 900 BP.  
 AC Q04039;  
 DT 06-SEP-1990 (first entry)  
 DE Anti-leu 3a light chain variable region gene, 206 Vx.  
 KW HIV; AIDS; anti-leu3A; vaccine; ds.  
 OS Mus musculus.  
 FH Key Location/Qualifiers  
 FT exon 259..307  
 FT /tag= a 308..537  
 FT intron



Mar 19 08:18

US-08-612-929-19.mg

13

FT /\*tag= b 538..882  
FT exon  
FT /\*tag= c  
PN EF-365209-A.  
PD 25-APR-1990.  
PF 11-OCT-1989; 010415.  
PR 17-OCT-1988; US-260558.  
PA (BECT) Becton Dickinson Co.  
PI Hinton R, OI VT;  
DR MPI; 90-126329/17.  
DR P-PSDB; R04132.  
PT New chimeric variants of murine antibody anti-leucine -  
PT contg. human antibody regions, and DNA encoding sequences.  
PS Claim 1; Fig 2; 12pp; English.  
CC Variants of murine monoclonal anti-CD4 antibody, anti-leu3A can be  
CC used to form chimeric mouse-variable, human-constant region Abs  
CC suggested as being useful as a vaccine to HIV.  
SQ Sequence 900 BP; 261 A; 206 C; 187 G; 246 T;

Query Match 81.5%; Score 22; DB 1; Length 900;  
Best Local Similarity 92.3%; Pred. No. 1.75e-03;  
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 825 caacaaagtatgaggtatcctccgac 850  
Qy 1 CAGCAAGTAATGAGGATCCTCCGAC 26

Search completed: Wed Mar 19 08:20:40 1997  
Job time : 14 secs.

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W A P S E H (TW)

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MPsrch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed Mar 19 08:19:08 1997; MaePar time 55.30 Seconds  
402.100 Million cell updates/sec

Tabular output not generated.

Title: >US-08-612-929-19

Description: (1-27) from US08612929.seq

Perfect Score: 27

N.A. Sequence: 1 CAGCAAGTATGAGGATCTCCGAGC 27

Comp: GTCGTTTCATTACTCTAGGAGGCTGC

Scoring table: TABLE default

Gap 10

Nmatch STD : Dbase 0; Query 0

Searched: 279077 seqs, 411808665 bases x 2

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

1:BCT 2:FUN 3:INV1 4:INV2 5:ORG 6:MAM 7:VRT 8:PLN 9:PRI  
10:PRO1 11:PRO2 12:ROD 13:SYN 14:UNC 15:VIR  
genbank94

Database:

16:BCT1 17:BCT2 18:BCT3 19:BCT4 20:BCT5 21:BCT6 22:BCT7  
23:BCT8 24:BCT9 25:INV1 26:INV2 27:INV3 28:INV4 29:INV5  
30:INV6 31:INV7 32:MAM1 33:MAM2 34:MAM3 35:VRT1 36:VRT2  
37:VRT3 38:VRT4 39:VRT5 40:VRT6 41:VRT7 42:VRT8 43:VRT9  
44:PLN1 45:PLN2 46:PLN3 47:PLN4 48:PLN5 49:PLN6 50:PLN7  
51:PRI1 52:PRI2 53:PRI3 54:PRI4 55:PRI5 56:PRI6 57:PRI7  
58:PRI8 59:PRI9 60:PRI10 61:PRI11 62:PRI12 63:PRI13  
64:ROD1 65:ROD2 66:ROD3 67:ROD4 68:ROD5 69:ROD6 70:ROD7  
71:STR 72:SYN 73:UNA 74:VRL1 75:VRL2 76:VRL3 77:VRL4  
78:VRL5 79:VRL6 80:VRL7 81:VRL8  
genbank-news

Database:

82:BCT 83:INV1 84:INV2 85:MAM 86:VRT 87:PAT 88:PHG  
89:PLN 90:PRI 91:ROD 92:STR 93:SYN 94:UNA 95:VRL  
u-embl46 94  
96:part1

Statistics: Mean 7.242; Variance 2.620; scale 2.765

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description	Pred. No.
1	25	92.6	195	66	MUSIGKAAAC	Mouse Igk chain mRNA, 5.58e-07
2	25	92.6	228	65	MMU18577	Mus musculus immunogl 5.58e-07
3	25	92.6	273	67	MUSIGKCNL	Mouse Ig rearranged k 5.58e-07
4	25	92.6	307	64	MMIGGLA	Mus musculus (DBA/1) 5.58e-07
5	25	92.6	336	67	MUSIGKCHK	Mouse Ig rearranged k 5.58e-07
6	25	92.6	336	64	MMIGLC310	M.musculus mRNA for I 5.58e-07
7	25	92.6	336	64	MMIGLC404	M.musculus mRNA for I 5.58e-07
8	25	92.6	393	70	S50265	Ig VJ=anti-CD4 mAb M- 5.58e-07
9	25	92.6	394	64	MMU01973	Mus musculus Balb/c a 5.58e-07
10	24	88.9	841	67	MUSIGKVR3	Mouse Ig germline kap 4.14e-06
11	23	85.2	312	66	MUSIGKABK	Mouse Ig kappa-chain 2.97e-05
12	23	85.2	318	65	MMVL2D4	M.musculus mRNA for i 2.97e-05
13	23	85.2	333	63	MDIGKVBV	M.domesticus Igk vari 2.97e-05
14	23	85.2	363	67	MUSL931GKV	Mouse hybridoma Ig re 2.97e-05
15	22	81.5	363	67	MUSL341GKV	Mouse hybridoma Ig re 2.97e-05
16	22	81.5	333	70	S54207	V kappa 21-immunoglob 2.06e-04
17	22	81.5	360	67	MUSIGKAF	Mouse Ig active kappa 2.06e-04
18	22	81.5	671	67	MUSIGKVS	Mouse Ig germline kap 2.06e-04
19	22	81.5	841	67	MUSIGKVR2	Mouse Ig germline kap 2.06e-04
20	22	81.5	900	40	I08223	Sequence 1 from paten 2.06e-04
21	21	77.8	195	66	MUSIGKAAAB	Mouse Igk chain mRNA, 1.38e-03
22	21	77.8	272	65	MUSANTDNAB	Mouse anti-DNA antibo 1.38e-03
23	21	77.8	279	66	MUSIGKAAA	Mouse Igk chain mRNA, 1.38e-03
24	21	77.8	292	65	MMU18599	Mus musculus immunogl 1.38e-03
25	21	77.8	302	67	MUSIGLAFJ	Mouse Ig kappa-chain 1.38e-03
26	21	77.8	330	67	MUSIGKCSJ	Mouse active rheumato 1.38e-03
27	21	77.8	330	67	MUSIGKCSI	Mouse active rheumato 1.38e-03
28	21	77.8	333	66	MUSCMVB	Mouse mRNA sequence, 1.38e-03
29	21	77.8	363	67	MUSL2021GK	Mouse hybridoma Ig re 1.38e-03
30	21	77.8	451	38	A07951	Artificial sequence f 1.38e-03
31	20	74.1	245	64	MMIGKCVRH	M.musculus immunoglob 8.85e-03
32	20	74.1	255	64	MMIGKCVRD	M.musculus immunoglob 8.85e-03
33	20	74.1	264	64	MMIGKCVRI	M.musculus immunoglob 8.85e-03
34	20	74.1	266	64	MMIGKCVRC	M.musculus immunoglob 8.85e-03
35	20	74.1	270	64	MMIGKCVRB	M.musculus immunoglob 8.85e-03
36	20	74.1	270	64	MMIGKCVRG	M.musculus immunoglob 8.85e-03
37	20	74.1	297	65	MMU29629	Mus musculus anti-DNA 8.85e-03
38	20	74.1	323	70	S52318	Ig VJ=anti-carcinoemb 8.85e-03
39	20	74.1	333	70	S42888	Ig V kappa =immunogl 8.85e-03
40	20	74.1	333	65	MMVLIE10	Mouse mRNA for kappa- 8.85e-03
41	20	74.1	336	67	MUSIGKCM1	Mouse Ig rearranged k 8.85e-03
42	20	74.1	396	70	SYN4C10L	Murine/Human chimeric 8.85e-03
43	20	74.1	469	67	MUSIGKKB	Mouse Ig aberrantly r 8.85e-03
44	20	74.1	694	67	MUSIGKAM2	Mouse Ig kappa aberria 8.85e-03
45	20	74.1	833	64	MMIGK2	Part of the gene for 8.85e-03

## ALIGNMENTS

RESULT 1  
LOCUS MUSIGKAAAC 195 bp mRNA  
DEFINITION Mouse Igk chain mRNA, VJ1 region.  
ACCESSION M57980  
NID g196406  
KEYWORDS J-region; V-region; anti-cytochrome c antibody;  
immunoglobulin kappa-chain; immunoglobulin light chain.  
SOURCE Mouse (BALB/c) secondary B cell hybridoma 2B5 mRNA, clone 2B5.F8.  
ORGANISM Mus musculus

Mar 19 08:18

US-08-612-929-19.rge

3

Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;  
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.  
REFERENCE 1 (bases 1 to 195)  
AUTHORS Goshorn, S.C., Betzel, E. and Jemerson, R.  
TITLE Common structural features among monoclonal antibodies binding the  
same antigenic region of cytochrome c  
JOURNAL J. Biol. Chem. 266 (4), 2134-2142 (1991)  
MEDLINE 91115823  
FEATURES  
Location/Qualifiers  
source  
1..195  
/organism="Mus musculus"  
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/cell\_line="2B5"  
/cell\_type="secondary B cell"  
/sequenced\_mol="cDNA to mRNA"  
/tissue\_type="hybridoma"  
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/gene="IgM"  
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1..195  
CDS  
1..195  
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/map="chromosome 6"  
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/product="Ig kappa chain"  
/db\_xref="PID:g196407"  
/translation="PKLLIYAASNLESGIPARFSGSGGDTFTNIHPVEEDGATY  
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19..39  
misc\_feature  
19..39  
/gene="IgM"  
/map="chromosome 6"  
/note="CDR2"  
misc\_feature  
136..162  
/gene="IgM"  
/map="chromosome 6"  
/note="CDR3"  
J\_segment  
156..195  
/gene="IgM"  
/map="chromosome 6"  
/note="J1"  
BASE COUNT 52 a 50 c 51 g 42 t  
ORIGIN Chromosome 6.  
Query Match 92.6%; Score 25; DB 66; Length 195;  
Best Local Similarity 96.3%; Pred. No. 5.58e-07;  
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Db 136 cagcaagaagtaagagatcctcgagc 162  
|||||  
Qy 1 CAGCAAGTAATGAGATCCTCGGACG 27  
RESULT 2  
LOCUS MMU18577 228 bp mRNA ROD 21-JUN-1995  
DEFINITION Mus musculus immunoglobulin kappa light chain, variable region  
mRNA, clone BALB/c-5i, partial cds.  
ACCESSION U18577  
NID g619707  
KEYWORDS mouse.  
SOURCE Mus musculus  
ORGANISM

Mar 19 08:18

US-08-612-929-19.rge

4

Eukaryota; Mitochondrial eukaryotes; eukaryote crown group;  
Metazoa/Eumycota group; Metazoa; Eumetazoa; Bilateria; Coelomata;  
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;  
Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;  
Eutheria; Glires; Rodentia; Sciurognathi; Myomorpha; Muridae; Mus.  
REFERENCE 1 (bases 1 to 228)  
AUTHORS Roark, J.H., Kuntz, C.L., Nguyen, K.A., Caton, A.J. and Erikson, J.  
TITLE Breakdown of B cell tolerance in a mouse model of systemic lupus  
erythematosus  
J. Exp. Med. 181 (3), 1157-1167 (1995)  
MEDLINE 95173583  
REFERENCE 2 (bases 1 to 228)  
AUTHORS Roark, J.H.  
TITLE Direct Submission  
JOURNAL Submitted (14-DEC-1994) Jessica H. Roark, Wistar Institute, 3601  
Spruce St., Philadelphia, PA 19104, USA  
FEATURES  
Location/Qualifiers  
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/tissue\_type="spleen"  
/dev\_stage="adult"  
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1..>228  
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FTNIHPVEEDATYCCQSNEDPPTFGSGT"  
BASE COUNT 61 a 57 c 57 g 53 t  
ORIGIN  
Query Match 92.6%; Score 25; DB 65; Length 228;  
Best Local Similarity 96.3%; Pred. No. 5.58e-07;  
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Db 187 cagcaagaagtaagagatcctcgagc 213  
|||||  
Qy 1 CAGCAAGTAATGAGATCCTCGGACG 27  
RESULT 3  
LOCUS MUS18577 273 bp mRNA ROD 15-MAR-1989  
DEFINITION Mouse Ig rearranged kappa-chain V-region mRNA from hybridoma  
H37-63, partial cds.  
ACCESSION M21525  
NID g196987  
KEYWORDS C-region; V-region; immunoglobulin light chain;  
immunoglobulin-kappa; rearranged gene.  
SOURCE Mouse (strain BALB/c) hybridoma H37-63, cDNA to mRNA.  
ORGANISM Mus musculus  
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;  
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.  
REFERENCE 1 (bases 1 to 273)  
AUTHORS Clarke, S.H., Huppi, K., Ruzinsky, D., Staudt, L., Gerhard, W. and  
Weigert, M.  
TITLE Inter- and intracolon diversity in the antibody response to  
influenza hemagglutinin  
J. Exp. Med. 161, 687-704 (1985)  
MEDLINE 85159415  
FEATURES Location/Qualifiers  
source  
1..273  
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Mar 1908:18

US-08-612-929-19-rgc

5

## CDS

&lt;1..&gt;273

/note="Ig kappa-chain VJ-regions"

/codon\_start=1

/db\_xref="PID:q196988"

/translation="SCRASESDYXGSLMHWYQKQPQPKLLISRASNLSEGIPAR  
FSGVGRDFTLTINVEADVDATYYCQSNEDPPTFGAGTKLEIKR"

BASE COUNT

69 a 72 c 66 g

65 t 1 others

ORIGIN

Chromosome 6.

Query Match

Best Local Similarity 92.6%; Score 25; DB 67; Length 273;

Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 214

cagcaagaatgagatctccacg 240

Qy 1 CAGCAAGTAATGAGATCTCCGACG 27

RESULT 4

LOCUS MMIGGL4

DEFINITION Mus musculus (DBA/1) mRNA for immunoglobulin gamma light chain

ACCESSION 226771

NID g436888

KEYWORDS immunoglobulin; immunoglobulin gamma; light chain joining region;

SOURCE house mouse.

ORGANISM

Mus musculus

Eukaryotes; mitochondrial eukaryotes; Metazoa/Eumycota group;

Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;

Vertebrata; Gnathostomata; Osteichthyes; Sarcopharygii; Chondata;

Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;

Sciurognathi; Myomorpha; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 307)

AUTHORS Mo, J.A., Scheynius, A., Nilsson, S. and Holmdahl, R.

TITLE Germline encoded IgG antibodies bind mouse cartilage in vivo

epitope and idiotype specific binding and inhibition

JOURNAL Scand. J. Immunol. (1993) In press

REFERENCE 2 (bases 1 to 307)

AUTHORS Mo, J.A.

TITLE Direct Submission

JOURNAL Submitted (30-SEP-1993) to the EMBL/GenBank/DBSJ databases. John A

Mo, Department of Medical and Physiological, Department of, Medical

and Physiological Chemistry, Husargatan 3, Uppsala, 75123, Sweden

REFERENCE 3 (bases 1 to 307)

AUTHORS Mo, J.A., Scheynius, A., Nilsson, S. and Holmdahl, R.

TITLE Germline-encoded IgG antibodies bind mouse cartilage in vivo:

epitope- and idiotype-specific binding and inhibition

JOURNAL Scand. J. Immunol. 39 (2), 122-130 (1994)

MEDLINE

FEATURES

Location/Qualifiers

source

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/organism="Mus musculus"

/strain="DBA/1"

/dev\_stage="Adult"

/tissue\_type="Lymph node"

/cell\_type="B cell hybridoma"

/cell\_line="CIIF4 hybridoma"

/chromosome="6"

V\_segment

/note="Light chain variable region"

J\_segment

273..307

/note="Joining region JK2"

BASE COUNT

81 a 77 c 77 g 72 t

Mar 1908:18

US-08-612-929-19-rgc

6

## ORIGIN

Query Match 92.6%; Score 25; DB 64; Length 307;

Best Local Similarity 96.3%; Pred. No. 5.58e-07;

Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 250

cagcaagaatgagatctccacg 276

Qy 1 CAGCAAGTAATGAGATCTCCGACG 27

RESULT 5

LOCUS MUSICKCKK

DEFINITION Mouse Ig rearranged kappa-chain V-region mRNA from hybridoma

ACCESSION M21524

NID g196985

KEYWORDS C-region; V-region; immunoglobulin light chain;

immunoglobulin-kappa; rearranged gene.

SOURCE Mouse (strain BALB/c) hybridoma H37-77, cDNA to mRNA.

ORGANISM

Mus musculus

Eukaryotes; Animalia; Chordata; Vertebrata; Mammalia; Theria;

Eutheria; Rodentia; Myomorpha; Muridae; Murinae.

REFERENCE 1 (bases 1 to 336)

AUTHORS Clarke, S.H., Huppi, K., Ruzinskiy, D., Staudt, L., Gerhard, W. and

Weigert, M.

TITLE Inter- and intracolon diversity in the antibody response to

influenza hemagglutinin

JOURNAL J. Exp. Med. 161, 687-704 (1985)

MEDLINE

FEATURES

source

1..336

/organism="Mus musculus"

&lt;1..&gt;336

/note="Ig kappa-chain VJ-regions"

/codon\_start=1

/db\_xref="PID:q196988"

/translation="DIELTQPSLASVLCQRTATISCRASESVYSGKSPHWYQKRP

GQPKLLIYRASNLSEGIPAREFSGSRDFTLTINVEADVDATYYCQSNEDPPTF

GAGTKLEIKR"

BASE COUNT 84 a 88 c 84 g 80 t

ORIGIN

Chromosome 6.

Query Match

Best Local Similarity 92.6%; Score 25; DB 67; Length 336;

Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 277

cagcaagaatgagatctccacg 303

Qy 1 CAGCAAGTAATGAGATCTCCGACG 27

RESULT 6

LOCUS MMIGLC310

DEFINITION M.musculus mRNA for IG light chain VJ region (M-T310).

ACCESSION X65091

NID g52288

KEYWORDS Ig light chain; VJ domain.

SOURCE

house mouse.

ORGANISM

Mus musculus

Eukaryotes; mitochondrial eukaryotes; Metazoa/Eumycota group;

Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;

Vertebrata; Gnathostomata; Osteichthyes; Sarcopharygii; Chondata;

Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;

Mar 19 08:18

US-08-612-929-19.rge

7

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REFERENCE
AUTHORS 1 (bases 1 to 336)
TITLE Direct Submission
JOURNAL Submitted (10-MAR-1992) to the EMBL/GenBank/DBJ databases. W.
Weissenhorn, Institut fuer Immunologie, Goethestraasse 31, W-8000
Muenchen 2, FRG

REFERENCE
AUTHORS 2 (bases 1 to 336)
TITLE Structural characterization of CD4 mAb
JOURNAL Unpublished
FEATURES
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        Location/Qualifiers
            1..336
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                /strain="Balb/c"
                /cell_type="B-cell"
                /cell_line="Hybridoma M-T310"
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                /codon_start=1
                /product="alpha CD4 mAb immunoglobulin light chain VJ
                region"
                /db_xref="PID:g52289"
                /translation="DIVLTQSPASLPMSIGQRTISCKASQSLDYGDSYMNWYQKRP
                GQPKLLIYAASNLSESGIPARFSGSGGDTFTIHHPVEEDAATYYCQGSSEDPPTF
                GGGTKLEIKR"
BASE COUNT 89 a 90 c 81 g 76 t
ORIGIN
Query Match 92.6%; Score 25; DB 64; Length 336;
Best Local Similarity 96.3%; Pred. No. 5.58e-07;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 277 cagcaagtagtgagatcctccgacg 303
|||||
QY 1 CAGCAAGTAGTGAGATCCTCCGACG 27
GGGTKLEIKR"

LOCUS MMIGLC404 336 bp RNA ROD 07-MAY-1992
DEFINITION M.musculus mRNA for IG light chain VJ region (M-T404).
ACCESSION X65092
NID g52292
KEYWORDS Ig light chain; VJ domain.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryotes; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.

REFERENCE
AUTHORS 1 (bases 1 to 336)
TITLE Direct Submission
JOURNAL Submitted (10-MAR-1992) to the EMBL/GenBank/DBJ databases. W.
Weissenhorn, Institut fuer Immunologie, Goethestraasse 31, W-8000
Muenchen 2, FRG

REFERENCE
AUTHORS 2 (bases 1 to 336)
TITLE Structural characterization of CD4 mAb
JOURNAL Unpublished
FEATURES
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                /strain="Balb/c"

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Mar 19 08:18

US-08-612-929-19.rge

8

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CDS
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    GQPKLLIYAASNLSESGIPARFSGSGGDTFTIHHPVEEDAATYYCQGSSEDPPTF
    GGGTKLEIKR"
BASE COUNT 89 a 90 c 81 g 76 t
ORIGIN
Query Match 92.6%; Score 25; DB 64; Length 336;
Best Local Similarity 96.3%; Pred. No. 5.58e-07;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 277 cagcaagtagtgagatcctccgacg 303
|||||
QY 1 CAGCAAGTAGTGAGATCCTCCGACG 27
GGGTKLEIKR"

LOCUS S50265 393 bp mRNA ROD 02-APR-1993
DEFINITION Ig VI-anti-CD4 mAb M-T310 variable region light chain [J1, chimeric
antibody] [mice, hybridoma cells, mRNA Partial, 393 nt].
ACCESSION S50265
NID g260765
KEYWORDS mice hybridoma cells.
SOURCE Mus sp.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 393)
AUTHORS Weissenhorn, W., Scheuer, W., Kaluza, B., Schwirzke, M., Reiter, C.,
Flieger, D., Lenz, H., Weiss, E.H., Rieber, E.P., Riethmuller, G. et.al.
TITLE Combinatorial functions of two chimeric antibodies directed to
human CD4 and one directed to the alpha-chain of the human
interleukin-2 receptor
JOURNAL Gene 121 (2), 271-278 (1992)
MEDLINE 93077041
REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI gibbsq 119503] from the original journal article.
This sequence comes from Fig. 1c.
FEATURES
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            1..393
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            1..393
                /partial
                /genes="Ig VL"
                /note="Method: conceptual translation supplied by author.
                This sequence comes from Fig. 1c."
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            /product="anti-CD4 mAb M-T310 variable region light chain"
            /db_xref="PID:g260766"
            /translation="METDTILLWILLWPGSTGDIVLTQSPASLPMSIGQRTISCK
            ASQSLDYGDSYMNWYQKRPQPKLLIYAASNLSESGIPARFSGSGGDTFTIHHPV
            EEEDAATYYCQGSSEDPPTFGGGTKLEIK"
BASE COUNT 100 a 105 c 98 g 90 t
ORIGIN
Query Match 92.6%; Score 25; DB 70; Length 393;
Best Local Similarity 96.3%; Pred. No. 5.58e-07;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Mar 19 08:18

US-08-612-929-19.rge

9

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Db 337 cagcaagtagtgaggtactctcgagc 363
|||||
Qy 1 CAGCAAGTAATGAGGATCTCCGAGC 27

RESULT 9
LOCUS MMU01973 394 bp mRNA ROD 24-SEP-1993
DEFINITION Mus musculus Balb/c anti-CD18 Ig light chain variable region mRNA,
partial cds.
ACCESSION U01973
NID g403071
KEYWORDS .
SOURCE mouse.
ORGANISM Mus musculus
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
Eutheria; Rodentia; Myomorpha; Muridae; Mus.
REFERENCE 1 (bases 1 to 394)
AUTHORS Heiao,K., Bajorath,J. and Harris,L.J.
TITLE Humanization of 60.3, an anti-CD18 antibody
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 394)
AUTHORS Harris,L.J.
TITLE Direct Submission
JOURNAL Submitted (21-SEP-1993) Linda J. Harris, Molecular Immunology,
Bristol-Myers Squibb, Pharmaceutical Research Institute, 3005 First
Avenue, Seattle, WA 98121 USA
FEATURES
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location/Qualifiers
1..394
/strain="Balb/c"
/organism="Mus musculus"
/cell_line="60.3 hybridoma"
/cell_type="hybridoma (B-cell)"
/tissue_type="spleen"
/dev_stage="adult"
1..60
/notes="nucleotides 1-29 derived from PCR primer and may
not reflect mRNA sequence"
1..49
/number=1
/product="partial signal peptide"
1..394
/partial
/notes="V gene is identical to VK21c germline gene; uses
Jk1"
/codon_start=1
/product="Ig variable region, light chain"
/db_xref="PID:g403072"
/translation="METDTLLVLLWVPGSTGDIVLTQSPASVLSLQQRATISCR
ASESVDSYGNFPMHWYQKQPQPKLLIYRASNLGSGIPARTSGSGSRDTFTLTNPV
EADDVATYYCQSSNEDPRTFTGGTKLEIK"
50..394
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/product="carboxyl end of signal peptide and mature heavy
chain"
61..135
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61..393
/mat_peptide
/product="Ig variable region, light chain"
136..168
/misc_feature
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169..219
/misc_feature
/standard_name="FR2"
220..228
/misc_feature
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Mar 19 08:18

US-08-612-929-19.rge

10

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misc_feature /standard_name="CDR2"
229..339
misc_feature /standard_name="FR3"
340..357
misc_feature /standard_name="CDR3"
358..393
misc_feature /standard_name="FR4"
99 a 100 c 98 g 97 t

BASE COUNT
ORIGIN

Query Match 92.6%; Score 25; DB 64; Length 394;
Best Local Similarity 96.3%; Pred. No. 5.58e-07;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 337 cagcaagtagtgaggtactctcgagc 363
|||||
Qy 1 CAGCAAGTAATGAGGATCTCCGAGC 27

RESULT 10
LOCUS MUSICKVR3 841 bp DNA ROD 14-APR-1994
DEFINITION Mouse Ig germline kappa V-region 9.5kb-V-kappa, V-kappa-21C.
ACCESSION K02161
NID g197492
KEYWORDS C-region; V-region; germline; immunoglobulin light chain;
immunoglobulin-kappa; immunoglobulin-kappa subgroup vk-21.
SEGMENT 3 of 3
SOURCE Mouse BALB/c embryo DNA, clones KM23 and KE5e.
ORGANISM Mus musculus
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE 1 (bases 1 to 841)
AUTHORS Heinrich,G., Traunecker,A. and Tonegawa,S.
TITLE Somatic mutation creates diversity in the major group of mouse
immunoglobulin kappa-light chains
JOURNAL J. Exp. Med. 159, 417-435 (1984)
MEDLINE 84113346
FEATURES
source location/Qualifiers
1..841
/organism="Mus musculus"
<198..246
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/number=1
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exon 1; putative"
join(198..246,486..793)
/partial
/notes="Ig kappa V-region 9.5kb-V-kappa"
/codon_start=1
/db_xref="PID:g197496"
/translation="METDTLLVLLWVPGSTGDIVLTQSPASVLSLQQRATISCR
ASESVDSYGNFPMHWYQKQPQPKLLIYRASNLGSGIPARTSGSGSRDTFTLTNPV
EADDVATYYCQSSNEDP"
198..246
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198..246
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247..485
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/notes="VK9.5 intron A"
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Mar 19 08:18

US-08-612-929-19.rge

11

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exon          486..793
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exon          486..794
              /note="Ig kappa V-region 9.5kb-V-kappa"
              /number=2
exon          486..496
              /note="Ig kappa V-region 9.5kb-V-kappa signal peptide,
              exon 2; putative"
              /codon_start=1
              /partial
mat_peptide    497..794
              /note="Ig kappa V-region 9.5kb-V-kappa mature peptide"
              /codon_start=1
idna           795..841
              /note="V-J intervening DNA (5' end +/- 1 bp)"
misc_signal    796..823
              /note="putative recombination recognition sequence;
              putative"
BASE COUNT    218 a 196 c 191 g 236 t
ORIGIN         About 39 kb after segment 2; chromosome 6.

Query Match   88.9%; Score 24; DB 67; Length 841;
Best Local Similarity 96.2%; Pred. No. 4.14e-06;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 773 cagcaaatgaatgagatctctccac 798
   |||||||
Qy 1 CAGCAAGTAATGAGATCTCTCCGAC 26

RESULT 11
LOCUS      MUSIGKABK 312 bp mRNA ROD 15-SEP-1990
DEFINITION Mouse Ig kappa-chain (anti-insulin Ab 127) mRNA V region, partial
            cds.
ACCESSION  M34529
NID        g196507
KEYWORDS    V-region; immunoglobulin heavy chain; immunoglobulin-kappa;
            processed gene.
SOURCE      Mouse (strain Balb/c), cDNA to mRNA.
ORGANISM    Mus musculus
            Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
            Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE   1 (bases 1 to 312)
AUTHORS     Ewulonu,U.K., Nelli,L.J. and Thomas,J.W.
TITLE       V-H and V-L gene usage by murine IgG antibodies that bind
            autologous insulin
JOURNAL     J. Immunol. 144, 3091-3098 (1990)
MEDLINE     90217518
FEATURES
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        /codon_start=1
        /db_xref="PID:g196508"
        /translation="DIVLTQSPASLAIVLQQRATISCRASEVDSYGNSEFMHWYQKRP
        GQPKLLIYRASNLSEGIPIARFSGSGSRDTLTINPVEADDVASYVYQQSQNEEPITF
        GG"
BASE COUNT    78 a 81 c 77 g 76 t
ORIGIN

Query Match   85.2%; Score 23; DB 66; Length 312;
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Mar 19 08:18

US-08-612-929-19.rge

12

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Best Local Similarity 92.6%; Pred. No. 2.97e-05;
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 277 cagcaaatgaatgaggaacctccacg 303
   |||||||
Qy 1 CAGCAAGTAATGAGGATCTCTCCGACG 27

RESULT 12
LOCUS      MWVL2D4 318 bp RNA ROD 16-MAY-1995
DEFINITION M.musculus mRNA for immunoglobulin light chain variable region
            (VL2D4) .
ACCESSION  X86545
NID        g809058
KEYWORDS    immunoglobulin; immunoglobulin light chain; kappa chain;
            light chain; variable region.
SOURCE      house mouse.
ORGANISM    Mus musculus
            Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
            Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE   1 (bases 1 to 318)
AUTHORS     Cerato,E., Birkle,S., Portoukalian,J. and Aubry,J.
JOURNAL     Unpublished
REFERENCE   2 (bases 1 to 318)
AUTHORS     Cerato,E.M.
TITLE       Direct Submission
JOURNAL     Submitted (24-APR-1995) to the EMBL/GenBank/DBSJ databases. E.M.
            Cerato, INSEEM U211, Institut de Biologie, 9 qual Moncoussu, 44035
            Nantes Cedex 01, FRANCE
FEATURES
    source             Location/Qualifiers
        1..318
        /organism="Mus musculus"
        /strain="BALB/c"
        /dev_stage="adult"
        /tissue_type="spleen"
        /cell_type="B cell hybridoma"
        /cell_line="2D4 hybridoma"
        /chromosome="12"
        /rearranged
        16..318
        /note="anti-ganglioside asialo CM2 immunoglobulin"
        /product="immunoglobulin light chain variable region VL
        2D4"
BASE COUNT    75 a 84 c 80 g 79 t
ORIGIN

Query Match   85.2%; Score 23; DB 65; Length 318;
Best Local Similarity 92.6%; Pred. No. 2.97e-05;
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 262 cagcaaatgaatgagatctctccacg 288
   |||||||
Qy 1 CAGCAAGTAATGAGGATCTCTCCGACG 27

RESULT 13
LOCUS      MDICKVBV 333 bp RNA ROD 05-NOV-1994
DEFINITION M.domesticus Igk variable region.
ACCESSION  Z22133
NID        g297695
KEYWORDS    anti-DNA antibody; IgK gene; IgK variable region; immunoglobulin.
            western European house mouse.
SOURCE      Mus musculus domesticus
            Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;
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Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Mus.

## REFERENCE

1 (bases 1 to 333)

Tillman,D.M., Jou,N.T., Hill,R.J. and Marion,T.N.

Both IgM and IgG anti-DNA antibodies are the products of clonally

selective B cell stimulation in (NZB x NZW)F1 mice

J. Exp. Med. 176 (3), 761-779 (1992)

## MEDLINE

92381444

## REFERENCE

2 (bases 1 to 333)

Marion,T.N.

Direct Submission

Submitted (23-MAR-1993) to the EMBL/GenBank/DBJ databases. Tony N.

Marion, Microbiology and Immunology, University of Tennessee,

Memphis, 858 Madison Avenue, Memphis, TN, 38163, USA

## FEATURES

source

1..333

/organism="Mus domesticus"

/strain="(NZB x NZW)F1"

/dev stage="somatic variant"

/tissue\_type="spleen"

/cell\_type="hybridoma"

/cell\_line="202p.38"

/isolate="mouse #202"

/chromosome="6"

/sex="Female"

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/gene="IgK"

/codon start=1

/function="kappa light chain variable region for anti-DNA

antibody; VK21 family"

/product="immunoglobulin variable region"

/db xref="PID:g297696"

/translation="DIVLTQSPASIVSLGQRATISCRASEVDNYGISFMNWFQKRP

GQPKLLIYANSGSQVPARFSGSGTDFSIHPMEEDDTAMFCQSQKEVPTTF

GGGKLEIK"

BASE COUNT

84 a

86 c

84 g

78 t

1 others

## ORIGIN

Query Match

85.2%; Score 23; DB 63; Length 333;

Best Local Similarity 92.6%; Pred. No. 2.97e-05;

Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 277 cagcaagaaggaaggtctccgacg 303

||||| ||||| ||||| ||||| |||||

QY 1 CAGCAAGTAATCAGGATCTCCGACG 27

## RESULT

14

LOCUS

MUSL931GKV

363 bp

mRNA

ROD

29-OCT-1994

DEFINITION

Mouse hybridoma Ig rearranged kappa-chain mRNA V-region, partial

cde.

ACCESSION

M97879

NID

g198681

KEYWORDS

V-region; immunoglobulin light chain; immunoglobulin-kappa;

processed gene.

SOURCE

Mus musculus

(strain BALB/c, sub\_species domesticus) SP20-BALB/c

fusion hybridoma cDNA to mRNA.

ORGANISM

Mus musculus

Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;

Eutheria; Rodentia; Myomorpha; Muridae; Murinae.

REFERENCE

1 (bases 1 to 363)

Lohman,K.L., Buck,D.W., Carrillo,M.A. and Kennedy,R.C.

TITLE Characterization of murine monoclonal anti-CD4; epitope recognition, idiotope expression, and variable gene sequence

## JOURNAL

Unpublished (1992)

## FEATURES

source

1..363

/organism="Mus musculus"

/strain="BALB/c"

/sub\_species="domesticus"

/sequenced\_mol="cDNA to mRNA"

/tissue\_type="SP20-BALB/c fusion hybridoma"

1..363

/gene="IgK"

/standard\_name="L93; monoclonal antibody (CD4 antigen

specificity)"

/map="6"

BASE COUNT

94 a

97 c

89 g

83 t

## ORIGIN

Query Match

85.2%; Score 23; DB 67; Length 363;

Best Local Similarity 92.6%; Pred. No. 2.97e-05;

Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 277 cagcaagaatcaggatctccgacg 303

||||| ||||| ||||| ||||| |||||

QY 1 CAGCAAGTAATCAGGATCTCCGACG 27

## RESULT

15

LOCUS

MUSL341GKV

363 bp

mRNA

ROD

29-OCT-1994

DEFINITION

Mouse hybridoma Ig rearranged kappa-chain mRNA V-region, partial

cde.

ACCESSION

M97871

NID

g198669

KEYWORDS

V-region; immunoglobulin light chain; immunoglobulin-kappa;

processed gene.

SOURCE

Mus musculus

(strain BALB/c, sub\_species domesticus) SP20-BALB/c

fusion hybridoma cDNA to mRNA.

ORGANISM

Mus musculus

Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;

Eutheria; Rodentia; Myomorpha; Muridae; Murinae.

REFERENCE

1 (bases 1 to 363)

Lohman,K.L., Buck,D.W., Carrillo,M.A. and Kennedy,R.C.

Characterization of murine monoclonal anti-CD4; epitope

recognition, idiotope expression, and variable gene sequence

Unpublished (1992)

## JOURNAL

Unpublished (1992)

## FEATURES

source

1..363

/organism="Mus musculus"

/strain="BALB/c"

/sub\_species="domesticus"

/sequenced\_mol="cDNA to mRNA"

/tissue\_type="SP20-BALB/c fusion hybridoma"

1..363

/gene="IgK"

/standard\_name="L34; monoclonal antibody (CD4 antigen

specificity)"

/map="6"

BASE COUNT

92 a

95 c

90 g

86 t

## ORIGIN

Query Match

85.2%; Score 23; DB 67; Length 363;

Best Local Similarity 92.6%; Pred. No. 2.97e-05;

Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;



Db 277 cagcaactatgaggatcctccgacg 303  
||||||| || |||||||||||||||  
Qy 1 CAGCAACTATCAGGATCCTCCGACG 27

Search completed: Wed Mar 19 08:20:08 1997  
Job time : 60 secs.



Query Match 78.6%; Score 44; DB 5; Length 111;  
 Best Local Similarity 88.9%; Pred. No. 8.48e-01;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 93 qgsnedp 101  
 |||||  
 Qy 1 QQSNEPPT 9

RESULT 2  
 ID KV3M MOUSE STANDARD; PRT; 111 AA.  
 AC P01665;  
 DT 21-JUL-1986 (REL. 01, CREATED)  
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)  
 DE IG KAPPA CHAIN V-III REGION (PC 7043).  
 OS MUS MUSCULUS (MOUSE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; RODENTIA.  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE; 79073152.  
 RA WEIGERT M., GATWALTAN L., LOH E., SCHILLING J., HOOD L.E.;  
 RL NATURE 276:785-790(1978).  
 DR PIR; A01937; KVM543.  
 DR HSP; P01679; IGGB.  
 KW IMMUNOGLOBULIN V REGION.  
 FT DOMAIN 1 23  
 FT DOMAIN 24 38  
 FT DOMAIN 39 53  
 FT DOMAIN 54 60  
 FT DOMAIN 61 92  
 FT DOMAIN 93 101  
 FT DOMAIN 102 111  
 FT DISULFID 23 92  
 FT NON TER 111 111  
 SQ SEQUENCE 111 AA; 12002 MW; ADC728CA CRC32;

Query Match 76.8%; Score 43; DB 5; Length 111;  
 Best Local Similarity 100.0%; Pred. No. 1.50e+00;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 93 qgsnedp 99  
 |||||  
 Qy 1 QQSNEP 7

RESULT 3  
 ID KV3O MOUSE STANDARD; PRT; 111 AA.  
 AC P01667;  
 DT 21-JUL-1986 (REL. 01, CREATED)  
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)  
 DE IG KAPPA CHAIN V-III REGION (PC 6308).  
 OS MUS MUSCULUS (MOUSE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; RODENTIA.  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE; 79073152.  
 RA WEIGERT M., GATWALTAN L., LOH E., SCHILLING J., HOOD L.E.;  
 RL NATURE 276:785-790(1978).  
 DR PIR; C01937; KVM508.

DR HSP; P01679; IGGB.  
 KW IMMUNOGLOBULIN V REGION.  
 FT DOMAIN 1 23  
 FT DOMAIN 24 38  
 FT DOMAIN 39 53  
 FT DOMAIN 54 60  
 FT DOMAIN 61 92  
 FT DOMAIN 93 101  
 FT DOMAIN 102 111  
 FT DISULFID 23 92  
 FT NON TER 111 111  
 SQ SEQUENCE 111 AA; 12071 MW; F7865271 CRC32;

Query Match 76.8%; Score 43; DB 5; Length 111;  
 Best Local Similarity 100.0%; Pred. No. 1.50e+00;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 93 qgsnedp 99  
 |||||  
 Qy 1 QQSNEP 7

RESULT 4  
 ID KV3L MOUSE STANDARD; PRT; 111 AA.  
 AC P01664;  
 DT 21-JUL-1986 (REL. 01, CREATED)  
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)  
 DE IG KAPPA CHAIN V-III REGION (CBPC 101).  
 OS MUS MUSCULUS (MOUSE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; RODENTIA.  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE; 79012520.  
 RA MCKEAN D.J., BELL M., POTTER M.;  
 RL PROC. NATL. ACAD. SCI. U.S.A. 75:3913-3917(1978).  
 CC -!- THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.  
 DR HSP; A01936; KVM5C1.  
 DR HSP; P01679; IGGB.  
 KW IMMUNOGLOBULIN V REGION.  
 FT DOMAIN 1 23  
 FT DOMAIN 24 38  
 FT DOMAIN 39 53  
 FT DOMAIN 54 60  
 FT DOMAIN 61 92  
 FT DOMAIN 93 101  
 FT DOMAIN 102 111  
 FT DISULFID 23 92  
 FT NON TER 111 111  
 SQ SEQUENCE 111 AA; 11964 MW; A2AC84C7 CRC32;

Query Match 76.8%; Score 43; DB 5; Length 111;  
 Best Local Similarity 100.0%; Pred. No. 1.50e+00;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 93 qgsnedp 99  
 |||||  
 Qy 1 QQSNEP 7

RESULT 5  
 ID KV3H MOUSE STANDARD; PRT; 111 AA.  
 AC P01660;

Mar 18 10:10

US-08-612-929-20.rsp

5

DT 21-JUL-1986 (REL. 01, CREATED)  
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)  
 DE IG KAPPA CHAIN V-III REGION (PC 3741 AND TEPC 111).  
 OS MUS MUSCULUS (MOUSE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; RODENTIA.  
 RN [1]  
 RP SEQUENCE (PC 3741).  
 RX MEDLINE; 79073152.  
 RA WEIGERT M., GATMAITAN L., LOH E., SCHILLING J., HOOD L.E.;  
 RL NATURE 276:785-790(1978).  
 RN [2]  
 RP SEQUENCE (TEPC 111).  
 RX MEDLINE; 79012520.  
 RA MCKEAN D.J., BELL M., POTTER M.;  
 RL PROC. NATL. ACAD. SCI. U.S.A. 75:3913-3917(1978).  
 CC -/- THE PC 3741 AND TEPC 111 SEQUENCES ARE IDENTICAL.  
 DR PIR; A01934; KWS37.  
 DR HSP; P01679; IGGB.  
 KW IMMUNOGLOBULIN V REGION.  
 FT DOMAIN 1 23  
 FT DOMAIN 24 38  
 FT DOMAIN 39 53  
 FT DOMAIN 54 60  
 FT DOMAIN 61 92  
 FT DOMAIN 93 101  
 FT DOMAIN 102 111  
 FT DISULFID 23 92  
 FT NON TER 111 111  
 SQ SEQUENCE 111 AA; 12099 MW; 76502E89 CRC32;

Query Match 76.8%; Score 43; DB 5; Length 111;  
 Best Local Similarity 100.0%; Pred. No. 1.50e+00;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 93 qgsndp 99  
 Qy 1 QQSNDP 7

RESULT 6  
 ID KV3Q MOUSE STANDARD; PRT; 111 AA.  
 AC P01669;  
 DT 21-JUL-1986 (REL. 01, CREATED)  
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)  
 DE IG KAPPA CHAIN V-III REGION (PC 7169).  
 OS MUS MUSCULUS (MOUSE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; RODENTIA.  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE; 79073152.  
 RA WEIGERT M., GATMAITAN L., LOH E., SCHILLING J., HOOD L.E.;  
 RL NATURE 276:785-790(1978).  
 DR PIR; E01937; KWS69.  
 DR HSP; P01679; IACY.  
 KW IMMUNOGLOBULIN V REGION.  
 FT DOMAIN 1 23  
 FT DOMAIN 24 38  
 FT DOMAIN 39 53  
 FT DOMAIN 54 60  
 FT DOMAIN 61 92  
 FT DOMAIN 93 101  
 FT DOMAIN 102 111  
 FT DISULFID 23 92  
 FT NON TER 111 111  
 SQ SEQUENCE 111 AA; 12099 MW; 76502E89 CRC32;

Mar 18 10:10

US-08-612-929-20.rsp

6

FT DOMAIN 93 101  
 FT DOMAIN 102 111  
 FT DISULFID 23 92  
 FT NON TER 111 111  
 SQ SEQUENCE 111 AA; 12011 MW; 9CB705B9 CRC32;  
 Query Match 76.8%; Score 43; DB 5; Length 111;  
 Best Local Similarity 100.0%; Pred. No. 1.50e+00;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 93 qgsndp 99  
 Qy 1 QQSNDP 7

RESULT 7  
 ID KV3F MOUSE STANDARD; PRT; 132 AA.  
 AC P01658;  
 DT 21-JUL-1986 (REL. 01, CREATED)  
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)  
 DE IG KAPPA CHAIN PRECURSOR V-III REGION (MOPC 321).  
 OS MUS MUSCULUS (MOUSE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; RODENTIA.  
 RN [1]  
 RP SEQUENCE OF 1-37.  
 RX MEDLINE; 78235887.  
 RA BURSTEIN Y., SCHECHTER I.;  
 RL BIOCHEMISTRY 17:2392-2400(1978).  
 RN [2]  
 RP SEQUENCE OF 21-132.  
 RX MEDLINE; 73140224.  
 RA MCKEAN D.J., POTTER M., HOOD L.E.;  
 RL BIOCHEMISTRY 12:749-759(1973).

CC -/- THE PARTIAL SEQUENCE OF THE C REGION OF THIS BENCE-JONES PROTEIN  
 WAS ALSO DETERMINED. IT DIFFERS FROM THAT REPORTED FOR MOUSE  
 MOPC 21 ONLY IN THE TRANSPOSITION OF TWO NEARBY RESIDUES.  
 DR PIR; A01933; KWS32.  
 DR HSP; P01679; IGGB.  
 KW IMMUNOGLOBULIN V REGION; BENCE-JONES PROTEIN; SIGNAL.  
 FT SIGNAL 1 20  
 FT CHAIN 21 132  
 FT DOMAIN 21 43  
 FT DOMAIN 44 58  
 FT DOMAIN 59 73  
 FT DOMAIN 74 80  
 FT DOMAIN 81 112  
 FT DOMAIN 113 121  
 FT DOMAIN 122 131  
 FT DISULFID 43 112  
 FT NON TER 132 132  
 SQ SEQUENCE 132 AA; 14523 MW; E572F824 CRC32;

Query Match 76.8%; Score 43; DB 5; Length 132;  
 Best Local Similarity 28.6%; Pred. No. 1.50e+00;  
 Matches 2; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 113 zszbzbp 119  
 Qy 1 QQSNDP 7

RESULT 8  
 ID KV3F MOUSE STANDARD; PRT; 132 AA.  
 AC P01658;  
 DT 21-JUL-1986 (REL. 01, CREATED)  
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)  
 DE IG KAPPA CHAIN PRECURSOR V-III REGION (MOPC 321).  
 OS MUS MUSCULUS (MOUSE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; RODENTIA.  
 RN [1]  
 RP SEQUENCE OF 1-37.  
 RX MEDLINE; 78235887.  
 RA BURSTEIN Y., SCHECHTER I.;  
 RL BIOCHEMISTRY 17:2392-2400(1978).  
 RN [2]  
 RP SEQUENCE OF 21-132.  
 RX MEDLINE; 73140224.  
 RA MCKEAN D.J., POTTER M., HOOD L.E.;  
 RL BIOCHEMISTRY 12:749-759(1973).

CC -/- THE PARTIAL SEQUENCE OF THE C REGION OF THIS BENCE-JONES PROTEIN  
 WAS ALSO DETERMINED. IT DIFFERS FROM THAT REPORTED FOR MOUSE  
 MOPC 21 ONLY IN THE TRANSPOSITION OF TWO NEARBY RESIDUES.  
 DR PIR; A01933; KWS32.  
 DR HSP; P01679; IGGB.  
 KW IMMUNOGLOBULIN V REGION; BENCE-JONES PROTEIN; SIGNAL.  
 FT SIGNAL 1 20  
 FT CHAIN 21 132  
 FT DOMAIN 21 43  
 FT DOMAIN 44 58  
 FT DOMAIN 59 73  
 FT DOMAIN 74 80  
 FT DOMAIN 81 112  
 FT DOMAIN 113 121  
 FT DOMAIN 122 131  
 FT DISULFID 43 112  
 FT NON TER 132 132  
 SQ SEQUENCE 132 AA; 14523 MW; E572F824 CRC32;

Query Match 76.8%; Score 43; DB 5; Length 132;  
 Best Local Similarity 28.6%; Pred. No. 1.50e+00;  
 Matches 2; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 113 zszbzbp 119  
 Qy 1 QQSNDP 7

RESULT 8  
 ID KV3F MOUSE STANDARD; PRT; 132 AA.  
 AC P01658;  
 DT 21-JUL-1986 (REL. 01, CREATED)  
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)  
 DE IG KAPPA CHAIN PRECURSOR V-III REGION (MOPC 321).  
 OS MUS MUSCULUS (MOUSE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; RODENTIA.  
 RN [1]  
 RP SEQUENCE OF 1-37.  
 RX MEDLINE; 78235887.  
 RA BURSTEIN Y., SCHECHTER I.;  
 RL BIOCHEMISTRY 17:2392-2400(1978).  
 RN [2]  
 RP SEQUENCE OF 21-132.  
 RX MEDLINE; 73140224.  
 RA MCKEAN D.J., POTTER M., HOOD L.E.;  
 RL BIOCHEMISTRY 12:749-759(1973).

ID GLHR ANTEL STANDARD; PRT; 925 AA.  
AC P35409;  
DT 01-JUN-1994 (REL. 29, CREATED)  
DT 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)  
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)  
DE PROBABLE GLYCOPROTEIN HORMONE G-PROTEIN COUPLED RECEPTOR PRECURSOR.  
OS ANTHOLEURA ELEGANTISSIMA (SEA ANEMONE).  
OC EUKARYOTA; METAZOA; CNIDARIA; ANTHOZOA; ZOANTHARIA; ACTINOTARIA.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 94107299.  
RA NOTHACKER H.-P., GRIMMELIKHUIJZEN C.J.P.;  
RL BIOCHEM. BIOPHYS. RES. COMMUN. 197:1062-1069(1993).  
CC -/- FUNCTION: PROBABLE RECEPTOR FOR A GLYCOPROTEIN HORMONE.  
CC -/- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
CC -/- SIMILARITY: HIGHLY SIMILAR TO FSH, LSH AND TSH RECEPTORS.  
CC -/- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
DR EMBL; Z28332; G452811; --  
DR PIR; S41908; S41908.  
DR PIR; JC2033; JC2033.  
DR GCRDB; GCR 0876; --  
DR PROSITE; PS00237; G-PROTEIN RECEPTOR.  
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL;  
KW ALTERNATIVE SPLICING; REPEAT.  
FT SIGNAL 1 27 POTENTIAL.  
FT CHAIN 28 925 PROBABLE GLYCOPROTEIN HORMONE G-PROTEIN COUPLED RECEPTOR.  
FT DOMAIN 28 529 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 530 551 1 (POTENTIAL).  
FT DOMAIN 552 561 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 562 584 2 (POTENTIAL).  
FT DOMAIN 585 606 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 607 628 3 (POTENTIAL).  
FT DOMAIN 629 651 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 652 673 4 (POTENTIAL).  
FT DOMAIN 674 691 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 692 712 5 (POTENTIAL).  
FT DOMAIN 713 739 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 740 763 6 (POTENTIAL).  
FT DOMAIN 764 774 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 775 795 7 (POTENTIAL).  
FT DOMAIN 796 925 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 925 925 5 X APPROXIMATE TANDEM REPEATS.  
FT REPEAT 333 349 1 (INCOMPLETE).  
FT REPEAT 350 384 2.  
FT REPEAT 385 419 3.  
FT REPEAT 420 453 4.  
FT REPEAT 454 461 5 (INCOMPLETE).  
FT VARSPLIC 235 925 MISSING (IN SPLICED VARIANT).  
FT CARBOHYD 61 61 POTENTIAL.  
FT CARBOHYD 152 152 POTENTIAL.  
FT CARBOHYD 212 212 POTENTIAL.  
FT CARBOHYD 435 435 POTENTIAL.  
FT CARBOHYD 495 495 POTENTIAL.  
FT CARBOHYD 558 558 POTENTIAL.  
SQ SEQUENCE 925 AA; 100059 MW; 168E8B81 CRC32;

Query Match 75.0%; Score 42; DB 4; Length 925;  
Best Local Similarity 66.7%; Pred. No. 2.62e+00;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
Db 477 hqstdpdt 485  
: || ||||  
QY 1 QQSNDPPT 9

RESULT 9  
ID KY3K MOUSE STANDARD; PRT; 111 AA.  
AC P01663;  
DT 21-JUL-1986 (REL. 01, CREATED)  
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)  
DE IG KAPPA CHAIN V-III REGION (PC 4050).  
OS MUS MUSCULUS (MOUSE).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUThERIA; RODENTIA.  
RN [1]  
RP SEQUENCE.  
RX MEDLINE; 79073152.  
RA WEIGERT M., GATMAITAN L., LOH E., SCHILLING J., HOOD L.E.;  
RL NATURE 276:785-790(1978).  
DR PIR; A01935; KVM5M6.  
DR HSP; P01679; LACY.  
KW IMMUNOGLOBULIN V REGION.  
FT DOMAIN 1 23 FRAMEWORK 1.  
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING 1.  
FT DOMAIN 39 53 FRAMEWORK 2.  
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING 2.  
FT DOMAIN 61 92 FRAMEWORK 3.  
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING 3.  
FT DOMAIN 102 111 FRAMEWORK 4.  
FT DISULFID 23 92 BY SIMILARITY.  
FT NON TER 111 111  
SQ SEQUENCE 111 AA; 12005 MW; 5EBF3264 CRC32;  
Query Match 73.2%; Score 41; DB 5; Length 111;  
Best Local Similarity 77.8%; Pred. No. 4.55e+00;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
Db 93 qgmedplt 101  
: || |||| |  
QY 1 QQSNDPPT 9  
RESULT 10  
ID YF7 YEAST STANDARD; PRT; 557 AA.  
AC P43609;  
DT 01-NOV-1995 (REL. 32, CREATED)  
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)  
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)  
DE HYPOTHETICAL 63.2 KD PROTEIN IN CDC26-YMR31 INTERGENIC REGION.  
GN YF037C.  
OS SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOCYCETES.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-S288C / AB972;  
RA MURAKAMI Y., NAITOU M., HAGIWARA H., SHIBATA T., OZAWA M.,  
RA SASANUMA S.-I., SASANUMA M., TSUCHIYA Y., SOEDA E., YOKOYAMA K.,  
RA YAMAZAKI M., TASHIRO H., EKI T.;  
RL NAT. GENET. 10:261-268(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-S288C / AB972;  
RA EKI T., NAITOU M., HAGIWARA H., ABE M., OZAWA M., SASANUMA S.-I.,  
RA SASANUMA M., TSUCHIYA Y., SHIBATA T., WTANABE K., ONO A.,  
RA YAMAZAKI M.-A., TASHIRO H., HANAOKA F., MURAKAMI Y.;  
RL YEAST 12:177-190(1996).

CC -!- SIMILARITY: TO YEAST TRANSCRIPTION REGULATORY PROTEIN SW13.

DR EMBL; D50617; G836792; --

DR EMBL; D44602; G893432; --

KW HYPOTHETICAL PROTEIN.

SQ SEQUENCE 557 AA; 63168 MW; D2C310A3 CRC32;

Query Match 73.2%; Score 41; DB 10; Length 557;

Best Local Similarity 44.4%; Pred. No. 4.55e+00;

Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Db 16 heateeppt 24

!!! :|||

Qy 1 QOSNEDPPT 9

RESULT 11

ID ERG7 YEAST STANDARD; PRT; 730 AA.

AC P38604;

DT 01-OCT-1994 (REL. 30, CREATED)

DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)

DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)

DE LANOSTEROL SYNTHASE (EC 5.4.99.7) (OXIDOSQUALENE--LANOSTEROL CYCLASE)

DE (2,3-EPOXSQUALENE--LANOSTEROL CYCLASE) (OSC).

GN ERG7 OR YHR072M.

OS SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST).

OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.

RN [1]

RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-8.

RX MEDLINE; 94181562.

RA COREY E.J., MATSUDA S.P.T., BARTEL B.;

RL PROC. NATL. ACAD. SCI. U.S.A. 91:2211-2215(1994).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE; 94316697.

RA SHI Z., BUNTEL C.J., GRIFFIN J.H.;

RL PROC. NATL. ACAD. SCI. U.S.A. 91:7370-7374(1994).

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=S288C / AB972;

RX MEDLINE; 94378003.

RA JOHNSTON M., ANDREWS S., BRINKMAN R., COOPER J., DING H., DOVER J.,

RA DU Z., FAVELLO A., FULTON L., GATTUNG S., GEISEL C., KIRSTEN J.,

RA KUCABA T., HILLIER L., JIER M., JOHNSTON L., LANGSTON Y.,

RA LATREILLE P., LOUIS E.J., MACRI C., MARDIS E., MENEZES S., MOUSER L.,

RA NIAN M., RIFKIN L., RILES L., ST.PETER H., TREVASKIS E., VAUGHAN K.,

RA VIGNATI D., WILCOX L., WORLDMAN P., WATERSTON R., WILSON R.,

RA VAUDIN M.;

RL SCIENCE 265:2077-2082(1994).

CC -!- FUNCTION: CATALYZES THE CYCLIZATION OF (S)-2,3 OXIDOSQUALENE TO

CC LANOSTEROL, A REACTION THAT FORMS THE STEROL NUCLEUS.

CC -!- CATALYTIC ACTIVITY: (S)-2,3-EPOXSQUALENE = LANOSTEROL.

CC -!- PATHWAY: EARLY STAGES OF ERGOSTEROL BIOSYNTHESIS.

CC -!- SIMILARITY: BELONGS TO THE FAMILY OF TERPENE CYCLASES/MUTASES.

DR EMBL; U04841; G465105; --

DR EMBL; U23488; G733000; --

DR EMBL; U10556; G500834; --

DR PIR; A53493; A53493.

DR LISTA; SC00322; ERG7.

DR SGD; L0000573; ERG7.

DR PROSITE; PS01074; TERPENE SYNTHASES.

KW ISOMERASE; STEROID BIOSYNTHESIS.

FT INIT MET 0 0

FT CONFLICT 60 60 H -> N (IN REF. 3).

FT CONFLICT 529 529 N -> D (IN REF. 1).

SQ SEQUENCE 730 AA; 83329 MW; 22EB7C8C CRC32;

Query Match 73.2%; Score 41; DB 3; Length 730;

Best Local Similarity 55.6%; Pred. No. 4.55e+00;

Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 36 qqandpps 44

!!! :|||

Qy 1 QOSNEDPPT 9

RESULT 12

ID ACVS CEPAC STANDARD; PRT; 3712 AA.

AC P25464;

DT 01-MAY-1992 (REL. 22, CREATED)

DT 01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)

DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)

DE DELTA-(L-ALPHA-AMINOADIPYL)-L-CYSTEINYL-D-VALINE SYNTHETASE

DE (EC 6.-.-.-) (ACV SYNTHETASE) (ACVS).

GN PCBAB.

OS CEPHALOSPORIUM ACREMONIUM (ACREMONIUM CHRYSOGENUM).

OC EUKARYOTA; FUNGI; ASCOMYCOTINA; PLECTOMYCETES; EUROTIALES.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE; 91177827.

RA GUTIERREZ S., DIEZ B., MONTENEGRO E., MARTIN J.F.;

RL J. BACTERIOL. 173:2354-2365(1991).

RN [2]

RP PARTIAL SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RC STRAIN=ATCC 11550;

RX MEDLINE; 91168300.

RA HOSKINS J.A., O'CALLAGHAN N., QUEENER S.W., CANTWELL C.A., WOOD J.S.,

RA CHEN V.J., SKATRUD P.L.;

RL CURR. GENET. 18:523-530(1990).

CC -!- FUNCTION: EACH OF THE CONSTITUENT AMINO ACIDS OF THE TRIPEPTIDE

CC ACV ARE ACTIVATED AS AMONACYL-ADENYLATES WITH PEPTIDE BONDS

CC FORMED THROUGH THE PARTICIPATION OF AMINO ACID THIOLESTER

CC INTERMEDIATES.

CC -!- PATHWAY: FIRST STEP IN THE BIOSYNTHESIS OF PENICILLIN AND

CC CEPHALOSPORIN.

CC -!- COFACTOR: CONTAINS THREE COVALENTLY BOUND PHOSPHOPANTHETHEINES

CC (POTENTIAL).

CC -!- SIMILARITY: TO OTHER ENZYMES WHICH ACT VIA AN ATP-DEPENDENT

CC COVALENT BINDING OF AMP TO THEIR SUBSTRATE.

DR PIR; A38531; YGCEVC.

DR PROSITE; PS00012; PHOSPHOPANTHETHEINE.

DR PROSITE; PS00455; AMP BINDING.

KW LIGASE; ANTIBIOTIC BIOSYNTHESIS; MULTIFUNCTIONAL ENZYME;

KW REPEAT; PHOSPHOPANTHETHEINE.

FT REPEAT 234 1062

FT REPEAT 1335 2162 DOMAIN 1 (ADIPATE-ACTIVATING).

FT REPEAT 2409 3387 DOMAIN 2 (CYSTEINE-ACTIVATING).

FT BINDING 827 827 DOMAIN 3 (VALINE-ACTIVATING).

FT BINDING 1916 1916 PHOSPHOPANTHETHEINE (BY SIMILARITY).

FT BINDING 2990 2990 PHOSPHOPANTHETHEINE (BY SIMILARITY).

FT ACT SITE 3568 3568 THIOESTERASE (BY SIMILARITY).

SQ SEQUENCE 3712 AA; 414767 MW; D6048F12 CRC32;

Query Match 73.2%; Score 41; DB 1; Length 3712;

Best Local Similarity 66.7%; Pred. No. 4.55e+00;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 2569 qqskentptt 2577

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US-08-612-929-20.rsp

11

Qy 1 QQSNEPPT 9

RESULT 13

ID KV3J MOUSE STANDARD; PRT; 111 AA.  
AC P01662;  
DT 21-JUL-1986 (REL. 01, CREATED)  
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)  
DE IG KAPPA CHAIN V-III REGION (ABPC 22 AND PC 9245).  
OS MUS MUSCULUS (MOUSE).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; RODENTIA.  
RN [1]  
RP SEQUENCE (ABPC 22).  
RX MEDLINE; 79012520.  
RA MCKEAN D.J., BELL M., POTTER M.;  
RL PROC. NATL. ACAD. SCI. U.S.A. 75:3913-3917(1978).  
[2]  
RP SEQUENCE (PC 9245).  
RX MEDLINE; 79073152.  
RA WEIGERT M., GATMAITAN L., LOH E., SCHILLING J., HOOD L.E.;  
RL NATURE 276:785-790(1978).  
CC -/- THE ABPC22 AND PC9241 SEQUENCES ARE IDENTICAL.  
DR PIR; A01935; KVM56.  
DR HSP; P01679; IACY.  
KW IMMUNOGLOBULIN V REGION.  
FT DOMAIN 1 23 FRAMEWORK 1.  
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING 1.  
FT DOMAIN 39 53 FRAMEWORK 2.  
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING 2.  
FT DOMAIN 61 92 FRAMEWORK 3.  
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING 3.  
FT DOMAIN 102 111 FRAMEWORK 4.  
FT DISULFID 23 92 BY SIMILARITY.  
FT NON\_TER 111 111  
SQ SEQUENCE 111 AA; 12041 MW; 711C554A CRC32;

Query Match 71.4%; Score 40; DB 5; Length 111;  
Best Local Similarity 85.7%; Pred. No. 7.83e+00;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 93 qgmndp 99

|||||

Qy 1 QQSNEP 7

RESULT 14

ID KV3I MOUSE STANDARD; PRT; 131 AA.  
AC P01661;  
DT 21-JUL-1986 (REL. 01, CREATED)  
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)  
DE IG KAPPA CHAIN PRECURSOR V-III REGION (MOPC 63).  
OS MUS MUSCULUS (MOUSE).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; RODENTIA.  
RN [1]  
RP SEQUENCE OF 1-35.  
RX MEDLINE; 78235887.  
RA BURSTEIN Y., SCHECHTER I.;  
RL BIOCHEMISTRY 17:2392-2400(1978).  
RN [2]  
RP SEQUENCE OF 21-131.

Mar 18 10:10

US-08-612-929-20.rsp

12

RA MEDLINE; 73140225.

RA MCKEAN D.J., POTTER M., HOOD L.E.;

RL BIOCHEMISTRY 12:760-771(1973).

RN [3]

RP REVISIONS.

RX MEDLINE; 79012520.

RA MCKEAN D.J., BELL M., POTTER M.;

RL PROC. NATL. ACAD. SCI. U.S.A. 75:3913-3917(1978).

DR PIR; A01935; KVM56.

DR HSP; P01679; IACY.

KW IMMUNOGLOBULIN V REGION; SIGNAL.

FT SIGNAL 1 20

FT CHAIN 21 131 IG KAPPA CHAIN V-III REGION (MOPC 63).

FT DOMAIN 21 43 FRAMEWORK 1.

FT DOMAIN 44 58 COMPLEMENTARITY-DETERMINING 1.

FT DOMAIN 59 73 FRAMEWORK 2.

FT DOMAIN 74 80 COMPLEMENTARITY-DETERMINING 2.

FT DOMAIN 81 112 FRAMEWORK 3.

FT DOMAIN 113 121 COMPLEMENTARITY-DETERMINING 3.

FT DOMAIN 122 131 FRAMEWORK 4.

FT DISULFID 43 112 BY SIMILARITY.

FT NON\_TER 131 131

SQ SEQUENCE 131 AA; 14291 MW; 9D55A06B CRC32;

Query Match 71.4%; Score 40; DB 5; Length 131;

Best Local Similarity 85.7%; Pred. No. 7.83e+00;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 113 qgmndp 119

|||||

Qy 1 QQSNEP 7

RESULT 15

ID LMP2 EBV STANDARD; PRT; 497 AA.  
AC P13285;  
DT 01-JAN-1990 (REL. 13, CREATED)  
DT 01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)  
DT 01-DEC-1992 (REL. 24, LAST ANNOTATION UPDATE)  
DE GENE TERMINAL PROTEIN (MEMBRANE PROTEIN LMP-2A/LMP-2B).  
OS ERSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).  
OC VIRIDAE; DS-DNA ENVELOPED VIRUSES; HERPESVIRIDAE; GAMMAHERPESVIRINAE.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 88283646.  
RA LAUX G., PERRICAUDET M., FARRELL P.J.;  
RL EMBO J. 7:769-774(1988).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 89095024.  
RA SAMPLE J., LIEBOWITZ D., KIEFF E.;  
RL J. VIROL. 63:933-937(1989).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 84270667.  
RA BAER R., BANKIER A.T., BIGGIN M.D., DEININGER P.L., FARRELL P.J.,  
RA GIBSON T.J., HATFULL G., HUDSON G.S., SATCHWELL S.C., SEGUIN C.,  
RA TUFFNELL P.S., BARRELL B.G.;  
RL NATURE 310:207-211(1984).  
CC -/- FUNCTION: MAY BE IMPORTANT FOR IMMORTALIZATION OF CELLS BY EBV.  
CC -/- SUBCELLULAR LOCATION: MEMBRANE (PROBABLE).  
DR EMBL; M24212; G522187; -.  
DR EMBL; Y00835; G59184; -.  
DR EMBL; V01555; -; NOT\_ANNOTATED\_CDS.

DR PIR; A30178; MWBEIM.  
KW TRANSMEMBRANE.  
FT CHAIN 1 497 MEMBRANE PROTEIN LMP-2A.  
FT CHAIN 120 497 MEMBRANE PROTEIN LMP-2B.  
FT TRANSMEM 122 141 POTENTIAL.  
FT TRANSMEM 150 168 POTENTIAL.  
FT TRANSMEM 178 198 POTENTIAL.  
FT TRANSMEM 208 235 POTENTIAL.  
FT TRANSMEM 242 259 POTENTIAL.  
FT TRANSMEM 267 288 POTENTIAL.  
FT TRANSMEM 300 316 POTENTIAL.  
FT TRANSMEM 321 339 POTENTIAL.  
FT TRANSMEM 355 373 POTENTIAL.  
FT TRANSMEM 392 411 POTENTIAL.  
FT TRANSMEM 419 443 POTENTIAL.  
FT TRANSMEM 450 470 POTENTIAL.  
SQ SEQUENCE 497 AA; 53011 MW; 6F2B2E7D CRC32;

Query Match 71.4%; Score 40; DB 5; Length 497;  
Best Local Similarity 62.5%; Pred. No. 7.83e+00;  
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 50 resnepp 57  
::|::|  
Qy 1 QOSNEDPP 8

Search completed: Tue Mar 18 10:12:11 1997  
Job time : 10 secs.



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WQESREH

(TM)

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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Mar 18 10:12:28 1997; MacPar time 2.30 Seconds  
100.591 Million cell updates/sec

Tabular output not generated.

Title: >US-08-612-929-20  
Description: (1-9) from US08612929.pep  
Perfect Score: 56  
Sequence: 1 QOSNEDPPT 9

Scoring table: PAM 150  
Gap 15

Searched: 82182 seqs, 25727515 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: pir48  
1:ann1 2:ann2 3:ann3 4:unann1 5:unann2 6:unann3 7:unann4  
8:unann5 9:unann6 10:unann7 11:unann8 12:unann9 13:unenc  
14:unrev

Statistics: Mean 18.801; Variance 24.382; scale 0.771

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	52	92.9	112	5	S19971 Ig kappa chain V reg	8.89e-02
2	52	92.9	131	5	PH1226 Ig kappa chain precu	8.89e-02
3	47	83.9	65	12	C38601 Ig kappa chain V reg	1.13e+00
4	44	78.6	96	12	B49442 Ig light chain V reg	4.85e+00
5	44	78.6	111	2	KVMS83 Ig kappa chain V reg	4.85e+00
6	44	78.6	111	12	D45722 anti-glycoprotein H	4.85e+00
7	43	76.8	81	12	S42193 Ig kappa chain V reg	7.80e+00
8	43	76.8	85	12	S42189 Ig kappa chain V reg	7.80e+00
9	43	76.8	87	12	S42190 Ig kappa chain V reg	7.80e+00
10	43	76.8	88	12	S42194 Ig kappa chain V reg	7.80e+00
11	43	76.8	90	12	S42187 Ig kappa chain V reg	7.80e+00
12	43	76.8	107	5	S26344 Ig kappa chain V reg	7.80e+00

13	43	76.8	107	5	S26343 Ig kappa chain V reg	7.80e+00
14	43	76.8	111	2	KVMS08 Ig kappa chain V reg	7.80e+00
15	43	76.8	111	5	A3936 Ig kappa chain V reg	7.80e+00
16	43	76.8	111	2	KVMS37 Ig kappa chain V reg	7.80e+00
17	43	76.8	111	2	KVMS43 Ig kappa chain V reg	7.80e+00
18	43	76.8	111	5	S09666 Ig kappa chain V-J r	7.80e+00
19	43	76.8	111	2	KVMS01 Ig kappa chain V reg	7.80e+00
20	43	76.8	111	2	KVMS69 Ig kappa chain V reg	7.80e+00
21	43	76.8	132	2	KVMS32 Ig kappa chain precu	7.80e+00
22	42	75.0	102	5	PH1079 Ig light chain V reg	1.25e+01
23	42	75.0	925	10	JC2033 G protein-coupled re	1.25e+01
24	41	73.2	65	12	B38601 Ig kappa chain V reg	1.97e+01
25	41	73.2	93	12	A38601 Ig kappa chain V reg	1.97e+01
26	41	73.2	557	10	S56292 hypothetical protein	1.97e+01
27	41	73.2	731	10	S46813 lanosterol synthase	1.97e+01
28	41	73.2	731	10	A57741 lanosterol synthase	1.97e+01
29	41	73.2	3712	2	YGCEVC alpha-aminoadipyl-cy	1.97e+01
30	40	71.4	102	5	PH1078 Ig light chain V reg	3.11e+01
31	40	71.4	131	2	KVMSW6 Ig kappa chain precu	3.11e+01
32	40	71.4	209	6	JQ2347 hypothetical 23.6K p	3.11e+01
33	40	71.4	297	10	S55085 hypothetical protein	3.11e+01
34	40	71.4	497	3	WBEELM membrane protein LMP	3.11e+01
35	40	71.4	914	14	S61671 hypothetical protein	3.11e+01
36	40	71.4	914	9	S46593 asparagine-rich zinc	3.11e+01
37	40	71.4	943	10	S28400 gag-like protein - f	3.11e+01
38	40	71.4	1655	14	S61617 nucleoporin Np188 -	3.11e+01
39	40	71.4	1655	9	S47446 hypothetical protein	3.11e+01
40	39	69.6	112	5	S19972 Ig kappa chain V reg	4.86e+01
41	39	69.6	148	6	D49530 16K vascular endothe	4.86e+01
42	39	69.6	509	9	S59210 hypothetical protein	4.86e+01
43	39	69.6	509	10	S45413 probable membrane pr	4.86e+01
44	39	69.6	692	9	S59833 DNA polymerase epsilon	4.86e+01
45	39	69.6	698	9	A39698 DNA-directed DNA pol	4.86e+01

## ALIGNMENTS

RESULT 1  
ENTRY S19971 #type fragment  
TITLE Ig kappa chain V region (CD4 mAb clone M-T310 and others) -  
mouse (fragment)  
ORGANISM #formal name Mus musculus #common name house mouse  
DATE 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 01-Dec-1995  
ACCESSIONS S19971; S19973  
REFERENCE S19963  
#authors Weissenhorn, W.; Riethmuller, G.; Weiss, E.M.; Rieber, E.P.  
#submission submitted to the EMBL Data Library, March 1992  
#description Structural characterization of CD4 mAb.  
#accession S19971  
#molecule\_type mRNA  
#residues 1-112 #label WEI  
#cross-references EMBL:X65091  
#experimental\_source clone M-T310  
#accession S19973  
#molecule\_type mRNA  
#residues 1-112 #label WEW  
#cross-references EMBL:X65092  
#experimental\_source M-T404  
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology  
SUMMARY #length 112 #checksum 4782  
Query Match 92.9%; Score 52; DB 5; Length 112;  
Best Local Similarity 88.9%; Pred. No. 8.89e-02;

Mar 18 10:11

US-08-612-929-20.rpr

3

Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 93 qqsedpdt 101  
|||||  
Qy 1 QQSNEPPT 9

RESULT 2  
ENTRY #type fragment  
TITLE Ig kappa chain precursor V region (M-T310) - human (fragment)  
ORGANISM #formal name Homo sapiens #common name man  
DATE 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 30-Apr-1995

ACCESSIONS PH1226  
REFERENCE PH1224  
#authors Weissenhorn, W.; Scheuer, W.; Kaluza, B.; Schwirzke, M.; Reiter, C.; Flieger, D.; Lenz, H.; Weiss, E.H.; Rieber, E.P.; Riethmüller, G.; Weidle, U.H.

#journal Gene (1992) 121:271-278  
#title Combinatorial functions of two chimeric antibodies directed to human CD4 and one directed to the alpha-chain of the human interleukin-2 receptor.

#accession PH1226  
#molecule\_type mRNA  
#residues 1-131 #label WEI

CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology  
KEYWORDS immunoglobulin  
FEATURE 1-20 #domain signal sequence #status predicted #label SIG  
21-131 #product Ig light chain V region #status predicted #label MAT

SUMMARY #length 131 #checksum 4648

Query Match 92.9%; Score 52; DB 5; Length 131;  
Best Local Similarity 88.9%; Pred. No. 8.89e-02;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 113 qqsedpdt 121  
|||||  
Qy 1 QQSNEPPT 9

RESULT 3  
ENTRY #type fragment  
TITLE Ig kappa chain V region (2B5) - mouse (fragment)  
ORGANISM #formal name Mus musculus #common name house mouse  
DATE 30-Aug-1991 #sequence\_revision 30-Aug-1991 #text\_change 23-Mar-1993

ACCESSIONS C38601  
REFERENCE A38601  
#authors Goshorn, S.C.; Retzel, E.; Jermerson, R.  
#journal J. Biol. Chem. (1991) 266:2134-2142  
#title Common structural features among monoclonal antibodies binding the same antigenic region of cytochrome c.

#cross-references M01D:91115823  
#accession C38601  
#status preliminary  
#molecule\_type mRNA  
#residues 1-65 #label GOS  
#cross-references GB:M57980  
SUMMARY #length 65 #checksum 8125

Query Match 83.9%; Score 47; DB 12; Length 65;  
Best Local Similarity 88.9%; Pred. No. 1.13e+00;

Mar 18 10:11

US-08-612-929-20.rpr

4

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 46 qqsedpdt 54  
|||||  
Qy 1 QQSNEPPT 9

RESULT 4  
ENTRY #type fragment  
TITLE Ig light chain V region (50.1) - mouse (fragment)  
ORGANISM #formal name Mus musculus #common name house mouse  
DATE 21-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 21-Jul-1995

ACCESSIONS B49442  
REFERENCE A49442  
#authors Stura, E.A.; Stanfield, R.L.; Fieser, G.G.; Silver, S.; Roguska, M.; Hincapie, L.M.; Simmerman, H.K.B.; Profy, A.T.; Wilson, I.A.

#journal Proteins (1992) 14:499-508  
#title Crystallization, sequence, and preliminary crystallographic data for an antipeptide Fab 50.1 and peptide complexes with the principal neutralizing determinant of HIV-1 gp120.

#accession B49442  
#status preliminary; not compared with conceptual translation  
#molecule\_type DNA  
#residues 1-96 #label STU

SUMMARY #length 96 #checksum 7322

Query Match 78.6%; Score 44; DB 12; Length 96;  
Best Local Similarity 88.9%; Pred. No. 4.85e+00;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 85 qqsedpdt 93  
|||||  
Qy 1 QQSNEPPT 9

RESULT 5  
ENTRY #type complete  
TITLE Ig kappa chain V region (PC7183) - mouse  
ORGANISM #formal name Mus musculus #common name house mouse  
DATE 30-Jun-1993 #sequence\_revision 30-Jun-1993 #text\_change 30-Sep-1993

ACCESSIONS B01937; A01937  
REFERENCE A93204  
#authors Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.  
#journal Nature (1978) 276:785-790  
#title Rearrangement of genetic information may produce immunoglobulin diversity.

#cross-references M01D:79073152  
#accession B01937  
#molecule\_type protein  
#residues 1-111 #label WEI

CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology  
KEYWORDS immunoglobulin  
FEATURE 23-92 #disulfide bonds #status predicted  
SUMMARY #length 111 #molecular-weight 11952 #checksum 9

Query Match 78.6%; Score 44; DB 2; Length 111;  
Best Local Similarity 88.9%; Pred. No. 4.85e+00;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 93 qqsedpdt 101

Mar 18 10:11

US-08-612-929-20 rpt

5

Qy 1 QQSNEPPT 9  
||||||| I

RESULT 6

ENTRY D45722 #type fragment  
TITLE anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 109) - mouse (fragment)  
ORGANISM #formal\_name Mus musculus #common\_name house mouse  
DATE 22-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 18-Nov-1994  
ACCESSIONS D45722  
REFERENCE A45722  
#authors Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Vasquez, M.; Britt, W.J.; Coelingh, K.L.  
#journal J. Virol. (1993) 67:489-496  
#title Neutralizing monoclonal antibodies that distinguish three antigenic sites on human cytomegalovirus glycoprotein H have conformationally distinct binding sites.  
#cross-references MUID:93100833  
#accession D45722  
##status preliminary; not compared with conceptual translation  
##molecule\_type nucleic acid  
##residues 1-111 ##label SIM  
##cross-references NCBIP:120592  
##note sequence extracted from NCBI backbone  
SUMMARY #length 111 #checksum 811

Query Match 78.6%; Score 44; DB 12; Length 111;  
Best Local Similarity 77.8%; Pred. No. 4.85e+00;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 93 qnnedprt 101  
||||||| I  
Qy 1 QQSNEPPT 9

RESULT 7

ENTRY S42193 #type fragment  
TITLE Ig kappa chain V region - mouse (fragment)  
ORGANISM #formal\_name Mus musculus #common\_name house mouse  
DATE 07-Oct-1994 #sequence\_revision 26-May-1995 #text\_change 26-May-1995  
ACCESSIONS S42193  
REFERENCE S42176  
#authors Mo, J.A.; Bona, C.A.; Holmdahl, R.  
#journal Eur. J. Immunol. (1993) 23:2503-2510  
#title Variable region gene selection of immunoglobulin G-expressing B cells with specificity for a defined epitope on type II collagen.  
#accession S42193  
##status preliminary  
##molecule\_type DNA  
##residues 1-81 ##label MOJ  
##cross-references EMBL:225456  
##note the authors translated the codon GTT for residue 36 as Ala  
SUMMARY #length 81 #checksum 9746

Query Match 76.8%; Score 43; DB 12; Length 81;  
Best Local Similarity 100.0%; Pred. No. 7.80e+00;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Mar 18 10:11

US-08-612-929-20 rpt

6

Db 75 qgsnedp 81  
||||||| I  
Qy 1 QQSNEDP 7

RESULT 8

ENTRY S42189 #type fragment  
TITLE Ig kappa chain V region - mouse (fragment)  
ORGANISM #formal\_name Mus musculus #common\_name house mouse  
DATE 28-Sep-1994 #sequence\_revision 21-Jul-1995 #text\_change 21-Jul-1995  
ACCESSIONS S42189  
REFERENCE S42176  
#authors Mo, J.A.; Bona, C.A.; Holmdahl, R.  
#journal Eur. J. Immunol. (1993) 23:2503-2510  
#title Variable region gene selection of immunoglobulin G-expressing B cells with specificity for a defined epitope on type II collagen.  
#accession S42189  
##status preliminary  
##molecule\_type DNA  
##residues 1-85 ##label MOJ  
##cross-references EMBL:225448  
SUMMARY #length 85 #checksum 7866

Query Match 76.8%; Score 43; DB 12; Length 85;  
Best Local Similarity 100.0%; Pred. No. 7.80e+00;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 79 qgsnedp 85  
||||||| I  
Qy 1 QQSNEDP 7

RESULT 9

ENTRY S42190 #type fragment  
TITLE Ig kappa chain V region - mouse (fragment)  
ORGANISM #formal\_name Mus musculus #common\_name house mouse  
DATE 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 13-Jan-1995  
ACCESSIONS S42190  
REFERENCE S42176  
#authors Mo, J.A.; Bona, C.A.; Holmdahl, R.  
#journal Eur. J. Immunol. (1993) 23:2503-2510  
#title Variable region gene selection of immunoglobulin G-expressing B cells with specificity for a defined epitope on type II collagen.  
#accession S42190  
##status preliminary  
##molecule\_type DNA  
##residues 1-87 ##label MOJ  
##cross-references EMBL:225450  
SUMMARY #length 87 #checksum 2354

Query Match 76.8%; Score 43; DB 12; Length 87;  
Best Local Similarity 100.0%; Pred. No. 7.80e+00;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 81 qgsnedp 87  
||||||| I  
Qy 1 QQSNEDP 7

RESULT 10

Mar 18 10:11

US-08-612-929-20.rpr

7

```
ENTRY          S42194      #type fragment
TITLE          Ig kappa chain V region - mouse (fragment)
ORGANISM       #formal name Mus musculus #common name house mouse
DATE           28-Sep-1994 #sequence_revision 21-Jul-1995 #text_change
                21-Jul-1995
ACCESSIONS
REFERENCE      S42176
#authors      Mo, J.A.; Bona, C.A.; Holmdahl, R.
#journal      Eur. J. Immunol. (1993) 23:2503-2510
#title        Variable region gene selection of immunoglobulin G-expressing
                B cells with specificity for a defined epitope on type II
                collagen.
#accession    S42194
#status       preliminary
#molecule_type DNA
#residues     1-88 #label MOJ
#cross-references EMBL:Z25458
SUMMARY        #length 88 #checksum 4364
```

```
Query Match      76.8%; Score 43; DB 12; Length 88;
Best Local Similarity 100.0%; Pred. No. 7.80e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Db 82 qgsndp 88
|||||||
Qy 1 QQSNEDP 7
```

```
RESULT 11
ENTRY          S42187      #type fragment
TITLE          Ig kappa chain V region - mouse (fragment)
ORGANISM       #formal name Mus musculus #common name house mouse
DATE           28-Sep-1994 #sequence_revision 21-Jul-1995 #text_change
                21-Jul-1995
ACCESSIONS
REFERENCE      S42176
#authors      Mo, J.A.; Bona, C.A.; Holmdahl, R.
#journal      Eur. J. Immunol. (1993) 23:2503-2510
#title        Variable region gene selection of immunoglobulin G-expressing
                B cells with specificity for a defined epitope on type II
                collagen.
#accession    S42187
#status       preliminary
#molecule_type DNA
#residues     1-90 #label MOJ
#cross-references EMBL:Z25444
SUMMARY        #length 90 #checksum 9303
```

```
Query Match      76.8%; Score 43; DB 12; Length 90;
Best Local Similarity 100.0%; Pred. No. 7.80e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Db 84 qgsndp 90
|||||||
Qy 1 QQSNEDP 7
```

```
RESULT 12
ENTRY          S26344      #type complete
TITLE          Ig kappa chain V region - mouse
ORGANISM       #formal name Mus musculus #common name house mouse
DATE           13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
                12-Apr-1995
ACCESSIONS     S26344
```

Mar 18 10:11

US-08-612-929-20.rpr

8

```
REFERENCE      S26309
#authors      Stark, S.E.; Caton, A.J.
#journal      J. Exp. Med. (1991) 174:613-624
#title        Antibodies that are specific for a single amino acid
                interchange in a protein epitope use structurally distinct
                variable regions.
#accession    S26344
#status       preliminary
#molecule_type mRNA
#residues     1-107 #label STA
#cross-references EMBL:X59209
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
SUMMARY        #length 107 #molecular-weight 11646 #checksum 6789
```

```
Query Match      76.8%; Score 43; DB 5; Length 107;
Best Local Similarity 100.0%; Pred. No. 7.80e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Db 92 qgsndp 98
|||||||
Qy 1 QQSNEDP 7
```

```
RESULT 13
ENTRY          S26343      #type complete
TITLE          Ig kappa chain V region - mouse
ORGANISM       #formal name Mus musculus #common name house mouse
DATE           13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
                12-Apr-1995
ACCESSIONS     S26343
REFERENCE      S26309
#authors      Stark, S.E.; Caton, A.J.
#journal      J. Exp. Med. (1991) 174:613-624
#title        Antibodies that are specific for a single amino acid
                interchange in a protein epitope use structurally distinct
                variable regions.
#accession    S26343
#status       preliminary
#molecule_type mRNA
#residues     1-107 #label STA
#cross-references EMBL:X59207
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
SUMMARY        #length 107 #molecular-weight 11660 #checksum 6543
```

```
Query Match      76.8%; Score 43; DB 5; Length 107;
Best Local Similarity 100.0%; Pred. No. 7.80e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Db 92 qgsndp 98
|||||||
Qy 1 QQSNEDP 7
```

```
RESULT 14
ENTRY          KYMS08      #type complete
TITLE          Ig kappa chain V region (PC6308) - mouse
ORGANISM       #formal name Mus musculus #common name house mouse
DATE           30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change
                30-Sep-1993
ACCESSIONS     C01937; A01937
REFERENCE      A93204
#authors      Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
                Nature (1978) 276:785-790
#journal
#title        Rearrangement of genetic information may produce
```

Mar 18 10:11

US-08-612-929-20.rpr

9

```
#cross-references MUID:79073152
#accession C01937
#molecule_type protein
#residues 1-111 ##label WEI
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS immunoglobulin
FEATURE
23-92
SUMMARY #disulfide bonds #status predicted
#length 111 #molecular-weight 12071 #checksum 2195
```

```
Query Match 76.8%; Score 43; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 7.80e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Db 93 qqsndp 99
|||||
Oy 1 QQSNEDP 7
```

```
RESULT 15
ENTRY A33936 #type fragment
TITLE Ig kappa chain V region (VM201) - mouse (fragment)
ORGANISM #formal name Mus musculus #common name house mouse
DATE 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change
12-Apr-1995
ACCESSIONS A33936
REFERENCE
#authors Meek, K.; Johansson, B.; Schulman, J.; Bona, C.; Capra, J.D.
#journal Proc. Natl. Acad. Sci. U.S.A. (1989) 86:4664-4668
#title Nucleotide changes in sequential variants of influenza virus
hemagglutinin genes and molecular structures of
corresponding monoclonal antibodies specific for each
variant.
```

```
#cross-references MUID:89282831
#accession A33936
#status preliminary
#molecule_type mRNA
#residues 1-111 ##label MEE
#cross-references GB:J04575
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
SUMMARY #length 111 #checksum 1618
```

```
Query Match 76.8%; Score 43; DB 5; Length 111;
Best Local Similarity 100.0%; Pred. No. 7.80e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Db 93 qqsndp 99
|||||
Oy 1 QQSNEDP 7
```

Search completed: Tue Mar 18 10:12:34 1997  
Job time : 6 secs.

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WATERMAN

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MParch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Mar 18 10:12:52 1997; MacPar time 1.71 Seconds  
Tabular output not generated. 54.031 Million cell updates/sec

Title: &gt;US-08-612-929-20

Description: (1-9) from US08612929.pep

Perfect Score: 56

Sequence: 1 QQSNEPPT 9

Scoring table: PAM 150

Gap 15

Searched: 88003 seqs, 10295656 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: a-geneseq25

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13  
14:part14 15:part15 16:part16 17:part17 18:part18

Statistics: Mean 13.130; Variance 39.761; scale 0.330

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	56	100.0	9	13	R70197	MAB 3B9 light chain C 1.78e+00
2	56	100.0	131	13	R70202	Humanized antibody 3B 1.78e+00
3	56	100.0	131	6	R29008	p64-k4 protein produc 1.78e+00
4	56	100.0	132	13	R70189	Mouse MAB 3B9 light c 1.78e+00
5	52	92.9	131	6	R32123	Anti-CD4 antibody WT 5.29e+00
6	51	91.1	9	13	R70201	Humanized antibody 3B 6.92e+00
7	51	91.1	131	13	R75355	Humanized antibody 3B 6.92e+00
8	49	87.5	17	12	R66145	CD-4 antibody variabl 1.18e+01
9	49	87.5	103	9	R47933	Light chain region of 1.18e+01
10	49	87.5	111	9	R47935	Humanised light chain 1.18e+01
11	49	87.5	115	1	R04134	Anti-Leu 3a light cha 1.18e+01
12	49	87.5	131	1	R04132	Anti-Leu 3a light cha 1.18e+01

13	47	83.9	111	9	R47494	Murine anti-CD18 AB 6 2.01e+01
14	47	83.9	111	9	R47492	Humanised anti-CD18 A 2.01e+01
15	45	80.4	215	12	R74781	Light chain of 59.1 a 3.40e+01
16	44	78.6	112	3	R13089	Murine IB4 light chain 4.42e+01
17	43	76.8	9	14	R75478	Mouse antibody light 5.72e+01
18	43	76.8	9	14	R75477	Mouse antibody light 5.72e+01
19	43	76.8	106	6	R33309	MaE15 light chain. 5.72e+01
20	43	76.8	111	11	R60306	Chimeric anti HIV ant 5.72e+01
21	43	76.8	111	1	P90541	Immunoglobulin L chain 5.72e+01
22	43	76.8	111	10	R55123	Mouse anti-HIV mu5.5 5.72e+01
23	43	76.8	111	11	R60302	Anti HIV antibody lig 5.72e+01
24	43	76.8	111	10	R55127	Mouse-human chimeric 5.72e+01
25	43	76.8	112	5	R24575	Human x mouse modifie 5.72e+01
26	43	76.8	131	1	P90543	Amino acids sequence 5.72e+01
27	43	76.8	132	7	R37116	Mouse 4C10 anti-idiot 5.72e+01
28	41	73.2	111	13	R65172	Murine NM-01 variable 9.57e+01
29	41	73.2	111	13	R65174	Region producing huma 9.57e+01
30	41	73.2	111	9	R48623	Sequence of the human 9.57e+01
31	41	73.2	111	9	R48622	Sequence of the human 9.57e+01
32	41	73.2	112	2	R10539	Chimeric MAB 9.2.27 1 9.57e+01
33	41	73.2	111	9	R48616	Sequence of the monoc 9.57e+01
34	41	73.2	132	3	R10920	kappa light chain var 9.57e+01
35	41	73.2	3639	8	R40227	ACVS. 9.57e+01
36	41	73.2	3712	3	R13896	ACV synthetase. 9.57e+01
37	40	71.4	110	10	R60810	Light chain variable 1.23e+02
38	40	71.4	111	10	R53930	Light chain variable 1.23e+02
39	40	71.4	111	6	R33305	MaE11 light chain. 1.23e+02
40	40	71.4	112	14	R79158	Human IgE receptor-bi 1.23e+02
41	40	71.4	120	9	R48618	Sequence of the monoc 1.23e+02
42	40	71.4	121	9	R48615	Sequence of the monoc 1.23e+02
43	40	71.4	121	6	R33346	Sequence of the varia 1.23e+02
44	40	71.4	209	2	R12300	ORF-2 of Herpes Virus 1.23e+02
45	40	71.4	218	6	R33312	Humanised MaE11 Vers1 1.23e+02

## ALIGNMENTS

RESULT 1  
ID R70197 standard; Protein; 9 AA.  
AC R70197;  
DT 20-SEP-1995 (first entry)  
DE MAB 3B9 light chain CDR.  
KW Chimeric antibody; humanized antibody; antibody engineering;  
KW monoclonal antibody; MAB; interleukin-4; IL-4; allergy; CDR;  
KW complementarity determining region.  
OS Mus sp.  
PN W09507301-A.  
PD 16-MAR-1995.  
PF 07-SEP-1993; US-117366.  
PR 07-SEP-1993; US-117366.  
PR 14-OCT-1993; US-136783.  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
PA (SMIK ) SMITHKLINE BEECHAM PLC.  
PI Gross MS, Holmes SD, Sylvester DR;  
PI WPI; 95-123387/16.  
DR Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived  
PT from high affinity mAbs - useful in treatment of IL-4-mediated  
PT and IgE-mediated allergic conditions  
PS Disclosure; Page 56; 97pp; English.  
CC Spleen cells from mice immunized with human IL-4 were used to prepare  
CC hybridomas, which were screened for anti-IL-4 MAB secretion. Only  
CC clone 3B9 was positive. cDNA clones of the 3B9 light and heavy  
CC chains were cloned into pGEM7f+ and transformed into E. coli  
CC DH5-alpha. A light chain cDNA clone was sequenced (083490) that

Mar 18 10:11

US-08-612-929-20.rag

3

CC encoded the protein given in R70189. 3 CDRs (R70195-97) were  
 CC identified.  
 SQ Sequence 9 AA;

Query Match 100.0%; Score 56; DB 13; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.78e+00;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 qgsnedpdt 9  
 |||||  
 Qy 1 QQSNEPPT 9

## RESULT 2

ID R70202 standard; Protein; 131 AA.  
 AC R70202;  
 DT 20-SEP-1995 (first entry)  
 DE Humanized antibody 3B9 light chain.  
 KW Humanized antibody; antibody engineering; monoclonal antibody;  
 KW MAb; interleukin-4; IL-4; allergy.  
 OS Homo sapiens.  
 PN WO9507301-A.  
 PD 16-MAR-1995.  
 PF 07-SEP-1994; U10308.  
 PR 07-SEP-1993; US-117366.  
 PR 14-OCT-1993; US-136783.  
 PA (SMIK ) SMITHKLINE BEECHAM CORP.  
 PA (SMIK ) SMITHKLINE BEECHAM PLC.  
 PI Gross MS, Holmes SD, Sylvester DR;  
 DR WPI; 95-123387/16.  
 DR N-PSDB; Q83520.  
 PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived  
 PT from high affinity mAbs - useful in treatment of IL-4-mediated  
 PT and IgE-mediated allergic conditions  
 PS Disclosure; Page 71-72; 97pp; English.  
 CC A humanized antibody light chain variable region and signal  
 CC sequence is given in R75355. The signal sequence is also  
 CC provided in R70194. The sequences of the 3 CDRs  
 CC are identical to mouse anti-human IL-4 MAb 3B9 light chain  
 CC CDRs (given in R70195-97).  
 SQ Sequence 131 AA;

Query Match 100.0%; Score 56; DB 13; Length 131;  
 Best Local Similarity 100.0%; Pred. No. 1.78e+00;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 112 qgsnedpdt 120  
 |||||  
 Qy 1 QQSNEPPT 9

## RESULT 3

ID R29008 standard; Protein; 131 AA.  
 AC R29008;  
 DT 30-MAR-1993 (first entry)  
 DE p64-k4 protein product.  
 KW Human; antibody; interleukin-6; receptor; IL-6R; light chain; L; H;  
 KW heavy chain; variable region; mouse; monoclonal; hybridoma; AUK64-7;  
 KW plasmid; p64-k4; p64-h2.  
 OS Synthetic.  
 FH Key Location/Qualifiers  
 FT Peptide 1..20  
 FT /note= "Signal peptide" 21..131  
 FT Protein

Mar 18 10:11

US-08-612-929-20.rag

4

FT /note= "Mature peptide"  
 PN WO9219759-A.  
 PD 12-NOV-1992.  
 PF 24-APR-1992; J00544.  
 PR 25-APR-1991; JP-095476.  
 PR 19-FEB-1992; JP-032084.  
 PA (CHUS ) CHUGAI SEIYAKU KK.  
 PI Bendig MM, Jones ST, Saldanha JW, Sato K, Tsuchiya M;  
 DR WPI; 92-398882/48.  
 DR N-PSDB; Q30757.  
 PT Reconstituted human antibody to human interleukin-6 receptor -  
 PT has low antigenicity and contains mouse V-region complementarity  
 PT determining regions  
 PS Disclosure; Page 124-125; 207pp; Japanese.  
 CC The sequences given in R29008-09 were encoded by plasmids which were  
 CC used in example to illustrate the production of a human antibody which  
 CC recognises human interleukin-6 receptor (IL-6R). The antibody  
 CC comprises light (L) chain and heavy (H) chain variable regions which  
 CC were derived from a mouse monoclonal antibody produced from the  
 CC hybridoma AUK64-7 which contained the plasmids p64-k4 and p64-h2.  
 SQ Sequence 131 AA;

Query Match 100.0%; Score 56; DB 6; Length 131;  
 Best Local Similarity 100.0%; Pred. No. 1.78e+00;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 113 qgsnedpdt 121  
 |||||  
 Qy 1 QQSNEPPT 9

## RESULT 4

ID R70189 standard; Protein; 132 AA.  
 AC R70189;  
 DT 20-SEP-1995 (first entry)  
 DE Mouse MAb 3B9 light chain.  
 KW Chimeric antibody; humanized antibody; antibody engineering;  
 KW monoclonal antibody; MAb; interleukin-4; IL-4; allergy.  
 OS Mus sp.  
 FH Key Location/Qualifiers  
 FT Peptide 1..20  
 FT /label= sig\_peptide 44..58  
 FT /label= CDR 74..80  
 FT /note= "complementarity determining region"  
 FT /label= CDR 113..121  
 FT /note= "complementarity determining region"  
 FT /label= CDR 113..121  
 FT /note= "complementarity determining region"

PN WO9507301-A.  
 PD 16-MAR-1995.  
 PF 07-SEP-1994; U10308.  
 PR 07-SEP-1993; US-117366.  
 PR 14-OCT-1993; US-136783.  
 PA (SMIK ) SMITHKLINE BEECHAM CORP.  
 PA (SMIK ) SMITHKLINE BEECHAM PLC.  
 PI Gross MS, Holmes SD, Sylvester DR;  
 DR WPI; 95-123387/16.  
 DR N-PSDB; Q83490.  
 PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived  
 PT from high affinity mAbs - useful in treatment of IL-4-mediated  
 PT and IgE-mediated allergic conditions

PS Disclosure; Fig.1; 97pp; English.

CC Spleen cells from mice immunized with human IL-4 were used to prepare  
CC hybridomas, which were screened for anti-IL-4 MAB secretion. Only  
CC clone 3B9 was positive. cDNA clones of the 3B9 light and heavy  
CC chains were cloned into pGEMTf+ and transformed into E. coli  
CC DH5-alpha. The clones were sequenced (Q83490-91), and used for  
CC antibody engineering.

SQ Sequence 132 AA;

Query Match 100.0%; Score 56; DB 13; Length 132;

Best Local Similarity 100.0%; Pred. No. 1.78e+00;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 113 qgsnedppt 121

|||||

Qy 1 QGSNEDPPT 9

RESULT 5

ID R32123 standard; Protein; 131 AA.

AC R32123;

DT 02-JUN-1993 (first entry)

DE Anti-CD4 antibody MT 3.10 light chain variable region.

KW Immunosuppression; tissue transplantation; graft; L chain; V region;

KW T-helper cell inhibition; transplant rejection; MAB;

KW Interleukin-2 receptor.

FH Key Location/Qualifiers

FT Peptide 1..20

FT /Label= signal

FT Region 21..120

FT /Label= Variable

FT Region 121..131

FT /Label= J1

PN DE4143214-A.

PD 28-JAN-1993.

PF 30-DEC-1991; 143214.

PR 25-JUL-1991; DE-124759.

PR 30-DEC-1991; DE-143214.

PA (BOEF ) BOEHRINGER MANNHEIM GMBH.

PI Kaluza B, Riethmüller G, Scheuer W, Weidle U;

DR WPI; 93-037582/05.

DR N-PSDB; Q36609.

PT Synergistic antibody compsn. for use as immunosuppressant -

PT comprises monoclonal anti-CD4 antibodies and monoclonal anti-IL2R

PT alpha- or anti-IL2R beta antibodies

PS Claim 5; Page 11; 18pp; German.

CC This sequence is the light chain variable region of a preferred

CC anti-CD4 monoclonal antibody for use in the claimed synergistic

CC composition. MAB MT 3.10 is deposited as clone 3.101/sB10 (ECACC

CC 90090702). The anti-CD4 antibody is used with at least one anti-IL2R

CC alpha or beta antibody. Individually the antibodies are strongly

CC inhibiting and when used together their immunosuppressive properties

CC are improved; they synergistically inhibit T-helper cell

CC proliferation to effectively inhibit transplant rejection at low

CC doses without significantly reducing the general immune response.

CC See also Q36608-Q36616.

SQ Sequence 131 AA;

Query Match 92.9%; Score 52; DB 6; Length 131;

Best Local Similarity 88.9%; Pred. No. 5.29e+00;

Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 113 qgsnedppt 121

|||||

Qy 1 QGSNEDPPT 9

RESULT 6

ID R70201 standard; Protein; 9 AA.

AC R70201;

DT 20-SEP-1995 (first entry)

DE Humanized antibody 3B9 light chain CDR.

KW Humanized antibody; antibody engineering; monoclonal antibody;

KW MAB; interleukin-4; IL-4; allergy; CDR;

KW complementarity determining region.

OS Homo sapiens.

PN W09507301-A.

PD 16-MAR-1995.

PF 07-SEP-1994; U10308.

PR 07-SEP-1993; US-117366.

PR 14-OCT-1993; US-136783.

PA (SMIK ) SMITHKLINE BEECHAM CORP.

PA (SMIK ) SMITHKLINE BEECHAM PLC.

PI Gross MS, Holmes SD, Sylvester DR;

DR WPI; 95-123387/16.

PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived

PT from high affinity mAbs - useful in treatment of IL-4-mediated

PT and IgE-mediated allergic conditions

PS Disclosure; Page 28; 97pp; English.

CC A humanized antibody light chain variable region and signal

CC sequence is given in R75355. The signal sequence is also

CC provided in R70194. The sequences of the first 2 CDRs

CC are identical to mouse anti-human IL-4 MAB 3B9 light chain

CC CDRs (given in R70195-96), but the third (R70201) differs

CC by a single amino acid from the native mouse CDR (R70197).

SQ Sequence 9 AA;

Query Match 91.1%; Score 51; DB 13; Length 9;

Best Local Similarity 100.0%; Pred. No. 6.92e+00;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 qgsnedppt 8

|||||

Qy 1 QGSNEDPPT 8

RESULT 7

ID R75355 standard; Protein; 131 AA.

AC R75355;

DT 20-SEP-1995 (first entry)

DE Humanized antibody 3B9 light chain.

KW Humanized antibody; antibody engineering; monoclonal antibody;

KW MAB; interleukin-4; IL-4; allergy.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Peptide 1..20

FT /Label= Sig\_peptide

FT Region 43..57

FT /Label= CDR

FT /note= "complementarity determining region"

FT Region 73..79

FT /Label= CDR

FT /note= "complementarity determining region"

FT Region 112..120

FT /Label= CDR

FT /note= "complementarity determining region"

PN W09507301-A.

PD 16-MAR-1995.



Mar 18 10:11

7

US-08-612-929-20.rag

PF 07-SEP-1994; U10308.  
 PR 07-SEP-1993; US-117366.  
 PR 14-OCT-1993; US-136783.  
 PA (SMIK ) SMITHKLINE BEECHAM CORP.  
 PA (SMIK ) SMITHKLINE BEECHAM PLC.  
 PI Gross MS, Holmes SD, Sylvestre DR;  
 WPI; 95-123387/16.  
 DR N-PSDB; Q73986.  
 PT Chimeric and humanised IL-4 monoclonal antibodies (mAb), derived  
 PT from high affinity mAbs - useful in treatment of IL-4-mediated  
 PT and IgE-mediated allergic conditions  
 PS Disclosure; Fig.5; 97pp; English.  
 CC A humanized antibody light chain variable region and signal  
 CC sequence is given in R75355. The signal sequence is also  
 CC provided in R70194. The sequences of the first 2 CDRs  
 CC are identical to mouse anti-human IL-4 Mab 3B9 light chain  
 CC CDRs (given in R70195-96), but the third (R70201) differs  
 CC by a single amino acid from the native mouse CDR (R70197).  
 SQ Sequence 131 AA;

Query Match 91.1%; Score 51; DB 13; Length 131;  
 Best Local Similarity 100.0%; Pred. No. 6.92e+00;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 112 qqsndpp 119  
 |||||  
 Qy 1 QQSNEPPT 8

RESULT 8

ID R66145 standard; peptide; 17 AA.  
 AC R66145;  
 DT 12-JUL-1995 (first entry)  
 DE CD-4 antibody variable region complementary peptide.  
 KW CD-4 antibody variable region; complementary peptide;  
 KW extra-corporeal blood circulation; cell filter material.  
 OS Synthetic.  
 PN J06269663-A.  
 PD 27-SEP-1994.  
 PF 17-MAR-1993; 057206.  
 PR 17-MAR-1993; JP-057206.  
 PA (TOYM ) TOYODO KK.  
 DR WPI; 94-346316/43.  
 PT Material for collecting cells positive for CD-4 antibody -  
 PT comprises nonwoven fabric having keto-alkyl halide functional gp  
 PS Example 3; Page 8; 9pp; Japanese.  
 CC R66140-R66146 are peptides complementary to the variable region  
 CC of the CD-4 antibody, these peptides are fixed onto a claimed  
 CC nonwoven fabric (average fibre dia. of 1-30 microns) coated with  
 CC keto-alkyl halide functional groups. This material can be used  
 CC as a filter for CD-4 positive cells in a medical treatment  
 CC involving the extra-corporeal circulation of blood.  
 SQ Sequence 17 AA;

Query Match 87.5%; Score 49; DB 12; Length 17;  
 Best Local Similarity 88.9%; Pred. No. 1.18e+01;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 9 qqsyedp 17  
 |||||  
 Qy 1 QQSNEPPT 9

RESULT 9

Mar 18 10:11

8

US-08-612-929-20.rag

ID R47933 standard; Protein; 103 AA.  
 AC R47933;  
 DT 24-JUL-1994 (first entry)  
 DE Light chain region of 23F2G.  
 KW Amplification; 23F2G; humanised antibody; heavy chain; light chain;  
 KW hybridoma; inflammation; CD18; human leukocyte integrins; mAb 60.3;  
 KW monoclonal antibody; LFA-1; adhesion; migration; multiple  
 KW sclerosis; MS.  
 PN W09402175-A.  
 PD 03-FEB-1994.  
 PF 16-JUL-1993; U06734.  
 PR 16-JUL-1992; US-915068.  
 PR 10-MAY-1993; US-060699.  
 PA (ICOS-) ICOS CORP.  
 PA (UNIV ) UNIV WASHINGTON.  
 PI Rose LM;  
 DR WPI; 94-048551/06.  
 DR N-PSDB; Q55915.  
 PT Antibodies immunologically reactive with the CD18 of human  
 PT leukocyte integrins and/or competing with mAb 60.3 for binding to  
 PT human LFA-1 - for alleviating symptoms associated with  
 PT inflammatory disease states  
 PS Example 6; Page 43; 58pp; English.  
 CC Total RNA was isolated from the hybridoma cell line 23F2G and first  
 CC strand cDNA was synthesised using the total RNA as a template. The  
 CC first strand cDNA was used as a template for PCR to obtain double  
 CC stranded DNA fragments encoding the variable regions of both the  
 CC heavy and light chains of monoclonal antibody 23F2G. The sequence  
 CC shown is that of the light chain variable region of MAb 23F2G  
 CC The humanised form of MAb 23F2G may be administered to  
 CC for the inhibition of inflammatory processes associated with  
 CC for the inhibition of inflammatory processes associated with  
 CC multiple sclerosis. The MAb blocks leukocyte adhesion and  
 CC migration to inflammatory sites. The MAb is an anti-CD18 integrin  
 CC antibody which competes with MAb 60.3 for binding to LFA-1.  
 CC See also R47931-6.  
 SQ Sequence 103 AA;

Query Match 87.5%; Score 49; DB 9; Length 103;  
 Best Local Similarity 77.8%; Pred. No. 1.18e+01;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 85 hqndp 93  
 :|||  
 Qy 1 QQSNEPPT 9

RESULT 10

ID R47935 standard; Protein; 111 AA.  
 AC R47935;  
 DT 24-JUL-1994 (first entry)  
 DE Humanised light chain region of 23F2G.  
 KW Amplification; 23F2G; humanised antibody; heavy chain; light chain;  
 KW hybridoma; inflammation; CD18; human leukocyte integrins; mAb 60.3;  
 KW monoclonal antibody; LFA-1; adhesion; migration; multiple  
 KW sclerosis; MS.  
 PN W09402175-A.  
 PD 03-FEB-1994.  
 PF 16-JUL-1993; U06734.  
 PR 16-JUL-1992; US-915068.  
 PR 10-MAY-1993; US-060699.  
 PA (ICOS-) ICOS CORP.  
 PA (UNIV ) UNIV WASHINGTON.  
 PI Rose LM;

DR WPI; 94-048551/06.  
 DR N-PSDB; Q55917.  
 PT Antibodies immunologically reactive with the CD18 of human  
 PT leukocyte integrins and/or competing with mAb 60.3 for binding to  
 PT human LFA-1 - for alleviating symptoms associated with  
 PT inflammatory disease states  
 PS Example 6; Page 45; 58pp; English.  
 CC Total RNA was isolated from the hybridoma cell line 23F2G and first  
 CC strand cDNA was synthesised using the total RNA as a template. The  
 CC first strand cDNA was used as a template for PCR to obtain double  
 CC stranded DNA fragments encoding the variable regions of both the  
 CC heavy and light chains of monoclonal antibody 23F2G. The sequence  
 CC shown is a humanised form of the light chain variable region of MAb  
 CC 23F2G. The humanised form of MAb 23F2G may be administered to  
 CC alleviate symptoms associated with inflammatory disease states, esp.  
 CC for the inhibition of inflammatory processes associated with  
 CC multiple sclerosis. The MAb blocks leukocyte adhesion and  
 CC migration to inflammatory sites. The MAb is an anti-CD18 integrin  
 CC antibody which competes with MAb 60.3 for binding to LFA-1.  
 CC See also R47931-6.  
 SQ Sequence 111 AA;

Query Match 87.5%; Score 49; DB 9; Length 111;  
 Best Local Similarity 77.8%; Pred. No. 1.18e+01;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 93 hqnedpdt 101  
 : | | | | | | |  
 Qy 1 QQSNEDPPT 9

## RESULT 11

ID R04134 standard; protein; 115 AA.  
 AC R04134;  
 DT 06-SEP-1990 (first entry)  
 DE Anti-Leu 3a light chain variable region gene product, KOL/206 V1.  
 KW HIV; AIDS; anti-Leu3A; vaccine; ds.  
 OS Mus musculus.  
 PN EP-365209-A.  
 PD 25-APR-1990.  
 PF 11-OCT-1989; 010415.  
 PR 17-OCT-1988; US-260558.  
 PA (BECT) Becton Dickinson Co.  
 PI Hinton R, Oi VT;  
 DR WPI; 90-126329/17.  
 DR N-PSDB; Q04041.  
 PT New chimeric variants of murine antibody anti-leucine -  
 PT contg. human antibody regions, and DNA encoding sequences.  
 PS Claim 4; Fig 4; 12pp; English.  
 CC Variants of murine monoclonal anti-CD4 antibody, anti-leu3A can be  
 CC used to form chimeric mouse-variable, human-constant region Abs  
 CC suggested as being useful as a vaccine to HIV.  
 SQ Sequence 115 AA;

Query Match 87.5%; Score 49; DB 1; Length 115;  
 Best Local Similarity 88.9%; Pred. No. 1.18e+01;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 96 qgsyedpdt 104  
 : | | | | | | |  
 Qy 1 QQSNEDPPT 9

## RESULT 12

ID R04132 standard; protein; 131 AA.  
 AC R04132;  
 DT 06-SEP-1990 (first entry)  
 DE Anti-Leu 3a light chain variable region gene product, 206 Vx.  
 KW HIV; AIDS; anti-Leu3A; vaccine; ds.  
 OS Mus musculus.  
 PN EP-365209-A.  
 PD 25-APR-1990.  
 PF 11-OCT-1989; 010415.  
 PR 17-OCT-1988; US-260558.  
 PA (BECT) Becton Dickinson Co.  
 PI Hinton R, Oi VT;  
 DR WPI; 90-126329/17.  
 DR N-PSDB; Q04039.  
 PT New chimeric variants of murine antibody anti-leucine -  
 PT contg. human antibody regions, and DNA encoding sequences.  
 PS Claim 1; Fig 2; 12pp; English.  
 CC Variants of murine monoclonal anti-CD4 antibody, anti-leu3A can be  
 CC used to form chimeric mouse-variable, human-constant region Abs  
 CC suggested as being useful as a vaccine to HIV.  
 SQ Sequence 131 AA;

Query Match 87.5%; Score 49; DB 1; Length 131;  
 Best Local Similarity 88.9%; Pred. No. 1.18e+01;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 113 qgsyedpdt 121  
 : | | | | | | |  
 Qy 1 QQSNEDPPT 9

## RESULT 13

ID R47494 standard; Protein; 111 AA.  
 AC R47494;  
 DT 06-JUL-1994 (first entry)  
 DE Murine anti-CD18 Ab 60.3 light chain.  
 KW Monoclonal antibody; MAb; heavy chain; light chain;  
 KW constant region; variable region; amplification; primer;  
 KW polymerase chain reaction; PCR; chimera; Ig;  
 KW immunoglobulin; humanised antibody; leucocyte; integrin.  
 OS Mus sp.  
 PN EP-578515-A.  
 PD 12-JAN-1994.  
 PF 24-MAY-1993; 401328.  
 PR 26-MAY-1992; US-888233.  
 PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
 PI Bajorath J, Harris LJ, Hsiao K, Ku-Chuan H;  
 DR WPI; 94-010334/02.  
 DR N-PSDB; Q55002.  
 PT Humanised monoclonal antibodies prepn. - using comparative model  
 PT building, by computer database searching  
 PS Disclosure; Page 21; 68pp; English.  
 CC A humanised monoclonal antibody corresponding to the murine anti-CD18  
 CC antibody 60.3 was prepared. The variable (V) region sequences from  
 CC both the heavy (H) and light (L) chains were determined from cDNA  
 CC (amplified by PCR), and spliced onto human constant (C) regions,  
 CC resulting in a chimeric 60.3 Ab (IgG1, kappa). The chimeric Ab was  
 CC expressed in tissue culture (Aq8.653 mouse myeloma cells, detected  
 CC by ELISA), and examined in binding assays. The results from  
 CC competition and inhibition assays showed that the chimeric Ab was  
 CC as effective as the murine 60.3 MAb. The deduced murine VH and VL  
 CC protein sequences were compared to the protein sequence data base,  
 CC and two human Ig protein sequences were selected to be used as  
 CC templates. A murine 60.3 Fv was modeled according to the deduced

Mar 18 10:11

US-08-612-929-20.rag

11

CC VH and VL protein sequences. Based on the 60.3 Fv model and the two  
 CC human template sequences selected from the protein data base, a  
 CC humanised Fv was modeled. Construction of the humanised 60.3 was  
 CC done by piecing 5 pairs of complementary oligonucleotides together  
 CC (spanning the entire V region) to form the VH and VL. These were  
 CC then attached onto vectors containing genes for appropriate C regions  
 CC to form humanised Ab (IgG1, kappa). The humanised proteins were again  
 CC expressed in Aq8.653 cells and binding assays were done. FACS analyses  
 CC indicated that the humanised Ab recognised cells expressing CD18.  
 CC About a dozen of the humanised 60.3 Ab master wells were transferred  
 CC and assayed for Ig.  
 SQ Sequence 111 AA;

Query Match 83.9%; Score 47; DB 9; Length 111;  
 Best Local Similarity 88.9%; Pred. No. 2.01e+01;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 93 qgsnedprt 101  
 |||||||  
 Qy 1 QQSNEPPT 9

RESULT 14

ID R47492 standard; Protein; 111 AA.  
 AC R47492;  
 DT 06-JUL-1994 (first entry)  
 DE Humanised anti-CD18 Ab 60.3 light chain.  
 KW Monoclonal antibody; MAb; heavy chain; light chain;  
 KW constant region; variable region; amplification; primer;  
 KW polymerase chain reaction; PCR; chimera; Ig;  
 KW immunoglobulin; humanised antibody; leucocyte; integrin.  
 OS Chimeric; Homo sapiens.  
 PN Chimeric; Mus sp.  
 PN EP-578515-A.  
 PD 12-JAN-1994.  
 PF 24-MAY-1993; 401328.  
 PR 26-MAY-1992; US-888233.  
 PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
 PI BaJorath J, Harris LJ, Hsiao K, Ku-Chuan H;  
 DR WPI: 94-010334/02.  
 DR N-PSDB; Q55000.  
 PT Humanised monoclonal antibodies prepn. - using comparative model  
 PT building, by computer database searching  
 PS Disclosure; Page 19; 68pp; English.  
 CC A humanised monoclonal antibody corresponding to the murine anti-CD18  
 CC antibody 60.3 was prepared. The variable (V) region sequences from  
 CC both the heavy (H) and light (L) chains were determined from cDNA  
 CC (amplified by PCR), and spliced onto human constant (C) regions,  
 CC resulting in a chimeric 60.3 Ab (IgG1, kappa). The chimeric Ab was  
 CC expressed in tissue culture (Aq8.653 mouse myeloma cells, detected  
 CC by ELISA), and examined in binding assays. The results from  
 CC competition and inhibition assays showed that the chimeric Ab was  
 CC as effective as the murine 60.3 MAb. The deduced murine VH and VL  
 CC protein sequences were compared to the protein sequence data base,  
 CC and two human Ig protein sequences were selected to be used as  
 CC templates. A murine 60.3 Fv was modeled according to the deduced  
 CC VH and VL protein sequences. Based on the 60.3 Fv model and the two  
 CC human template sequences selected from the protein data base, a  
 CC humanised Fv was modeled. Construction of the humanised 60.3 was  
 CC done by piecing 5 pairs of complementary oligonucleotides together  
 CC (spanning the entire V region) to form the VH and VL. These were  
 CC then attached onto vectors containing genes for appropriate C regions  
 CC to form humanised Ab (IgG1, kappa). The humanised proteins were again  
 CC expressed in Aq8.653 cells and binding assays were done. FACS analyses

Mar 18 10:11

US-08-612-929-20.rag

12

CC indicated that the humanised Ab recognised cells expressing CD18.  
 CC About a dozen of the humanised 60.3 Ab master wells were transferred  
 CC and assayed for Ig.  
 SQ Sequence 111 AA;

Query Match 83.9%; Score 47; DB 9; Length 111;  
 Best Local Similarity 88.9%; Pred. No. 2.01e+01;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 93 qgsnedprt 101  
 |||||||  
 Qy 1 QQSNEPPT 9

RESULT 15

ID R74781 standard; peptide; 215 AA.  
 AC R74781;  
 DT 26-JUN-1995 (first entry)  
 DE Light chain of 59.1 an anti-HIV antibody.  
 KW Identifying compounds; anti-HIV antibodies; HIV treatment;  
 KW peptide RP142; antibody 59.1.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT Modified site 8  
 FT /label= OTHER  
 FT /note= "CPR no further definition"  
 FT Modified site 81  
 FT /label= OTHER  
 FT /note= "CPR no further definition"  
 FT Modified site 99  
 FT /label= OTHER  
 FT /note= "CPR no further definition"  
 FT Modified site 145  
 FT /label= OTHER  
 FT /note= "CPR no further definition"  
 PN WO9418232-A.  
 PD 18-AUG-1994.  
 PF 09-FEB-1994; U01458.  
 PR 12-FEB-1993; US-017485.  
 PA (REPK ) REPLIGEN CORP.  
 PA (SCRI ) SCRIPPS RES INST.  
 PI Profy AT, Wilson IA;  
 DR WPI: 94-332662/41.  
 PT Identifying cpds. which elicit, or bind to, anti-HIV antibodies -  
 PT and new antibodies which neutralise a broad range of HIV strains  
 PS Disclosure; Page 78; 137pp; English.  
 CC R74781 describes the amino acid sequence of the light chain of  
 CC 59.1 an anti-HIV antibody (Ab), it was used in the development of  
 CC the peptide RP142 (R74783). This peptide can bind to anti-HIV Abs or  
 CC elicit new Abs effective against a broad range of HIV strains,  
 CC that can be used in the treatment of HIV infection.  
 SQ Sequence 215 AA;

Query Match 80.4%; Score 45; DB 12; Length 215;  
 Best Local Similarity 77.8%; Pred. No. 3.40e+01;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 93 qgsnedprt 101  
 |||||||  
 Qy 1 QQSNEPPT 9

Search completed: Tue Mar 18 10:13:00 1997  
 Job time : 8 secs.

Mar 19:08:21

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1

Mar 19:08:21

US-08-612-929-21.rge

2

\*\*\*\*\*  
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\*\*\*\*\*  
MPSrch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm  
Run on: Wed Mar 19 08:22:29 1997; MasPar time 52.87 Seconds  
Tabular output not generated.  
\*\*\*\*\*  
Title: >US-08-612-929-21  
Description: (1-21) from US08612929.seq  
Perfect Score: 21  
N.A. Sequence: 1 ACTTCTGCTATGGTGTGAGC 21  
Comp: TGAAGACCATCCACACTCG  
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Scoring table: TABLE default  
Gap 10  
Nmatch STD : Dbase 0; Query 0  
Searched: 279077 seqs, 411808665 bases x 2  
Post-processing: Minimum Match 0%  
Listing first 45 summaries  
\*\*\*\*\*  
Database: emb1-new5  
1:BCT 2:FON 3:INV1 4:INV2 5:ORG 6:MAM 7:VRT 8:PLN 9:PRI  
10:PRO1 11:PRO2 12:ROD 13:SYN 14:UNC 15:VIR  
Database: genbank94  
16:BCT1 17:BCT2 18:BCT3 19:BCT4 20:BCT5 21:BCT6 22:BCT7  
23:BCT8 24:BCT9 25:INV1 26:INV2 27:INV3 28:INV4 29:INV5  
30:INV6 31:INV7 32:MAM1 33:MAM2 34:MAM3 35:VRT1 36:VRT2  
37:VRT3 38:PAT1 39:PAT2 40:PAT3 41:PHG 42:PLN1 43:PLN2  
44:PLN3 45:PLN4 46:PLN5 47:PLN6 48:PLN7 49:PLN8 50:PRI1  
51:PRI2 52:PRI3 53:PRI4 54:PRI5 55:PRI6 56:PRI7 57:PRI8  
58:PRI9 59:PRI10 60:PRI11 61:PRI12 62:PRI13 63:ROD1  
64:ROD2 65:ROD3 66:ROD4 67:ROD5 68:ROD6 69:ROD7 70:ROD8  
71:STR 72:SYN 73:UNA 74:VRL1 75:VRL2 76:VRL3 77:VRL4  
78:VRL5 79:VRL6 80:VRL7 81:VRL8  
Database: genbank-new5  
82:BCT 83:INV1 84:INV2 85:MAM 86:VRT 87:PAT 88:PHG  
89:PLN 90:PRI 91:ROD 92:STR 93:SYN 94:UNA 95:VRL  
96:part1  
Database: u-emb146\_94  
96:part1  
Statistics: Mean 6.886; Variance 2.651; scale 2.598  
\*\*\*\*\*

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MPSrch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed Mar 19 08:22:29 1997; MasPar time 52.87 Seconds  
327.119 Million cell updates/sec

Tabular output not generated.

Title: >US-08-612-929-21  
Description: (1-21) from US08612929.seq  
Perfect Score: 21  
N.A. Sequence: 1 ACTTCTGCTATGGTGTGAGC 21  
Comp: TGAAGACCATCCACACTCG

Scoring table: TABLE default  
Gap 10

Nmatch STD : Dbase 0; Query 0

Searched: 279077 seqs, 411808665 bases x 2

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: emb1-new5  
1:BCT 2:FON 3:INV1 4:INV2 5:ORG 6:MAM 7:VRT 8:PLN 9:PRI  
10:PRO1 11:PRO2 12:ROD 13:SYN 14:UNC 15:VIR

Database: genbank94  
16:BCT1 17:BCT2 18:BCT3 19:BCT4 20:BCT5 21:BCT6 22:BCT7  
23:BCT8 24:BCT9 25:INV1 26:INV2 27:INV3 28:INV4 29:INV5  
30:INV6 31:INV7 32:MAM1 33:MAM2 34:MAM3 35:VRT1 36:VRT2  
37:VRT3 38:PAT1 39:PAT2 40:PAT3 41:PHG 42:PLN1 43:PLN2  
44:PLN3 45:PLN4 46:PLN5 47:PLN6 48:PLN7 49:PLN8 50:PRI1  
51:PRI2 52:PRI3 53:PRI4 54:PRI5 55:PRI6 56:PRI7 57:PRI8  
58:PRI9 59:PRI10 60:PRI11 61:PRI12 62:PRI13 63:ROD1  
64:ROD2 65:ROD3 66:ROD4 67:ROD5 68:ROD6 69:ROD7 70:ROD8  
71:STR 72:SYN 73:UNA 74:VRL1 75:VRL2 76:VRL3 77:VRL4  
78:VRL5 79:VRL6 80:VRL7 81:VRL8

Database: genbank-new5  
82:BCT 83:INV1 84:INV2 85:MAM 86:VRT 87:PAT 88:PHG

Database: u-emb146\_94  
89:PLN 90:PRI 91:ROD 92:STR 93:SYN 94:UNA 95:VRL  
96:part1

Statistics: Mean 6.886; Variance 2.651; scale 2.598

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description	Pred. No.
1	21	100.0	286	65	MM023019	Mus musculus C57BL/6	1.35e-03
2	21	100.0	306	66	MUSB	Mus musculus immunogl	1.35e-03
3	21	100.0	318	65	MM022990	Mus musculus CB17 SCI	1.35e-03
4	21	100.0	318	12	MM022990	Mus musculus CB17 SCI	1.35e-03
5	21	100.0	318	91	MM022990	Mus musculus CB17 SCI	1.35e-03
6	21	100.0	320	65	MM022991	Mus musculus CB17 SCI	1.35e-03
7	21	100.0	320	91	MM022991	Mus musculus CB17 SCI	1.35e-03
8	21	100.0	320	12	MM022991	Mus musculus CB17 SCI	1.35e-03
9	21	100.0	326	91	MM022986	Mus musculus CB17 SCI	1.35e-03
10	21	100.0	326	12	MM022986	Mus musculus CB17 SCI	1.35e-03
11	21	100.0	330	91	MM022975	Mus musculus CB17 SCI	1.35e-03
12	21	100.0	353	65	MM022995	Mus musculus CB17 SCI	1.35e-03
13	21	100.0	353	91	MM022995	Mus musculus CB17 SCI	1.35e-03
14	21	100.0	353	12	MM022995	Mus musculus CB17 SCI	1.35e-03
15	21	100.0	358	65	MM023000	Mus musculus CB17 SCI	1.35e-03
16	21	100.0	359	65	MM023007	Mus musculus CB17 SCI	1.35e-03
17	21	100.0	360	65	MM022983	Mus musculus CB17 SCI	1.35e-03
18	21	100.0	360	12	MM022983	Mus musculus CB17 SCI	1.35e-03
19	21	100.0	360	12	MM022984	Mus musculus CB17 SCI	1.35e-03
20	21	100.0	360	65	MM023010	Mus musculus CB17 SCI	1.35e-03
21	21	100.0	360	65	MM022984	Mus musculus CB17 SCI	1.35e-03
22	21	100.0	360	91	MM022977	Mus musculus CB17 SCI	1.35e-03
23	21	100.0	360	91	MM022992	Mus musculus CB17 SCI	1.35e-03
24	21	100.0	360	91	MM022979	Mus musculus CB17 SCI	1.35e-03
25	21	100.0	360	91	MM022981	Mus musculus CB17 SCI	1.35e-03
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27	21	100.0	360	91	MM022984	Mus musculus CB17 SCI	1.35e-03
28	21	100.0	360	91	MM022983	Mus musculus CB17 SCI	1.35e-03
29	21	100.0	360	65	MM022992	Mus musculus CB17 SCI	1.35e-03
30	21	100.0	360	12	MM022977	Mus musculus CB17 SCI	1.35e-03
31	21	100.0	360	65	MM022988	Mus musculus CB17 SCI	1.35e-03
32	21	100.0	360	12	MM022997	Mus musculus CB17 SCI	1.35e-03
33	21	100.0	360	65	MM022977	Mus musculus CB17 SCI	1.35e-03
34	21	100.0	360	65	MM022979	Mus musculus CB17 SCI	1.35e-03
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38	21	100.0	360	65	MM022999	Mus musculus CB17 SCI	1.35e-03
39	21	100.0	360	12	MM022992	Mus musculus CB17 SCI	1.35e-03
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41	21	100.0	360	65	MM023005	Mus musculus CB17 SCI	1.35e-03
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43	21	100.0	360	12	MM022981	Mus musculus CB17 SCI	1.35e-03
44	21	100.0	360	12	MM022979	Mus musculus CB17 SCI	1.35e-03
45	21	100.0	360	65	MM023013	Mus musculus CB17 SCI	1.35e-03

# ALIGNMENTS

RESULT 1  
LOCUS MM023019 286 bp DNA ROD 06-MAY-1995  
DEFINITION Mus musculus C57BL/6 immunoglobulin heavy chain V region mRNA,  
clone CB17H-1, partial cds.  
ACCESSION U23019  
NID g780640  
KEYWORDS house mouse.  
SOURCE Mus musculus  
ORGANISM Mus musculus

Mar 19 08:21

US-08-612-999-21.rge

3

Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;  
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;  
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;  
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;  
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.

REFERENCE

AUTHORS Young, D.C. and Kearney, J.F.  
TITLE Sequence analysis and antigen binding characteristics of immunoglobulins from SCID Ig+ mice  
JOURNAL Int. Immunol. 7 (1995) In press  
AUTHORS 2 (bases 1 to 286)  
Young, D.C.

AUTHORS

Direct Submission  
TITLE Submitted (17-MAR-1995) David C. Young, University of Texas Health  
JOURNAL Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137,  
Houston, TX 77030, USA

FEATURES

source Location/Qualifiers

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/clone="CB17H-1"

/strain="C57BL/6"

/organism="Mus musculus"

/sub\_species="domesticus"

/germline

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/codon\_start=2

/product="immunoglobulin heavy chain"

/db\_xref="PID:g780641"

/translation="QVTLKESGPGILQSSQTLISLTCFSFSLSTSGMGVSWIRQPSG  
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BASE COUNT

67 a 77 c 70 g 72 t

ORIGIN

Query Match 100.0%; Score 21; DB 65; Length 286;

Best Local Similarity 100.0%; Pred. No. 1.35e-03;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 92 acctctgtatgggtgagc 112

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Qy 1 ACTTCTGGTATGGGTGACG 21

RESULT 2

LOCUS MUSB 306 bp mRNA ROD 14-MAR-1994  
DEFINITION Mus musculus immunoglobulin heavy chain (IgH) mRNA, VDJ4 region,  
partial cds.

ACCESSION

L22743

NID

g348959

KEYWORDS

Ig heavy chain; diversity region; immunoglobulin; joining region;  
variable region.  
SOURCE Mus musculus (strain BALB/cByJ) female adult spleen cDNA to mRNA.

ORGANISM

Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;  
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.  
1 (bases 1 to 306)  
Sheehan, K.M., Mainville, C.A., Willert, S. and Brodeur, P.H.

REFERENCE

AUTHORS J. Immunol. 151 (10), 5364-5375 (1993)

MEDLINE

94044761

FEATURES

source Location/Qualifiers

1..306

/organism="Mus musculus"

Mar 19 08:21

US-08-612-999-21.rge

4

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/tissue\_type="spleen"  
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/db\_xref="PID:g348960"  
/translation="LTCFSFGSLSTSGMGVSWIRQPSGKGLELAHYWDDKRYNP  
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BASE COUNT 72 a 80 c 75 g 79 t

ORIGIN

Query Match 100.0%; Score 21; DB 66; Length 306;  
Best Local Similarity 100.0%; Pred. No. 1.35e-03;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 34 acctctgtatgggtgagc 54

|||||

Qy 1 ACTTCTGGTATGGGTGACG 21

RESULT 3

LOCUS MMU22990 318 bp mRNA ROD 26-APR-1995  
DEFINITION Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA,  
clone 45-24h, partial cds.

ACCESSION

U22990

NID

g780582

KEYWORDS

house mouse.

SOURCE

Mus musculus  
Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;  
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;  
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;  
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;  
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 318)  
Young, D.C. and Kearney, J.F.  
TITLE Sequence analysis and antigen binding characteristics of immunoglobulins from SCID Ig+ mice  
JOURNAL Int. Immunol. 7 (1995) In press

REFERENCE

2 (bases 1 to 318)

AUTHORS

Young, D.C.

TITLE

Direct Submission

JOURNAL

Submitted (17-MAR-1995) David C. Young, University of Texas Health  
Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137,  
Houston, TX 77030, USA

FEATURES

source Location/Qualifiers

1..318

/clone="45-24h"

/strain="CB17 SCID"

/organism="Mus musculus"

/sub\_species="domesticus"

/cell\_type="lymphocyte"

/tissue\_type="spleen"

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CDS

Mar 19 08:21

US-08-612-929-21.rge

5

BASE COUNT 74 a 84 c 79 g 81 t

ORIGIN

Query Match 100.0%; Score 21; DB 65; Length 318;

Best Local Similarity 100.0%; Pred. No. 1.35e-03;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 91 actctcgtatggtgtgagc 111

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Qy 1 ACTTCTGCTATGGGTGTGACC 21

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Best Local Similarity 100.0%; Pred. No. 1.35e-03;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 91 actctcgtatggtgtgagc 111

|||||

Qy 1 ACTTCTGCTATGGGTGTGACC 21

RESULT 5

LOCUS MMU22990 318 bp mRNA ROD 09-APR-1996

DEFINITION Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA,

clone 45-24h, partial cds.

ACCESSION U22990

NID g780582

KEYWORDS house mouse.

SOURCE Mus musculus

ORGANISM

Eukaryota; Eutheria; Rodentia; Sciurognathi; Muridae;

Vertebrata; Murinae; Mus.

REFERENCE 1 (bases 1 to 318)

AUTHORS Young, D. and Kearney, J.F.

TITLE Sequence analysis and antigen binding characteristics of Ig SCID

JOURNAL Ig+ mice

MEDLINE Int. Immunol. 7 (5), 807-819 (1995)

REFERENCE 2 (bases 1 to 318)

AUTHORS Young, D.C.

TITLE Direct Submission

JOURNAL Submitted (17-MAR-1995) David C. Young, University of Texas Health

Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137,

Houston, TX 77030, USA

COMMENT NCBI gi: 780582

FEATURES

source

1..318

/organism="Mus musculus"

/strain="CB17 SCID"

/sub\_species="domesticus"

/clone="45-24h"

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/note="NCBI gi: 780583"

/codon\_start=1

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/db\_xref="PID:g780583"

/translation="QVTIKESCPGILQSSQTLSTCSFSGFSLSTSCMGVSWIRQPSG

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GSTY"

BASE COUNT 74 a 84 c 79 g 81 t

ORIGIN

Query Match 100.0%; Score 21; DB 91; Length 318;

Best Local Similarity 100.0%; Pred. No. 1.35e-03;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 91 actctcgtatggtgtgagc 111

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Qy 1 ACTTCTGCTATGGGTGTGACC 21

GSTY\*

RESULT 6

LOCUS MMU22991 320 bp mRNA ROD 26-APR-1995

DEFINITION Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA,

clone 45-24h, partial cds.

ACCESSION U22991

NID g780582

KEYWORDS house mouse.

SOURCE Mus musculus

ORGANISM

Eukaryota; Eutheria; Rodentia; Sciurognathi; Muridae;

Vertebrata; Murinae; Mus.

REFERENCE 1 (bases 1 to 318)

AUTHORS Young, D. and Kearney, J.F.

TITLE Sequence analysis and antigen binding characteristics of Ig SCID

JOURNAL Ig+ mice

MEDLINE Int. Immunol. 7 (5), 807-819 (1995)

REFERENCE 2 (bases 1 to 318)

AUTHORS Young, D.C.

TITLE Direct Submission

JOURNAL Submitted (17-MAR-1995) David C. Young, University of Texas Health

Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137,

Houston, TX 77030, USA

BASE COUNT 74 a 84 c 79 g 81 t

ORIGIN

Query Match 100.0%; Score 21; DB 65; Length 318;

Best Local Similarity 100.0%; Pred. No. 1.35e-03;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 91 actctcgtatggtgtgagc 111

|||||

Qy 1 ACTTCTGCTATGGGTGTGACC 21

GSTY\*

RESULT 4

ID MMU22990 standard; RNA; ROD; 318 BP.

AC U22990;

DT 29-APR-1995 (Rel. 43, Created)

DT 09-APR-1996 (Rel. 47, Last updated, Version 2)

DE Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA,

clone 45-24h, partial cds.

DE clone 45-24h, partial cds.

KW Mus musculus (mouse)

OS Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;

OC Theria; Eutheria; Rodentia; Muridae; Murinae.

RN [1]

RP 1-318

RA Young D., Kearney J.F.;

RT "Sequence analysis and antigen binding characteristics of Ig SCID

Ig+ mice";

RL Int. Immunol. 7:807-819(1995).

RN [2]

RP 1-318

RA Young D.C.;

RT "Sequence analysis and antigen binding characteristics of Ig SCID

Ig+ mice";

RL Int. Immunol. 7:807-819(1995).

RN [2]

RP 1-318

RA Young D.C.;

RT "Sequence analysis and antigen binding characteristics of Ig SCID

Ig+ mice";

RL Int. Immunol. 7:807-819(1995).

RN [2]

RP 1-318

RA Young D.C.;

RT "Sequence analysis and antigen binding characteristics of Ig SCID

Ig+ mice";

RL Int. Immunol. 7:807-819(1995).

RN [2]

RP 1-318

RA Young D.C.;

RT "Sequence analysis and antigen binding characteristics of Ig SCID

Ig+ mice";

RL Int. Immunol. 7:807-819(1995).

RN [2]

RP 1-318

RA Young D.C.;

RT "Sequence analysis and antigen binding characteristics of Ig SCID

Ig+ mice";

RL Int. Immunol. 7:807-819(1995).

RN [2]

RP 1-318

RA Young D.C.;

RT "Sequence analysis and antigen binding characteristics of Ig SCID

Ig+ mice";

RL Int. Immunol. 7:807-819(1995).

RN [2]

RP 1-318

RA Young D.C.;

RT "Sequence analysis and antigen binding characteristics of Ig SCID

Ig+ mice";

RL Int. Immunol. 7:807-819(1995).

RN [2]

RP 1-318

RA Young D.C.;

RT "Sequence analysis and antigen binding characteristics of Ig SCID

Ig+ mice";

RL Int. Immunol. 7:807-819(1995).

RN [2]

RP 1-318

RA Young D.C.;

RT "Sequence analysis and antigen binding characteristics of Ig SCID

Ig+ mice";

RL Int. Immunol. 7:807-819(1995).

RN [2]

Mar 19 08:21

7

US-08-612-929-21.rge

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clone 45-25h, partial cds.
ACCESSION   U22991
NID         g780584
KEYWORDS    .
SOURCE      house mouse.
ORGANISM    Mus musculus
            Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;
            Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
            Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
            Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
            Sciurognathi; Myomorpha; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 320)
AUTHORS    Young, D.C. and Kearney, J.F.
TITLE      Sequence analysis and antigen binding characteristics of
            immunoglobulins from SCID Ig+ mice
JOURNAL    Int. Immunol. 7 (1995) In press
REFERENCE   2 (bases 1 to 320)
AUTHORS    Young, D.C.
TITLE      Direct Submission
JOURNAL    Submitted (17-MAR-1995) David C. Young, University of Texas Health
            Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137,
            Houston, TX 77030, USA
FEATURES   source
            Location/Qualifiers
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            AITY"

BASE COUNT   72 a   86 c   78 g   84 t
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Best Local Similarity 100.0%; Pred. No. 1.35e-03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 91 acctctggtatgggtgagc 111
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Qy 1 ACTTCTGGTATGGGTGAGC 21

RESULT 7
LOCUS       MM022991 320 bp mRNA ROD 09-APR-1996
DEFINITION Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA,
            clone 45-25h, partial cds.
ACCESSION   U22991
NID         g780584
KEYWORDS    .
SOURCE      house mouse.
ORGANISM    Mus musculus
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
            Murinae; Mus.
REFERENCE   1 (bases 1 to 320)
AUTHORS    Young, D. and Kearney, J.F.
TITLE      Sequence analysis and antigen binding characteristics of Ig SCID

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Mar 19 08:21

8

US-08-612-929-21.rge

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Ig+ mice
Int. Immunol. 7 (5), 807-819 (1995)
JOURNAL     96053543
MEDLINE     2 (bases 1 to 320)
REFERENCE   2 (bases 1 to 320)
AUTHORS    Young, D.C.
TITLE      Direct Submission
JOURNAL    Submitted (17-MAR-1995) David C. Young, University of Texas Health
            Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137,
            Houston, TX 77030, USA
COMMENT     NCBI gi: 780584
FEATURES   source
            Location/Qualifiers
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BASE COUNT   72 a   86 c   78 g   84 t
ORIGIN
Query Match      100.0%; Score 21; DB 91; Length 320;
Best Local Similarity 100.0%; Pred. No. 1.35e-03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 91 acctctggtatgggtgagc 111
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Qy 1 ACTTCTGGTATGGGTGAGC 21

RESULT 8
ID          MM022991 standard; RNA; ROD; 320 BP.
AC          U22991;
DT          29-APR-1995 (Rel. 43, Created)
DT          09-APR-1996 (Rel. 47, Last updated, Version 2)
DE          Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA,
            clone 45-25h, partial cds.
KW          .
OS          Mus musculus (mouse)
OC          Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
            Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
RN          [1]
RP          1-320
RA          Young D., Kearney J.F.;
RT          "Sequence analysis and antigen binding characteristics of Ig SCID
            clone 45-25h, partial cds."
RL          Int. Immunol. 7:807-819(1995).
RN          [2]
RP          1-320
RA          Young D.C.;
RT          .
RL          Submitted (17-MAR-1995) to the EMBL/GenBank/DBJ databases.
RL          David C. Young, University of Texas Health Science Center, Houston,
            Pathology, 6431 Fannin, MSMB 2.137, Houston, TX 77030, USA
CC          NCBI gi: 780584
FH          Key Location/Qualifiers

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FT /clone="45-25h"
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FT I
FT TYX"
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Best Local Similarity 100.0%; Pred. No. 1.35e-03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 91 actctcgtatgggtgtgagc 111
|||||
Qy 1 ACTTCTGATGGGTGTGAGC 21

RESULT 9
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DEFINITION Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA,
clone 45-20h, partial cds.
ACCESSION U22986
NID g780574
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
Murinae; Mus.
REFERENCE
AUTHORS Young, D. and Kearney, J.F.
TITLE Sequence analysis and antigen binding characteristics of Ig SCID
Ig+ mice
JOURNAL Int. Immunol. 7 (5), 807-819 (1995)
MEDLINE 96053543
REFERENCE
AUTHORS Young, D.C.
TITLE Direct Submission
JOURNAL Submitted (17-MAR-1995) David C. Young, University of Texas Health
Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137,
Houston, TX 77030, USA
NCBI gi: 780574
COMMENT Location/Qualifiers
FEATURES
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CDS
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BASE COUNT 76 a 82 c 81 g 87 t
ORIGIN

Query Match 100.0%; Score 21; DB 91; Length 326;
Best Local Similarity 100.0%; Pred. No. 1.35e-03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 91 actctcgtatgggtgtgagc 111
|||||
Qy 1 ACTTCTGATGGGTGTGAGC 21

RESULT 10
ID MM22986 standard; RNA; ROD; 326 BP.
AC U22986;
DT 29-APR-1995 (Rel. 43, Created)
DT 09-APR-1996 (Rel. 47, Last updated, Version 2)
DE Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA,
clone 45-20h, partial cds.
KW Mus musculus (mouse)
OS Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
OC Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
RN [1]
RP 1-326
RA Young D., Kearney J.F.;
RT "Sequence analysis and antigen binding characteristics of Ig SCID
RT Ig+ mice";
RL Int. Immunol. 7:807-819(1995).
RN [2]
RP 1-326
RA Young D.C.;
RT ;
RL Submitted (17-MAR-1995) to the EMBL/GenBank/DBJ databases.
RL David C. Young, University of Texas Health Science Center, Houston,
RL Pathology, 6431 Fannin, MSMB 2.137, Houston, TX 77030, USA
CC NCBI gi: 780574
FH Key Location/Qualifiers
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FT S SYFDX"
SQ Sequence 326 BP; 76 A; 82 C; 81 G; 87 T; 0 other;

Query Match 100.0%; Score 21; DB 12; Length 326;
Best Local Similarity 100.0%; Pred. No. 1.35e-03;
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Mar 19 08:21

US-08-612-929-21.rge

11

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 91 actctcgtatggtgtgagc 111  
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Qy 1 ACTTCGTATGGGTGTGAGC 21

RESULT 11

LOCUS MMU22975 330 bp mRNA ROD 09-APR-1996  
DEFINITION Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA,  
clone 45-10h, partial cds.

ACCESSION U22975

NID g780552

SOURCE house mouse.

ORGANISM Mus musculus

Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;  
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;  
Murinae; Mus.

REFERENCE 1 (bases 1 to 330)

AUTHORS Young, D. and Kearney, J.F.

TITLE Sequence analysis and antigen binding characteristics of Ig SCID  
Ig+ mice

JOURNAL Int. Immunol. 7 (5), 807-819 (1995)

MEDLINE 96053543

REFERENCE 2 (bases 1 to 330)

AUTHORS Young, D.C.

Direct Submission

TITLE Submitted (17-MAR-1995) David C. Young, University of Texas Health  
Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137,  
Houston, TX 77030, USA

COMMENT NCBI gi: 780552

FEATURES Location/Qualifiers

source 1..330

/organism="Mus musculus"

/strain="CB17 SCID"

/sub\_species="domesticus"

/clone="45-10h"

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/tissue\_type="spleen"

&lt;1..&gt;330

/note="NCBI gi: 780553"

/codon\_start=1

/product="immunoglobulin heavy chain"

/db\_xref="PID:g780553"

/translation="QVTLKESPGILOSQTLSLTCFSGLSTSGMGSVMIROPSSG  
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GSTYFDY"

BASE COUNT 76 a 86 c 81 g 87 t

ORIGIN

Query Match 100.0%; Score 21; DB 91; Length 330;

Best Local Similarity 100.0%; Pred. No. 1.35e-03;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 91 actctcgtatggtgtgagc 111  
|||||  
Qy 1 ACTTCGTATGGGTGTGAGC 21

RESULT 12

LOCUS MMU22995 353 bp mRNA ROD 26-APR-1995  
DEFINITION Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA,  
clone 45-28h, partial cds.

Mar 19 08:21

US-08-612-929-21.rge

12

ACCESSION U22995

NID g780592

KEYWORDS house mouse.

SOURCE Mus musculus

ORGANISM Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;  
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;  
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;  
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;  
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 353)

AUTHORS Young, D.C. and Kearney, J.F.

Sequence analysis and antigen binding characteristics of

immunoglobulins from SCID Ig+ mice

Int. Immunol. 7 (1995) In press

REFERENCE 2 (bases 1 to 353)

AUTHORS Young, D.C.

Direct Submission

TITLE Submitted (17-MAR-1995) David C. Young, University of Texas Health  
Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137,  
Houston, TX 77030, USA

FEATURES Location/Qualifiers

source 1..353

/clone="45-28h"

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/organism="Mus musculus"

/sub\_species="domesticus"

/cell\_type="lymphocyte"

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FFDYWGQGTTLTVSG"

BASE COUNT 81 a 96 c 87 g 89 t

ORIGIN

Query Match 100.0%; Score 21; DB 65; Length 353;

Best Local Similarity 100.0%; Pred. No. 1.35e-03;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 85 actctcgtatggtgtgagc 105

|||||

Qy 1 ACTTCGTATGGGTGTGAGC 21

RESULT 13

LOCUS MMU22995 353 bp mRNA ROD 09-APR-1996

DEFINITION Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA,  
clone 45-28h, partial cds.

ACCESSION U22995

NID g780592

KEYWORDS house mouse.

ORGANISM Mus musculus

Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;  
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;  
Murinae; Mus.

REFERENCE 1 (bases 1 to 353)

AUTHORS Young, D. and Kearney, J.F.

Sequence analysis and antigen binding characteristics of Ig SCID

Ig+ mice

JOURNAL Int. Immunol. 7 (5), 807-819 (1995)  
MEDLINE 96053543  
REFERENCE 2 (bases 1 to 353)  
AUTHORS Young,D.C.  
TITLE Direct Submission  
JOURNAL Submitted (17-MAR-1995) David C. Young, University of Texas Health  
Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137,  
Houston, TX 77030, USA

COMMENT NCBI gi: 780592

FEATURES Location/Qualifiers  
source

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BASE COUNT 81 a 96 c 87 g 89 t  
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Query Match 100.0%; Score 21; DB 91; Length 353;  
Best Local Similarity 100.0%; Pred. No. 1.35e-03;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 85 actctgtgtatgggtgtgagc 105  
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QY 1 ACTTCTGATGGGTGTGACC 21

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ID MM22995 standard; RNA; ROD; 353 BP.  
AC U22995;  
DT 29-APR-1995 (Rel. 43, Created)  
DT 09-APR-1996 (Rel. 47, Last updated, Version 2)  
DE Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA,  
clone 45-28h, partial cds.  
KW Mus musculus (mouse)  
OS Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;  
OC Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.  
RN [1]  
RP 1-353  
RA Young D., Kearney J.F.;  
RT "Sequence analysis and antigen binding characteristics of Ig SCID  
Ig<sup>+</sup> mice";  
RL Int. Immunol. 7:807-819(1995).  
RN [2]  
RP 1-353  
RA Young D.C.;

Submitted (17-MAR-1995) to the EMBL/GenBank/DBJ databases.  
RL David C. Young, University of Texas Health Science Center, Houston,  
RL Pathology, 6431 Fannin, MSMB 2.137, Houston, TX 77030, USA  
CC NCBI gi: 780592  
FH Key Location/Qualifiers

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FT /strain="CB17 SCID"  
FT /sub\_species="domesticus"  
FT /clone="45-28h"  
FT /cell\_type="lymphocyte"  
FT /tissue\_type="spleen"  
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FT /codon\_start=3  
FT /product="immunoglobulin heavy chain"  
FT /db\_xref="PID:g780593"  
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G  
FT VAGTHWDDKRYNPSLKSLTISKDTSRQVFLKITSVDYADTATYYCARRVLGSSF  
F  
FT DYYWGQGTTLTVSG"  
SQ Sequence 353 BP; 81 A; 96 C; 87 G; 89 T; 0 other;

Query Match 100.0%; Score 21; DB 12; Length 353;  
Best Local Similarity 100.0%; Pred. No. 1.35e-03;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 85 actctgtgtatgggtgtgagc 105  
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QY 1 ACTTCTGATGGGTGTGACC 21

RESULT 15  
LOCUS MMU23000 358 bp mRNA ROD 26-APR-1995  
DEFINITION Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA,  
clone 45-32h, partial cds.

ACCESSION U23000

NID g780602

KEYWORDS house mouse.

SOURCE Mus musculus

ORGANISM

Eukaryota; mitochondrial eukaryotes; Metazoa/Eumycota group;  
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;  
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;  
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;  
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 358)  
AUTHORS Young,D.C. and Kearney,J.F.  
TITLE Sequence analysis and antigen binding characteristics of  
immunoglobulins from SCID Ig<sup>+</sup> mice

JOURNAL Int. Immunol. 7 (1995) In press

REFERENCE 2 (bases 1 to 358)

AUTHORS Young,D.C.

TITLE Direct Submission

JOURNAL

Submitted (17-MAR-1995) David C. Young, University of Texas Health  
Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137,  
Houston, TX 77030, USA

FEATURES

source

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Location/Qualifiers  
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Mar 19 08:21

US-08-612-929-21.rge

15

/translation="VTIKESGPGILQSSQTLSTCSFSGFSINTSGMGVSWIRQPSGK  
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BASE COUNT      81 a      95 c      87 g      95 t  
ORIGIN

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Best Local Similarity 100.0%;    Pred. No. 1.35e-03;  
Matches    21;    Conservative    0;    Mismatches    0;    Indels    0;    Gaps    0;

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Qy    1    ACTTCTGTATGGGTGTGAGC 21

Search completed: Wed Mar 19 08:23:25 1997  
Job time : 56 secs.

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MASSIVE (TM)

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MPsrch\_nm n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed Mar 19 08:24:19 1997; MasPar time 57.38 Seconds  
161.419 Million cell updates/sec

Tabular output not generated.

Title: >US-08-612-929-21  
Description: (1-21) from US08612929.seq  
Perfect Score: 21  
N.A. Sequence: 1 ACTTCTGGTATGGGTGACG 21  
Comp: TGNAGACCATCCACATCG

Scoring table: TABLE default

Gap 10

Nmatch STD : Dbase 0; Query 0

Searched: 630489 seqs, 220513910 bases x 2

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: EST-STS  
1:EST1 2:EST2 3:EST3 4:EST4 5:EST5 6:EST6 7:EST7 8:EST8  
9:EST9 10:EST10 11:EST11 12:EST12 13:EST13 14:EST14  
15:EST15 16:EST16 17:EST17 18:EST18 19:EST19 20:EST20  
21:EST21 22:EST22 23:EST23 24:EST24 25:EST25 26:EST26  
27:EST27 28:EST28 29:EST29 30:EST30 31:EST31 32:EST32  
33:EST33 34:EST34 35:EST35 36:EST36 37:EST37 38:EST38  
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99:EST99  
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100:EST100 101:EST101 102:EST102 103:EST103 104:EST104  
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125:EST125 126:EST126 127:EST127 128:EST128 129:EST129

Database:

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136:STS8 137:STS9 138:STS10 139:STS11 140:STS12  
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146:STS18 147:STS19 148:STS20 149:STS21 150:STS22  
151:STS23 152:STS24 153:STS25 154:STS26 155:STS27  
156:STS28 157:STS29 158:STS30 159:STS31 160:STS32  
161:STS33 162:STS34 163:STS35 164:STS36 165:STS37  
166:STS38 167:STS39 168:STS40 169:STS41 170:STS42  
171:STS43 172:STS44 173:STS45 174:STS46

Statistics: Mean 6.550; Variance 1.345; scale 4.869

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	16	76.2	273 170	MM4172	ma08f03.r1 Soares mou	1.46e-03
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3	16	76.2	352 132	G08125	human STS CHLC.GATA10	1.46e-03
4	16	76.2	392 96	R83741	yp16a07.s1 Homo sapie	1.46e-03
5	16	76.2	402 159	HS154322	zc67f05.s1 Soares fet	1.46e-03
6	16	76.2	402 146	W02154	zc67f05.s1 Soares fet	1.46e-03
7	16	76.2	486 83	R42566	yg01dl1.s1 Homo sapie	1.46e-02
8	15	71.4	313 19	H42722	yo71h05.r1 Homo sapie	2.69e-02
9	15	71.4	316 5	CELR083A1R	C.elegans cDNA clone	2.69e-02
10	15	71.4	397 13	H23221	ym52f07.s1 Homo sapie	2.69e-02
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12	15	71.4	556 16	H32803	EST108258 Rattus sp.	2.69e-02
13	14	66.7	232 50	H0WGS02742	Human adult lung 3'di	4.37e-01
14	14	66.7	254 133	G13411	human STS WI-3806.	4.37e-01
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18	14	66.7	305 81	R36147	yh92f08.s1 Homo sapie	4.37e-01
19	14	66.7	342 123	T79663	yd71a12.r1 Homo sapie	4.37e-01
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29	14	66.7	403 127	T94984	ye38h05.r1 Homo sapie	4.37e-01
30	14	66.7	421 75	R14317	yf80e06.r1 Homo sapie	4.37e-01
31	14	66.7	422 25	H62080	yu40b03.r1 Homo sapie	4.37e-01
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33	14	66.7	446 25	H62101	yu40e07.r1 Homo sapie	4.37e-01
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42	14	66.7	537 20	H45847	yp22c02.r1 Homo sapie	4.37e-01

Mar 19 08:23

US-08-612-929-21.rst

3

43 14 66.7 537 107 T21646 3654 Arabidopsis thal 4.37e-01  
 44 14 66.7 589 147 W04275 za49a10.r1 Soares fet 4.37e-01  
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 DT 29-APR-1996 (Rel. 47, Last updated, Version 1)  
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 OS Mus musculus (mouse)  
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 OC Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.  
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 RA Marra M., Hillier L., Allen M., Bowles M., Dietrich N.,  
 RA Dubuque T., Geisel S., Kucaba T., Lacy M., Le M., Martin J.,  
 RA Morris M., Schellenberg K., Steptoe M., Tan F., Underwood K.,  
 RA Moore B., Theising B., Wylie T., Lennon G., Soares B., Wilson R.,  
 RA Waterston R.;  
 RT "The WashU-HHMI Mouse EST Project";  
 RL Unpublished.  
 CC Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project  
 CC Washington University School of MedicineP 4444 Forest Park Parkway,  
 CC Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810  
 CC Email: mouseest@wustl.edu This clone is available  
 CC royalty-free through LNL ; contact the IMAGE Consortium  
 CC (info@image.llnl.gov) for further information. Seq primer:  
 CC mob.REGA+ET High quality sequence stop: 261. NCBI gi: 1283734  
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 FT was primed with a Not I - oligo(dT) primer [5'  
 FT TGTACCAATCTGAAGTGGAGCGCGCATTTTTTTTTTTTTTTT 3'] ,  
 FT double-stranded cDNA was size selected, ligated to Eco RI  
 FT adapters (Pharmacia), digested with Not I and cloned into  
 FT the Not I and Eco RI sites of a modified pT73 vector  
 FT (Pharmacia). Library went through one round of  
 FT normalization to a Cot = 5. Library constructed by Bento  
 FT Soares and M.Fatima Bonaldo."  
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 Best Local Similarity 94.4%; Pred. No. 1.46e-03;  
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 QY 4 TCTGGTATGGGTGTGAGC 21

RESULT 2  
 LOCUS W09417 273 bp mRNA EST 26-APR-1996

Mar 19 08:23

US-08-612-929-21.rst

4

DEFINITION ma08f03.r1 Soares mouse p3NMF19.5 Mus musculus cDNA 5' .  
 ACCESSION W09417  
 NID g1283734  
 KEYWORDS EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus

Eukaryota; Eukaryotes; Mitochondrial eukaryotes; Metazoa; Chordata;  
 Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;  
 Murinae; Mus.

REFERENCE 1 (bases 1 to 273)  
 AUTHORS Marra M., Hillier L., Allen M., Bowles M., Dietrich N., Dubuque T.,  
 Geisel S., Kucaba T., Lacy M., Le M., Martin J., Morris M.,  
 Schellenberg K., Steptoe M., Tan F., Underwood K., Moore B.,  
 Theising B., Wylie T., Lennon G., Soares B., Wilson R. and  
 Waterston R.  
 TITLE The WashU-HHMI Mouse EST Project  
 JOURNAL Unpublished (1996)  
 COMMENT

Contact: Marra M/Mouse EST Project  
 WashU-HHMI Mouse EST Project  
 Washington University School of MedicineP  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: mouseest@wustl.edu  
 This clone is available royalty-free through LNL ; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 Seq primer: mob.REGA+ET  
 High quality sequence stop: 261.

NCBI gi: 1283734  
 Location/Qualifiers  
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 was primed with a Not I - oligo(dT) primer [5'  
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 double-stranded cDNA was size selected, ligated to Eco RI  
 adapters (Pharmacia), digested with Not I and cloned into  
 the Not I and Eco RI sites of a modified pT73 vector  
 (Pharmacia). Library went through one round of  
 normalization to a Cot = 5. Library constructed by Bento  
 Soares and M.Fatima Bonaldo."  
 /clone lib="Soares mouse p3NMF19.5"  
 /dev stage="19 weeks"  
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 mRNA  
 BASE COUNT 81 a 60 c 73 g 59 t  
 ORIGIN

Query Match 76.2%; Score 16; DB 148; Length 273;  
 Best Local Similarity 94.4%; Pred. No. 1.46e-03;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 126 tctggatgggtgtgagc 143  
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 QY 4 TCTGGTATGGGTGTGAGC 21

RESULT 3  
 LOCUS G08125 352 bp DNA STS 08-AUG-1995  
 DEFINITION human STS CHLC.GATA10H05.P7044 clone GATA10H05.  
 ACCESSION G08125

Mar 19 08:23

US-08-612-929-21.rst

5

NID q938675  
KEYWORDS STS sequence; primer; sequence tagged site.  
SOURCE human vector=pCPI host=E.coli dutung+ (DH10B) Marker Selected genomic DNA prepared from XY individual of French nationality.  
ORGANISM Homo Sapiens  
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 352)  
AUTHORS Murray,J., Sheffield,V, Weber,J.L., Duyk,G. and Bueto,K.H.  
TITLE Cooperative Human Linkage Center  
JOURNAL Unpublished (1995)  
COMMENT Synonyms: GATA10H05, CHLC.GATA10H05.#T7043  
Contact: Dr. Jeffrey C. Murray  
UofI

The University of Iowa  
Department of Pediatrics, Iowa City, IA 52242, USA  
Tel: (319) 356-3508  
Fax: (319) 356-3347  
Email: jeff-murray@uiowa.edu

Primer A: CCTAAATTGTGAGATCTTTTATC  
Primer B: TTTTCTAGACTACCCCTTACC

STS size: 216

PCR Profile:

denature: 30 seconds at 94 degrees C  
annealing: 75 seconds at 55 degrees C  
extension: 15 seconds at 72 degrees C  
PCR cycles: 27  
extension: 6 minutes at 72 degrees C

Protocol:  
Template: 30ng genomic DNA  
Primer: each 1.5 pmole  
dNTPs: each 200 uM  
Taq Polymerase: 0.3 units  
Total Vol: 10 ul

Buffer:

MgCl2: 1.5mM  
KCl: 50mM  
Tris: 10mM  
pH: 8.3.

Location/Qualifiers  
1..352  
/organism="Homo Sapiens"  
/note="human"

STS  
primer\_bind 2..217  
primer\_bind complement(195..217)  
BASE COUNT 109 a 47 c 65 g 128 t 3 others  
ORIGIN

Query Match 76.2%; Score 16; DB 132; Length 352;  
Best Local Similarity 94.4%; Pred. No. 1.46e-03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 327 ttccagtgatgggtgtgag 344

||||| |||||||

QY 3 TTCTGCTAGCGGTGTGAG 20

RESULT 4

LOCUS R83741 392 bp mRNA EST 04-AUG-1995

Mar 19 08:23

US-08-612-929-21.rst

6

DEFINITION YP16a07.s1 Homo sapiens cDNA clone 187572 3' .  
ACCESSION R83741  
NID 928618  
KEYWORDS EST.  
SOURCE human clones=187572 library=Soares breast 3nBBst vector=pT7T3D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) primer=T3 Reitel=Not I Reite2=Eco RI Adult human. 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTACCAATCTCAAGTGGAGCGCCCTTTTCTTTTCTTTTCTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 20. Library constructed by Bento Soares and M.Patima Bonaldo.

ORGANISM Homo sapiens  
Eukaryotae; Metazoa; Bumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 392)

AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Fan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.  
The WashU-Merck EST Project

TITLE The WashU-Merck EST Project  
JOURNAL Unpublished (1995)  
COMMENT

Contact: Wilson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.wustl.edu  
High quality sequence stops: 319  
Source: IMAGE Consortium, LIND

This clone is available royalty-free through LIND; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES  
source  
1..392  
/organism="Homo sapiens"  
/clone="187572"  
/note="human"

BASE COUNT 87 a 96 c 101 g 101 t 7 others  
ORIGIN

Query Match 76.2%; Score 16; DB 96; Length 392;  
Best Local Similarity 90.0%; Pred. No. 1.46e-03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 254 cttctgatgtggtgagc 273

||||| |||||||

QY 2 CTTCGGTATGGGTGAGC 21

RESULT 5

ID HS154322 standard; RNA; EST; 402 BP.

AC W02154;

DT 25-APR-1996 (Rel. 47, Created)

DT 25-APR-1996 (Rel. 47, Last updated, Version 1)

DE zc67f05.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone

DE 327393 3'.

KW EST.



cDNA was ligated to Hind III adaptors (Pharmacia), digested with Not I and directionally cloned into the Not I and Hind III sites of the LfaMid BA vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo.

## ORGANISM

Homo sapiens

Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.

## REFERENCE

1 (bases 1 to 486)

## AUTHORS

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.

The WashU-Merck EST Project

Unpublished (1995)

## COMMENT

GDB: G00-403-477

Contact: Wilson RK

WashU-Merck EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence stops: 352

Source: IMAGE Consortium, LML

This clone is available royalty-free through LML; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

## FEATURES

Location/Qualifiers

source

1..486

/organism="Homo sapiens"

/clone="31130"

/note="human"

BASE COUNT 120 a 94 c 111 g 157 t 4 others

## ORIGIN

Query Match

Best Local Similarity 76.2%; Score 16; DB 83; Length 486;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 348 actctgtatgctctgag 367

|||||

Qy 1 ACTTCTGATGGGTCTGAG 20

## RESULT

8

LOCUS

H42722

yo1h05.r1

Homo sapiens

cDNA clone

183417

EST

31-JUL-1995

DEFINITION

H42722

ACCESSION

H42722

NID

g918774

KEYWORDS

EST.

SOURCE

human clone=183417

library=Soares breast 3NbHbSt vector=pf7T3D

(Pharmacia) with a modified polylinker host=DH10B (ampicillin

resistant) primer=M13RP1 Rsite=Not I Rsite2=Eco RI Adult human.

1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAGTCGGAGGGCGGCTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pf7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 20. Library constructed by Bento Soares and M.Fatima Bonaldo.

## ORGANISM

Homo sapiens

Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.

## REFERENCE

1 (bases 1 to 486)

## AUTHORS

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.

The WashU-Merck EST Project

Unpublished (1995)

## COMMENT

GDB: G00-403-477

Contact: Wilson RK

WashU-Merck EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence stops: 352

Source: IMAGE Consortium, LML

This clone is available royalty-free through LML; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

## FEATURES

Location/Qualifiers

source

1..486

/organism="Homo sapiens"

/clone="31130"

/note="human"

BASE COUNT 120 a 94 c 111 g 157 t 4 others

## ORIGIN

Query Match

Best Local Similarity 76.2%; Score 16; DB 83; Length 486;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 348 actctgtatgctctgag 367

|||||

Qy 1 ACTTCTGATGGGTCTGAG 20

## RESULT

8

LOCUS

H42722

yo1h05.r1

Homo sapiens

cDNA clone

183417

EST

31-JUL-1995

DEFINITION

H42722

ACCESSION

H42722

NID

g918774

KEYWORDS

EST.

SOURCE

human clone=183417

library=Soares breast 3NbHbSt vector=pf7T3D

(Pharmacia) with a modified polylinker host=DH10B (ampicillin

resistant) primer=M13RP1 Rsite=Not I Rsite2=Eco RI Adult human.

## ORGANISM

Homo sapiens

Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.

## REFERENCE

1 (bases 1 to 313)

## AUTHORS

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.

The WashU-Merck EST Project

Unpublished (1995)

## TITLE

The WashU-Merck EST Project

## JOURNAL

Unpublished (1995)

## COMMENT

Contact: Wilson RK

WashU-Merck EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence stops: 237

Source: IMAGE Consortium, LML

This clone is available royalty-free through LML; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

## FEATURES

Location/Qualifiers

source

1..313

/organism="Homo sapiens"

/clone="183417"

/note="human"

BASE COUNT 69 a 74 c 100 g 66 t 4 others

## ORIGIN

Query Match

Best Local Similarity 71.4%; Score 15; DB 19; Length 313;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 182 ttctgtatgggtgt 196

|||||

Qy 3 TTCTGTATGGGTGT 17

## RESULT

9

LOCUS

CELK083A1R

316 bp

mRNA

EST

10-DEC-1995

DEFINITION

C.elegans cDNA clone yk83a1 : 3' end, single read.

ACCESSION

D71871

NID

g1111581

KEYWORDS

EST(expressed sequence tag).

Caenorhabditis elegans (strain N2, ) (library: Yuji Kohara

unpublished cDNA) Hermaphrodite embryo cDNA to mRNA.

SOURCE

Caenorhabditis elegans

Eukaryotae; mitochondrial eukaryotes; Metazoa; Nematoidea;

Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea;

Rhabditidae; Caenorhabditis.

REFERENCE

1 (bases 1 to 316)

## AUTHORS

Kohara, Y., Motohashi, T., Tabara, H., Sugimoto, A., Watanabe, H. and

Nishigaki, A.

TITLE

Toward an expression map of the C.elegans genome

JOURNAL

Unpublished (1995)

COMMENT

Submitted (23-Aug-1995) to DDBJ by:

Yuji Kohara

Gene Library Lab.

National Institute of Genetics

Yata 1111, Mishima Shizuoka



Mar 19 08:23

US-08-612-929-21.rst

11

411 Japan

Phone: 0559-81-6854

Fax : 0559-81-6855

Email:ykohara@dbj.nig.ac.jp.

Location/Qualifiers

## FEATURES

source  
1..316  
/organism="Caenorhabditis elegans"  
/strain="N2"  
/dev\_stage="embryo"  
/sequenced\_mol="cDNA to mRNA"  
/sex="Hermaphrodite"  
/tissue\_type="embryo"  
/clone\_lib="Yuji Kohara unpublished cDNA"  
120 a 45 c 49 g 97 t 5 others

## BASE COUNT

ORIGIN

Query Match 71.4%; Score 15; DB 5; Length 316;  
Best Local Similarity 84.2%; Pred. No. 2.69e-02;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 282 ttctgntgntgttgac 300

||||| t t t t t t t t

Qy 3 TTCTGGTATGGTGTGAC 21

## RESULT 10

LOCUS H23221 397 bp mRNA EST 06-JUL-1995

DEFINITION ym52107.s1 Homo sapiens cDNA clone 51884 3'.

ACCESSION H23221

NID g891916

KEYWORDS EST.

SOURCE human clone-51884 library=Soares infant brain IN1B vector=Lafmid BA host=DH10B (ampicillin resistant) primer=Promega -2lm13 Rsite1-Not I Rsite2=Hind III Whole brain from a 73 days post natal female. 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' AACTGGAGAAATTCGCGCCGACGAGATTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Hind III adaptors (Pharmacia), digested with Not I and directionally cloned into the Not I and Hind III sites of the Lafmid BA vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo.

## ORGANISM

Homo sapiens  
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.

## TITLE

The WashU-Merck EST Project

## JOURNAL

Unpublished (1995)

GDB: G00-424-820

Contact: Wilson RK

WashU-Merck EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence stops: 353

Mar 19 08:23

US-08-612-929-21.rst

12

Source: IMAGE Consortium, LNL

This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

## FEATURES

Location/Qualifiers  
source  
1..397  
/organism="Homo sapiens"  
/clone="51884"  
/note="human"  
96 a 85 c 88 g 121 t 7 others

## BASE COUNT

ORIGIN

Query Match 71.4%; Score 15; DB 13; Length 397;

Best Local Similarity 85.0%; Pred. No. 2.69e-02;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 307 ctcttgatggtgac 326

||||| t t t t t t t t

Qy 2 CTTCTGGTATGGTGTGAC 21

## RESULT 11

LOCUS H46104 431 bp mRNA EST 31-JUL-1995

DEFINITION y017d06.r1 Homo sapiens cDNA clone 178187 5'.

ACCESSION H46104

NID g922156

KEYWORDS EST.

SOURCE Homo sapiens clone=178187 library=Soares adult brain N2b5HB55Y vector=pTT73D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) primer=M13RPI Rsite1-Not I Rsite2-Eco RI 55-year old male. 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTCAAGTGGGAGCGCGCTTTTTTTTTTTT 3'],

double-stranded cDNA was size selected, ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pTT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 53. Library constructed by Bento Soares and M.Fatima Bonaldo. The adult brain RNA was provided by Dr. Donald H. Gilden. Tissue was acquired 17-18 hours after death which occurred in consequence of a ruptured aortic aneurysm. RNA was prepared from a pool of tissues representing the following areas of the brain: frontal, parietal, temporal and occipital cortex from the left and right hemispheres, subcortical white matter, basal ganglia, thalamus, cerebellum, midbrain, pons and medulla.

## ORGANISM

Homo sapiens  
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.

## TITLE

The WashU-Merck EST Project

Unpublished (1995)

Contact: Wilson RK

WashU-Merck EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Mar 19:08:23

US-08-612-929-21.rst

13

Email: est@watson.wustl.edu  
High quality sequence stops: 238  
Source: IMAGE Consortium, L1NL  
This clone is available royalty-free through L1NL ; contact the  
IMAGE Consortium (info@image.l1nl.gov) for further information.

FEATURES

source  
1..431  
/organism="Homo sapiens"  
/clone="178187"  
BASE COUNT 106 a 104 c 101 g 116 t 4 others  
ORIGIN  
Query Match 71.4%; Score 15; DB 20; Length 431;  
Best Local Similarity 85.7%; Pred. No. 2.69e-02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 364 actgctggcatgggtgtgggc 384

Oy 1 ACTTCTGGTATCGGTGTGAGC 21  
||||| ||||| ||||| |||

RESULT 12

LOCUS H32803 556 bp mRNA EST 08-SEP-1995  
DEFINITION EST108258 Rattus sp. cDNA 5' end.  
ACCESSION H32803  
NID g978220  
KEYWORDS EST.  
SOURCE rat primer=M13 Reverse library=Rat PC-12 cells, untreated  
vector=phuescript SK- RsaI=I-EcoRI RsaI=2-XhoI poly(A)+ RNA was  
purified from untreated PC12 cells cultured for 9 days. cDNA was  
constructed using an oligo-dT primer and directionally cloned using  
the Lambda ZAP II Vector Kit by Stratagene.

ORGANISM

Rattus sp.  
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;  
Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Myomorpha;  
Muridae; Murinae; Rattus.

REFERENCE

AUTHORS Lee,N.H., Weinstock,K.G., Kirkness,E.F., Earle-Hughes,J.A.,  
Fuldner,R.A., Marmaras,S., Glodek,A., Gocayne,J.D., Adams,M.D.,  
Kerlavage,A.R., Fraser,C.M. and Venter,J.C.

TITLE Comparative expressed sequence tag analysis of differential gene  
expression profiles in PC-12 cells before and after nerve growth  
factor treatment

JOURNAL Proc. Natl. Acad. Sci. USA 92, 8303-8307 (1995)

COMMENT

Contact: Lee NH  
The Institute for Genomic Research  
932 Clopper Rd, Gaithersburg, MD 20878  
Tel: 3018699056  
Fax: 3018699423  
Email: nhlee@tigr.org

For clone availability please contact the TIGR Database  
(tdbinfo@tdb.tigr.org).

FEATURES

source  
1..556  
/organism="Rattus sp."  
/note="rat"  
mRNA  
<1..>556  
BASE COUNT 128 a 134 c 150 g 140 t 4 others  
ORIGIN  
Query Match 71.4%; Score 15; DB 16; Length 556;  
Best Local Similarity 85.0%; Pred. No. 2.69e-02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Mar 19:08:23

US-08-612-929-21.rst

14

Db 469 acatcgmtatgggtgtgag 488

Oy 1 ACTTCTGGTATCGGTGTGAG 20  
||||| ||||| ||||| |||

RESULT 13

LOCUS HUMGS02742 232 bp mRNA EST 20-FEB-1995  
DEFINITION Human adult lung 3'directed MboI cDNA, HUMGS02742, clone lq0864.  
ACCESSION D45555  
NID g662509  
KEYWORDS EST(expressed sequence tag); gene signature(GS); lung.  
SOURCE Homo sapiens (library: Human adult lung 3'directed MboI cDNA) Adult  
Lung cDNA to mRNA.

ORGANISM

Homo sapiens  
Eukaryotae; Animalia; Chordata; Vertebrata; Mammalia; Theria;  
Eutheria; Primates; Haplorhini; Catarrhini; Homiidae.

REFERENCE

AUTHORS 1 (bases 1 to 232)  
Kohichi Ito, Kousaku,O., Junji,Y., Hideoki,Y. and Kenichi,M.  
TITLE An expression profile of active genes in human lung  
JOURNAL DNA Research 1, 279-287 (1994)

COMMENT

PROJECT = 'bodymapping'  
Submitted (02-FEB-1995) to DDBJ by:  
Kohichi Itoh  
Institute for Molecular and Cellular Biology  
Osaka University  
3-1, Yamadaoka  
Suita, Osaka, 565  
Japan  
Phone: 06-877-5111 x3910  
Fax : 06-877-1922.

FEATURES

source  
1..232  
/organism="Homo sapiens"  
/dev\_stage="Adult"  
/sequenced\_mol="cDNA to mRNA"  
/tissue\_type="Lung"  
/clone\_lib="Human adult lung 3'directed MboI cDNA"  
BASE COUNT 49 a 63 c 64 g 56 t  
ORIGIN  
Query Match 66.7%; Score 14; DB 50; Length 232;  
Best Local Similarity 100.0%; Pred. No. 4.37e-01;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 174 gtatgggtgtgagc 187

Oy 8 GTATCGGTGTGAGC 21  
||||| ||||| ||||| |||

RESULT 14

LOCUS GL3411 254 bp DNA STS 20-DEC-1995  
DEFINITION human STS WI-3806.  
ACCESSION GL3411  
NID g1127520  
KEYWORDS STS sequence; primer; sequence tagged site.  
SOURCE human STSs derived from random genomic DNA.  
ORGANISM Homo sapiens

Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;  
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;  
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;  
Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 254)

AUTHORS

Hudson,T.

TITLE Whitehead Institute/MIT Center for Genome Research; Physically

JOURNAL Mapped STSs

COMMENT Unpublished (1995)

Contact: Thomas Hudson

Whitehead Institute/MIT Center for Genome Research

Whitehead Institute for Biomedical Research

9 Cambridge Center, Cambridge MA 02142 USA

Tel: 617 252 1900

Fax: 617 252 1902

Email: thudson@genome.wi.mit.edu

Primer A: TACCTCTGGAATGGGTGTGG

Primer B: CTTCGTCTTTCATGACGAGAA

STS size: 200

PCR Profile:

Presoak:

Denaturation:

Annealing: 56 degrees C

Polymerization:

PCR Cycles: 35

Thermal Cycler:

Protocol:

Template: 10 ng

Primer: each 5 pM

dNTPs: each 4 mM

Taq Polymerase: 0.025 units/ul

Total Vol: 20 ul

Buffer:

MgCl2: 1.5 mM

KCl: 50 mM

Tris-HCl: 10 mM

pH: 9.3

Random genome wide STS.

Location/Qualifiers

FEATURES

source

1..254

/organism="Homo sapiens"

/note="human"

52..251

primer\_bind /map="373.9 cR from top of Chr11 linkage group"

52..71

primer\_bind /map="373.9 cR from top of Chr11 linkage group"

complement(230..251)

BASE COUNT /map="373.9 cR from top of Chr11 linkage group"

81 a 50 c 55 g 68 t

ORIGIN

Query Match

Best Local Similarity 66.7%; Score 14; DB 133; Length 254;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 53 acctctggaatgggtgtg 70

||||| |||||

Qy 1 ACTTCTGATGGGTGTC 18

RESULT 15

LOCUS HSC3AE011 295 bp RNA EST 21-SEP-1995

DEFINITION H. sapiens partial cDNA sequence; clone c-3ae01.

ACCESSION F12473

NTD 9708465

KEYWORDS partial cDNA sequence; transcribed sequence fragment.

SOURCE human.

ORGANISM Homo sapiens

Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;

Vertebrata; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 295)

AUTHORS Genexpress.

TITLE Direct Submission

JOURNAL Submitted (19-JAN-1995) Genethon, B.P. 60, 91002 Evry Cedex France

and Genetique Moleculaire et Biologie du developpement, CNRS UPR420

B.P. 8, 94801 Villejuif Cedex France. E-mail:

genexpress@genethon.fr

REFERENCE 2 (bases 1 to 295)

AUTHORS Genexpress.

TITLE The Genexpress cDNA program

JOURNAL Unpublished

REFERENCE 3 (bases 1 to 295)

AUTHORS Auffray, C., Behar, G., Bois, F., Bouchier, C., da Silva, C.,

Devignes, M.D., Duprat, S., Houlgatte, R., Jumeau, M.N., Lamy, B.,

Lorenzo, F., Mitchell, H., Mariage-Samson, R., Pietu, G., Pouliot, Y.,

Sebastiani-Kabaktchis, C. and Tessier, A.

IMAGE: molecular integration of the analysis of the human genome

and its expression

JOURNAL C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)

MEDLINE 95277534

COMMENT Cloning method: total mRNA was oligo-(dT) primed and directionally

cloned 5' -> 3' into the HindIII -> NotI sites of the laimid BA

vector;

Sequencing method: single read, full automatic;

Primer: M13 reverse

cDNA sequence colinear to mRNA

Stretch removed: nothing

Normalization method: Bento Soares, P.N.A.S. 91:9228-9232 (1994);

Genexpress library\_idt: C;

Genexpress\_sequence\_idt: y1c-3ae01.

FEATURES

source

1..295

/organism="Homo sapiens"

/isolate="muscular atrophy patient"

/clone\_lib="normalized infant brain cDNA from B.Souares,

Psychiatry Dept. Columbia University USA"

/sex="female"

/tissue\_type="total brain"

/dev\_stage="3 months old"

BASE COUNT 104 a 71 c 56 g 62 t 2 others

ORIGIN

Query Match

Best Local Similarity 66.7%; Score 14; DB 44; Length 295;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 33 cacacccacaccagaa 48

||||| |||||

Cp 18 CACACCATACAGAA 3

Search completed: Wed Mar 19 08:25:25 1997

Job time : 66 secs.

\*\*\*\*\*

WATERMAN

(TM)

\*\*\*\*\*

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MPsrch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed Mar 19 08:23:44 1997; MasPar time 10.31 Seconds  
177.715 Million cell updates/sec

Tabular output not generated.

Title: >US-08-612-929-21  
Description: (1-21) from US08612929.seq  
Perfect Score: 21  
N.A. Sequence: 1 ACTTCTGCTATGGGTGACG 21  
Comp: TGAAGACCATACCCACATCG

Scoring table: TABLE default  
Gap 10

Nmatch STD : Dbase 0; Query 0

Searched: 113505 seqs, 43611913 bases x 2

Post-processing: Minimum Match 0\$  
Listing first 45 summaries

Database: n-geneseq25  
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13  
14:part14 15:part15 16:part16 17:part17 18:part18  
19:part19 20:part20 21:part21 22:part22

Statistics: Mean 5.273; Variance 3.101; scale 1.700

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	21	100.0	423	14	Q83492 Chimeric antibody 3B9	5.62e-03
2	21	100.0	483	14	Q83491 Mouse MAb 3B9 heavy c	5.62e-03
3	21	100.0	738	12	Q70612 IL-6 binding inhibito	5.62e-03
c	4	20	95.2	91	Q51746 Oligonucleotide probe	2.11e-02
5	19	90.5	366	11	Q68709 Humanised MAb H-chain	7.80e-02
6	17	81.0	45	4	Q24650 PCR Primer C for ampl	9.99e-01
7	17	81.0	139	4	Q24653 Fragment CD of HUMDXC	9.99e-01
8	17	81.0	207	4	Q24652 Fragment AB of HUMDXC	9.99e-01

9	17	81.0	265	4	Q24654	Fragment AD of HUMDXC	9.99e-01	
10	17	81.0	360	19	T09300	Murine anti-Protein C	9.99e-01	
11	17	81.0	417	19	T09299	Murine anti-Protein C	9.99e-01	
12	16	76.2	429	11	Q64166	Sequence of mouse VH	3.45e+00	
13	16	76.2	630	13	Q78948	Human immunoglobulin	3.45e+00	
14	15	71.4	812	6	Q37056	Rat immunoglobulin H	1.16e+01	
15	15	71.4	2352	1	Q04729	Xylene oxygenase gene	1.16e+01	
c	16	14	66.7	25	10	Q56540	Nucleic acid detectio	3.76e+01
c	17	14	66.7	25	10	Q57121	Chromosomal transloca	3.76e+01
c	18	14	66.7	232	19	T21378	Human gene signature	3.76e+01
c	19	14	66.7	789	6	Q36376	NDP kinase gene.	3.76e+01
c	20	14	66.7	1159	7	Q40592	JSL precursor DNA.	3.76e+01
c	21	14	66.7	1422	16	Q95109	Human papillomavirus	3.76e+01
c	22	14	66.7	1564	21	T36701	Plasmid pNHK101.	3.76e+01
c	23	14	66.7	1650	13	Q74684	Early Ripening Tomato	3.76e+01
c	24	14	66.7	2438	1	N80408	Plasmid pRAJ220 inser	3.76e+01
c	25	14	66.7	2457	1	N81451	Sequence encoding fus	3.76e+01
c	26	14	66.7	2476	21	T18377	Plasmid pMKH1.	3.76e+01
c	27	14	66.7	2511	1	N92113	Polynucleotide encodi	3.76e+01
c	28	14	66.7	2673	1	N81449	Sequence encoding fus	3.76e+01
c	29	14	66.7	4284	12	Q74259	Stress-induced tobacc	3.76e+01
c	30	14	66.7	5406	1	N93197	Fragment of clone lam	3.76e+01
c	31	14	66.7	5642	8	Q51193	pDE4; Plasmid DNA rep	3.76e+01
c	32	14	66.7	7050	7	Q40419	Sequence of pTE4.	3.76e+01
c	33	13	61.9	43	9	Q50622	Canine coronavirus 1-	1.18e+02
c	34	13	61.9	97	21	T24468	Human gene signature	1.18e+02
c	35	13	61.9	370	20	T21289	Human gene signature	1.18e+02
c	36	13	61.9	382	8	Q59352	Human brain Expressed	1.18e+02
c	37	13	61.9	1191	14	Q85439	FCV DNA insert of clo	1.18e+02
c	38	13	61.9	2246	4	Q25541	Consensus sequence fo	1.18e+02
c	39	13	61.9	4074	20	T13950	B. thuringiensis VIP2	1.18e+02
c	40	13	61.9	4359	9	Q52447	Canine coronavirus 1-	1.18e+02
c	41	13	61.9	4365	4	Q25536	S gene of TS FIPV.	1.18e+02
c	42	13	61.9	4565	1	Q03704	Gene encoding plant e	1.18e+02
c	43	13	61.9	4669	9	Q52726	Sequence of human mul	1.18e+02
c	44	13	61.9	4800	4	N81533	Sequence of the peplo	1.18e+02
c	45	13	61.9	6785	3	Q20065	Plasmid pAZ112.	1.18e+02

## ALIGNMENTS

RESULT	1
ID	Q83492 standard; cDNA; 423 BP.
AC	Q83492;
DE	20-SEP-1995 (first entry)
DE	Chimeric antibody 3B9 heavy chain.
KW	Chimeric antibody; antibody engineering; monoclonal antibody;
KW	MAb; interleukin-4; IL-4; allergy; ds.
OS	Homo sapiens; Mus sp.
FH	Key Location/Qualifiers
FT	CDS 1..423
FT	/*tag= a
FT	sig_peptide 1..57
FT	/*tag= b
FT	mat_peptide 58..423
FT	/*tag= c
PN	W09507301-A.
PD	16-MAR-1995.
PF	07-SEP-1994; U10308.
PR	07-SEP-1993; US-117366.
PR	14-OCT-1993; US-136783.
PA	(SMIK ) SMITHKLINE BEECHAM CORP.
PA	(SMIK ) SMITHKLINE BEECHAM PLC.
PI	Gross MS, Holmes SD, Sylvester DR;

DR WPI; 95-123387/16.  
DR P-PSDB; R70191.  
PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived from high affinity mAbs - useful in treatment of IL-4-mediated PT and IgE-mediated allergic conditions  
PS Disclosure; Fig.3; 9pp; English.  
CC A human/mouse chimeric antibody heavy chain variable region was constructed (given in R70191) that contained the mouse anti-human IL-4 MAb 3B9 variable region including 3 CDRs (R70198-200) and a CC human antibody signal peptide (R70193). The construct was used CC for humanized antibody production.  
SQ Sequence 423 BP; 87 A; 115 C; 110 G; 111 T;  
  
Query Match 100.0%; Score 21; DB 14; Length 423;  
Best Local Similarity 100.0%; Pred. No. 5.62e-03;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Db 151 actctgtatgggtgtgagc 171  
|||||  
Qy 1 ACTTCTGATGGGTGTGAGC 21  
  
RESULT 2  
ID Q83491 standard; cDNA; 483 BP.  
AC Q83491;  
DT 20-SEP-1995 (first entry)  
DE Mouse MAb 3B9 heavy chain.  
KW Chimeric antibody; humanized antibody; antibody engineering;  
KW monoclonal antibody; MAb; interleukin-4; IL-4; allergy; ds.  
OS Mus sp.  
FH Key Location/Qualifiers  
FT CDS 64..483  
FT /\*tag= a  
FT sig\_peptide 64..120  
FT /\*tag= b  
FT mat\_peptide 121..483  
FT /\*tag= c  
PN W09507301-A.  
PD 16-MAR-1995.  
PF 07-SEP-1993; U10308.  
PR 07-SEP-1993; US-117366.  
PR 14-OCT-1993; US-136783.  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
PA (SMIK ) SMITHKLINE BEECHAM PLC.  
PI Gross MS, Holmes SD, Sylvestre DR;  
DR WPI; 95-123387/16.  
DR P-PSDB; R70190.  
PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived from high affinity mAbs - useful in treatment of IL-4-mediated PT and IgE-mediated allergic conditions  
PS Disclosure; Fig.2; 9pp; English.  
CC Spleen cells from mice immunized with human IL-4 were used to prepare CC hybridomas, which were screened for anti-IL-4 MAb secretion. Only CC clone 3B9 was positive. cDNA clones of the 3B9 light and heavy CC chains were cloned into pGEM7f+ and transformed into E. coli CC DH5-alpha. The clones were sequenced (Q83490-91), and used for CC antibody engineering.  
SQ Sequence 483 BP; 108 A; 130 C; 124 G; 121 T;  
  
Query Match 100.0%; Score 21; DB 14; Length 483;  
Best Local Similarity 100.0%; Pred. No. 5.62e-03;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Db 211 actctgtatgggtgtgagc 231

Qy 1 ACTTCTGATGGGTGTGAGC 21  
|||||  
RESULT 3  
ID Q70612 standard; DNA; 738 BP.  
AC Q70612;  
DT 28-APR-1995 (first entry)  
DE IL-6 binding inhibitor DNA.  
KW Human interleukin-6 binding inhibitor; IL-6; rheumatoid arthritis;  
KW septic shock; multiple myeloma; ss.  
OS Homo sapiens.  
PN EP-617126-A.  
PD 28-SEP-1994.  
PF 16-FEB-1994; 102346.  
PR 17-FEB-1993; JP-028173.  
PA (AJIN ) AJINOMOTO KK.  
PI Hamuro J, Nakazawa H, Shimamura T;  
DR WPI; 94-295777/37.  
DR P-PSDB; R58612.  
PT Polypeptide inhibiting binding of human interleukin-6 (IL-6) to PT its receptor - useful for treating auto-immune disease induced PT or aggravated by IL-6  
PS Claim 9; Page 19; 26pp; English.  
CC Q70612 codes for human interleukin-6 binding inhibitor, the CC polypeptide described in R58612. This polypeptide inhibits the CC binding of human IL-6 to its receptor, and can therefore be CC useful in the treatment of a variety of autoimmune diseases;  
CC specifically in the treatment of rheumatoid arthritis, septic CC shock due to bacterial infection and multiple myeloma.  
SQ Sequence 738 BP; 187 A; 189 C; 180 G; 182 T;  
  
Query Match 100.0%; Score 21; DB 12; Length 738;  
Best Local Similarity 100.0%; Pred. No. 5.62e-03;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Db 457 actctgtatgggtgtgagc 477  
|||||  
Qy 1 ACTTCTGATGGGTGTGAGC 21  
  
RESULT 4  
ID Q51746 standard; cDNA; 91 BP.  
AC Q51746;  
DT 31-MAY-1994 (first entry)  
DE Oligonucleotide probe MK14-A  
KW Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;  
KW ss.  
OS Synthetic.  
PN EP-571911-A.  
PD 01-DEC-1993.  
PF 24-MAY-1993; 108325.  
PR 26-MAY-1992; US-889651.  
PA (BECT ) BECTON DICKINSON CO.  
PI Shank DD, Spears PA;  
DR WPI; 93-378944/48.  
PT New oligonucleotide probes specific for Mycobacteria - used for PT detection and amplification of Mycobacteria nucleic acid in PT samples  
PS Claim 3; Page 14; 23pp; English.  
CC Oligonucleotide probe MK14-A consists of nucleotides 5-95 of MK14 CC (Q51735). It hybridized to all spp. of mycobacteria tested, but CC cross reacted to a few non-mycobacterial spp. The probe may CC be useful as an initial screen for mycobacterial infection.

```

CC See also Q5173S-45 and Q5174T-59.
SQ Sequence   91 BP;    5 A;   17 C;   15 G;    4 T;

Query Match      95.2%; Score 20; DB 9; Length 91;
Best Local Similarity 0.0%; Pred.No. 2.11e-02;
Matches          0; Conservative 20; Mismatches 0; Indels 0; Gaps 0;

Db       22 vshhsvhvhhvvhhvsvvv 41
        ::::~::~:~::~:~::~:~::
Cp       21 GCTCACACCATACAGAG 2

RESULT      5
ID Q68709 standard; cDNA to mRNA; 366 BP.
AC Q68709;
DT 08-FEB-1995 (first entry)
DE Humanised MAb H-chain coding sequence.
KW Human; mouse; murine; heavy; light; chain; monoclonal; antibody;
KW complementarity determining region; CDR; IgG; kappa; IIIB; IILN; ds.
OS Chimeric - Mus musculus.
OS Chimeric - Homo sapiens.
PN J06141885-A.
PD 24-MAY-1994.
PF 05-NOV-1992; 322476.
PR 05-NOV-1992; JP-322476.
PA (KAGA ) ZH KAKAKU & KESSEI RYOHO KENKYUSHO.
DR WPI; 94-205040/25.
PT P-PSDB; R54101.
PR Recombinant anti-HIV monoclonal antibody - capable of
PT neutralising strains which can not be neutralised by anti-IIIB
PT and IILN antibodies
PS PS Disclosure; Page 13; 23pp; Japanese.
CC The sequences given in Q68709-10 encode the heavy and light chains
CC respectively of the humanised monoclonal antibody (MAB) of the
CC invention. The antibody has the ability to neutralise human
CC immunodeficiency virus. The antibody is classified as IgG kappa and
CC has the sequence RIQPCR or RVQPCR in the principal neutralising
CC domain. The antibody may be used to neutralise the clinically
CC separate strains which cannot be neutralised by the neutralising
CC antibodies against IIIB and IILN strains.
SQ Sequence 366 BP; 85 A; 98 C; 84 G; 99 T;

Query Match      90.5%; Score 19; DB 11; Length 366;
Best Local Similarity 95.2%; Pred.No. 7.80e-02;
Matches          0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db       91 acttttggtggtgtgcac 111
        |||| ||||||~~~~~|
Qy       1 ACTTCTGGTATGGGTGTGACC 21

RESULT      6
ID Q24650 standard; DNA; 45 BP.
AC Q24650;
DT 10-NOV-1992 (first entry)
DE PCR Primer C for amplifying HUMDXCH.23.
KW Polymerase chain reaction; CAMPATH-IH; rat anti-digoxin MAb; DX48;
KW human IgG1 heavy chain; humanised antibody; PCR grafting; ss.
OS Synthetic.
PN W09207075-A.
PD 30-APR-1992.
PF 08-OCT-1991; G01744.
PR 10-OCT-1990; GB-022011.
PA (WELL ) WELLCOME FOUND LTD.

```

PI	Crowe JS, Lewis AP; WPI; 92-167155/20.	Prepn. of chimeric humanised antibodies - using a new polymerase chain reaction technique
PT	Example 1; Page 33; 67pp; English.	
PS	Primer C is made up of the positive strand sequence of DX48 CDRH1, complementary to the CDRH1 region of primer B (Q24649), running into the 5' end of the CAMPATH-1H FRH2. Primer C was used with primer D (Q24651) to PCR-amplify fragment CD (Q24653) of HUMDXCH.23 which contains the DX48 CDRH1 sequence. A second fragment (AB) was generated from the same template, but using primers A and B (Q24648-9), which also contained the DX48 CDRH1 sequence such that on denaturation and reannealing the overlapping sequences of AB and CD can anneal.	
SC	Sequence 45 BP; 9 A; 8 C; 18 G; 10 T;	
Query Match	81.0%; Score 17; DB 4; Length 45;	
Best Local Similarity	90.5%; Pred. No. 9.99e-01;	
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;		
Db	1 acttatgtatgggtctgggc 21 	
Qy	1 ACTTCTGGTATGGGTGAGC 21	
RESULT 7		
ID	Q24653 standard; DNA; 139 BP.	
AC	Q24653; 1992 (first entry)	
DT	10-NOV-1992	
DE	Fragment CD of HUMDXCH.23 humanised antibody.	
KW	Polymerase chain reaction; CAMPATH-1H; rat anti-digoxin Mab; DX48; human IgG1 heavy chain; humanised antibody; PCR grafting; ds.	
OS	Synthetic.	
FT	Key Location/Qualifiers	
FT	misc_feature 1..48	
FT	/*tag= a	
FT	/note= "DX48 CDRH1"	
FT	misc_feature 49..108	
FT	/*tag= b	
FT	/note= "Represents insert of 117bp"	
FT	misc_feature 109..139	
FT	/*tag= c	
FT	/note= "3' terminus of CAMPATH-1H CH3"	
PN	W09207075-A.	
PD	30-APR-1992.	
PF	08-OCT-1991; G01744.	
PR	10-OCT-1990; GB-022011.	
PA	(WELL ) WELLCOME FOUND LTD. Crowe JS, Lewis AP; WPI; 92-167155/20.	
DR	Prepn. of chimeric humanised antibodies - using a new polymerase chain reaction technique	
PT	Example 1; Page 36; 67pp; English.	
PS	Fragment CD was generated by PCR using the humanised antibody HUMDXCH.23 as template (see Q29298). Primers C and D were used in the PCR reaction; Primer C is made up of the positive strand sequence of DX48 CDRH1, complementary to the CDRH1 region of primer B (Q24649), running into the 5' end of the CAMPATH-1H FRH2 and Primer D corresponds to a negative strand oligonucleotide incorporating the HindIII site at the 3' terminus of HUMDXCH.23. Fragment CD overlaps with fragment AB (Q24652) and the two fragments were annealed to form a template for secondary PCR.	
SC	Sequence 139 BP; 17 A; 14 C; 31 G; 17 T;	

Mar 19 08:22

US-08-612-929-21.mg

7

Query Match 81.0%; Score 17; DB 4; Length 139;  
Best Local Similarity 90.5%; Pred. No. 9,99e-01;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 1 acttatggtatggtgtgggc 21  
||||| ||||||| ||||| ||

Qy 1 ACTTCTGGTATGGGTGTGACC 21

RESULT 8

ID Q24652 standard; DNA; 207 BP.  
AC Q24652;  
DT 10-NOV-1992 (first entry)  
DE Fragment AB of HUMDXCH.23 humanised antibody.  
KW Polymerase chain reaction; CAMPATH-1H; rat anti-digoxin MAb; DX48;  
KW human IgG1 heavy chain; humanised antibody; PCR grafting; ds.  
OS Synthetic.

FH Key Location/Qualifiers  
FT misc\_feature 1..42  
FT /\*tag= a  
FT /note= "5' end of HUMDXCH.23, including start codon  
FT of CAMPATH-1H leader sequence"  
FT misc\_feature 160..186  
FT /\*tag= b  
FT /note= "3' 27bp of CAMPATH-1H FRH1"  
FT misc\_feature 187..207  
FT /\*tag= c  
FT /note= "DX48 CDRH1 sequence"  
PN W09207075-A.

PD 30-APR-1992.  
PF 08-OCT-1991; G01744.  
PR 10-OCT-1990; GB-022011.  
PA (WELL ) WELLCOME FOUND LTD.  
PI Crowe JS, Lewis AP;  
DR WPI; 92-167155/20.  
PT Prepn. of chimeric humanised antibodies - using a new polymerase  
PT chain reaction technique  
PS Example 1; Page 34 and Fig 2; 67pp; English.  
CC Fragment AB was generated by PCR using the humanised antibody  
CC HUMDXCH.23 as template (see Q29298). Primers A and B were used  
CC in the PCR reaction; Primer A corresponds to a positive strand  
CC oligonucleotide incorporating the HindIII site at the 5' terminus  
CC of HUMDXCH.23 and Primer B possesses negative strand sequence from  
CC the 3' end of the CAMPATH-1H FRH1 region (with point mutations to  
CC convert Phe 27 and Thr 30 of CAMPATH-1H back to the Ser residues  
CC present in the NEW FRH1) together with the CDRH1 sequence of DX48  
CC in place of the CAMPATH-1H CDRH1. Fragment AB overlaps with  
CC fragment CD (Q24653) and the two fragments were annealed to form a  
CC template for secondary PCR.  
SQ Sequence 207 BP; 20 A; 24 C; 24 G; 22 T;

Query Match 81.0%; Score 17; DB 4; Length 207;  
Best Local Similarity 90.5%; Pred. No. 9,99e-01;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 187 acttatggtatggtgtgggc 207

||||| ||||||| ||||| ||

Qy 1 ACTTCTGGTATGGGTGTGACC 21

RESULT 9

ID Q24654 standard; DNA; 265 BP.  
AC Q24654;  
DT 10-NOV-1992 (first entry)

Mar 19 08:22

US-08-612-929-21.mg

8

DE Fragment AD of HUMDXCH.23 humanised antibody.  
KW Polymerase chain reaction; CAMPATH-1H; rat anti-digoxin MAb; DX48;  
KW human IgG1 heavy chain; humanised antibody; PCR grafting; ss.  
OS Synthetic.

FH Key Location/Qualifiers  
FT misc\_feature 1..42  
FT /\*tag= a  
FT /note= "5' end of HUMDXCH.23, including start codon  
FT of CAMPATH-1H leader sequence"  
FT misc\_feature 43..102  
FT /\*tag= b  
FT /note= "represents 117bp insert"  
FT misc\_feature 103..129  
FT /\*tag= c

FT /note= "3' 27bp of CAMPATH-1H FRH1 in which  
FT point mutations convert Phe 27 and Thr 30  
FT of CAMPATH-1H back to the Ser residues  
FT present in NEW FRH1"  
FT misc\_feature 130..150  
FT /\*tag= d  
FT /note= "DX48 CDRH1"  
FT misc\_feature 151..174  
FT /\*tag= e  
FT /note= "CAMPATH-1H FRH2"  
FT misc\_feature 175..234  
FT /\*tag= f  
FT /note= "represents insert of 1206bp"  
FT misc\_feature 235..265  
FT /\*tag= g

FT /note= "3' terminus of CAMPATH-1H CH3"  
PN W09207075-A.  
PD 30-APR-1992.  
PF 08-OCT-1991; G01744.  
PR 10-OCT-1990; GB-022011.  
PA (WELL ) WELLCOME FOUND LTD.  
PI Crowe JS, Lewis AP;  
DR WPI; 92-167155/20.  
PT Prepn. of chimeric humanised antibodies - using a new polymerase  
PT chain reaction technique  
PS Example 1; Page 36; 67pp; English.  
CC Primer A (Q24648) was used with Primer D (Q24651) in a secondary PCR  
CC reaction to generate fragment AD (Q24654). The secondary PCR  
CC used as template fragments AB and CD (see Q24652 and Q24653)  
CC annealed together. The two fragments constitute the whole length of  
CC the HUMDXCH.23 insert but with point mutations to convert Phe 27  
CC and Thr 30 of CAMPATH-1H back to Ser residues present in the NEW  
CC FRH1 and the CAMPATH-1H CDRH1 replaced by the CDRH1 sequence of  
CC DX48.

SQ Sequence 265 BP; 34 A; 36 C; 44 G; 31 T;  
Query Match 81.0%; Score 17; DB 4; Length 265;  
Best Local Similarity 90.5%; Pred. No. 9,99e-01;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 130 acttatggtatggtgtgggc 150

||||| ||||||| ||||| ||

Qy 1 ACTTCTGGTATGGGTGTGACC 21

RESULT 10

ID T09300 standard; DNA; 360 BP.  
AC T09300;  
DT 25-JUL-1996 (first entry)  
DE Murine anti-Protein C MAb HPC-4 VH gamma mature protein coding region.

KW Epitope; activation; heavy chain; protein C; vitamin K; plasma protein;  
 KW zymogen; cleavage; mouse; humanised antibody; variable region;  
 KW light chain; inhibition; anticoagulant; coagulation; tumour; ss.  
 OS Mus musculus.  
 PN W09534652-A1.  
 PD 21-DEC-1995.  
 PF 09-JUN-1995; 007372.  
 PR 10-JUN-1994; US-259321.  
 PA (OKLA-) OKLAHOMA MED RES FOUND.  
 PI Esmen CT, Rezaie A;  
 DR WPI; 96-049681/05.  
 DR P-PSDB; R88109.  
 PT Calcium-binding monoclonal antibody immunoreactive with Protein C -  
 PT inhibits Protein C anticoagulant activation by  
 PT thrombin-thrombomodulin, e.g. for treating tumours  
 PS Claim 4; Page 30; 41pp; English.  
 CC This is the nucleotide sequence encoding the mature protein from the  
 CC murine anti-protein C monoclonal antibody HPC-4 heavy chain variable  
 CC region (VH gamma). HPC-4 recognises the activation peptide region  
 CC (888106) of the heavy chain of protein C, a vitamin K-dependent plasma  
 CC protein zymogen. Protein C is activated to activated protein C (APC)  
 CC by cleavage between the Arg-Leu amino acid contained within the  
 CC activation peptide sequence. HPC-4 prevents protein C activation to  
 CC APC by binding to this region. The DNA sequences encoding the variable  
 CC regions of the heavy and light chains of the antibody (T09299-302) were  
 CC used to construct humanised antibodies using the PCR primers T09303-9.  
 CC The humanised antibodies are useful as inhibitors of coagulation and can  
 CC be used for the treatment of tumours by inhibiting the anticoagulant  
 CC activity of APC by preventing conversion of protein C to APC.  
 SQ Sequence 360 BP; 82 A; 91 C; 95 G; 92 T;

Query Match 81.0%; Score 17; DB 19; Length 360;  
 Best Local Similarity 100.0%; Pred. No. 9.99e-01;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 91 actctgtgtatgggtgt 107  
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 QY 1 ACTTCTGGTATGGGTGT 17

## RESULT 11

ID T09299 standard; DNA; 417 BP.  
 AC T09299;  
 DT 25-JUL-1996 (first entry)  
 DE Murine anti-Protein C MAb HPC-4 VH gamma coding region.  
 KW Epitope; activation; heavy chain; protein C; vitamin K; plasma protein;  
 KW zymogen; cleavage; mouse; humanised antibody; variable region;  
 KW light chain; inhibition; anticoagulant; coagulation; tumour; ss.  
 OS Mus musculus.  
 FH Key Location/Qualifiers  
 FT sig\_peptide 1..57  
 FT /tag= a  
 FT mat\_peptide 58..417  
 FT /tag= b  
 PN W09534652-A1.  
 PD 21-DEC-1995.  
 PF 09-JUN-1995; 007372.  
 PR 10-JUN-1994; US-259321.  
 PA (OKLA-) OKLAHOMA MED RES FOUND.  
 PI Esmen CT, Rezaie A;  
 DR WPI; 96-049681/05.  
 DR P-PSDB; R88107.  
 PT Calcium-binding monoclonal antibody immunoreactive with Protein C -  
 PT inhibits Protein C anticoagulant activation by

PT thrombin-thrombomodulin, e.g. for treating tumours  
 PS Claim 4; Page 29-30; 41pp; English.  
 CC This is the nucleotide sequence encoding the heavy chain variable region  
 CC from the murine anti-protein C monoclonal antibody HPC-4 which recognises  
 CC the activation peptide region (888106) of the heavy chain of protein C,  
 CC a vitamin K-dependent plasma protein zymogen. Protein C is converted to  
 CC activated protein C (APC) by cleavage between the Arg-Leu amino acid  
 CC contained within the activation peptide sequence. HPC-4 prevents protein  
 CC C activation to APC by binding to this region. The DNA sequences encoding  
 CC the variable regions of the heavy and light chains of the antibody  
 CC (T09299-302) were used to construct humanised antibodies using the PCR  
 CC primers T09303-9. The humanised antibodies are useful as inhibitors of  
 CC coagulation and can be used for the treatment of tumours by inhibiting  
 CC the anticoagulant activity of APC by preventing conversion of protein C  
 CC to APC.  
 SQ Sequence 417 BP; 89 A; 108 C; 106 G; 114 T;

Query Match 81.0%; Score 17; DB 19; Length 417;  
 Best Local Similarity 100.0%; Pred. No. 9.99e-01;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 148 actctgtgtatgggtgt 164  
 |||||  
 QY 1 ACTTCTGGTATGGGTGT 17

## RESULT 12

ID Q64166 standard; cDNA to mRNA; 429 BP.  
 AC Q64166;  
 DT 29-DEC-1994 (first entry)  
 DE Sequence of mouse VH showing the sequences of recombinant  
 DE anti-FHV-1 antibody CDRs 1, 2 and 3.  
 KW Feline herpes virus; FHV-1; monoclonal antibody; CDR;  
 KW complementarity determining region; ss.  
 OS Mus musculus.  
 FH Key Location/Qualifiers  
 FT CDS 1..429  
 FT /tag= a  
 FT misc feature 19  
 FT /tag= b  
 FT /label= MHL341  
 FT misc feature 385..429  
 FT /tag= c  
 FT /label= MJH3  
 PN W09412661-A.  
 PD 09-JUN-1994.  
 PF 25-NOV-1993; J01724.  
 PR 28-NOV-1992; JP-341255.  
 PA (KAGA) CEMO SERO THERAPEUTIC RES INST.  
 PI Kimachi K, Maeda H, Nishiyama K, Tokiyoshi S;  
 DR WPI; 94-200288/24.  
 DR P-PSDB; R54092.  
 PT Feline monoclonal antibody and recombinant antibodies specific  
 PT for FHV-1 - for detection, treatment and prevention of FHV-1  
 PT infection.  
 PS Disclosure; Page 17-18; 53pp; Japanese.  
 CC The inventors claim a monoclonal antibody against feline herpes  
 CC virus (FHV-1). They also claim a recombinant antibody against FHV-1  
 CC and fragments of VH and VL CDR1, CDR2 and CDR3. The antibodies are  
 CC used in the detection, treatment and prevention of FHV-1. The  
 CC sequences of the CDRs in the VH of the recombinant anti-FHV-1  
 CC antibody are given in R54092. The sequences of the CDRs in the VL of  
 CC the recombinant anti-FHV-1 antibody are given in R54093. These CDR  
 CC sequences are claimed.



SQ Sequence 429 BP; 84 A; 116 C; 109 G; 120 T;  
Query Match 76.2%; Score 16; DB 11; Length 429;  
Best Local Similarity 100.0%; Pred. No. 3.45e+00;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 148 actctggtatggtg 163  
|||||  
Qy 1 ACTTCTGATGGG 16

RESULT 13  
ID Q78948 standard; DNA; 630 BP.  
DT 01-AUG-1995 (first entry)  
DE Human immunoglobulin Vh gene #10.  
KW Primer; PCR; amplify; human; immunoglobulin; variable; heavy chain;  
KW cosmid; placenta; vector; pJB81; E.coli; mammalian; ds.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT CDS 71..495  
FT /tag= a  
FT /product= human immunoglobulin variable heavy chain  
FT intron 114..199  
FT /tag= b  
FT misc\_signal 322..324  
FT /tag= c  
FT /transl\_except= unused termination codon  
FT misc\_signal 373..375  
FT /tag= d  
FT /transl\_except= unused termination codon  
FT misc\_signal 496..498  
FT /tag= e  
FT /note= "miscellaneous signal, does not conform to  
FT termination or splice site sequence"  
PN W09426895-A.  
PD 24-NOV-1994.  
PF 10-MAY-1993; J00603.  
PR 10-MAY-1993; W0-J00603.  
PA (NIBS) JAPAN TOBACCO INC.  
PI Honjo T, Matsuda F;  
DR WPI; 95-006791/01.  
DR P-PSDB; R66304.  
PT DNA fragment comprising human immunoglobulin Vh genes - for the  
PT production of human immunoglobulin in mammalian hosts  
PS Claim 19; Page 43-44; 130pp; Japanese.  
CC A series of genes (Q78939-79002) encoding human immunoglobulin variable  
CC heavy chains. The genes were isolated and cloned from a series of cosmid  
CC constructs: Y202; Y103; Y21; Y6; Y24; 3-31; M84; M18 and M131, by PCR  
CC amplification using primers Q78917-38. The genes are subdivided into 5  
CC families of Vh genes. The fragments cover a region of 800 kb. The DNA  
CC fragments were isolated from high molecular weight DNA from human  
CC placenta. The DNA was partially digested with TaqI restriction enzyme.  
CC The fragments were separated by gel electrophoresis and 35-45 kb fractions  
CC were collected. The fragments were ligated with ClaI-digested cosmid  
CC vector pJB81. The ligation products were in vitro packed and infected  
CC into E.coli 490A. The fragments were then subcloned by colony  
CC hybridisation. The Vh genes and the DNA fragments encoding them are  
CC useful in producing human immunoglobulin in mammalian hosts.  
SQ Sequence 630 BP; 141 A; 179 C; 148 G; 162 T;

Query Match 76.2%; Score 16; DB 13; Length 630;  
Best Local Similarity 94.4%; Pred. No. 3.45e+00;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 301 actctggaatggtgtg 318  
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Qy 1 ACTTCTGATGGGTG 18

RESULT 14  
ID Q37056 standard; DNA; 812 BP.  
AC Q37056;  
DT 12-JUL-1993 (first entry)  
DE Rat immunoglobulin H chain promoter and variable region coding sequence.  
KW Promoter; variable; region; rat; immunoglobulin; heavy; H; chain;  
KW humanised; chimeric; antibody; expression vector; ss.  
OS Rattus rattus.  
FH Key Location/Qualifiers  
FT CDS 300..806  
FT /tag= a  
FT exon 300..345  
FT /tag= b  
FT /number= Exon 1  
FT intron 346..429  
FT /tag= c  
FT /number= Intron 1  
FT exon 430..806  
FT /tag= d  
FT /number= Exon 2  
FT sig\_peptide 300..441  
FT /tag= e  
FT mat\_peptide 442..806  
FT /tag= f  
FT TATA\_signal 256..262  
FT /tag= g  
PN EP-533199-A.  
PD 24-MAR-1993.  
PF 18-SEP-1992; 116026.  
PR 18-SEP-1991; JP-238375.  
PA (KYOW) KYOWA HAKKO KOGYO CO LTD.  
PI Hanai N, Hasegawa M, Kuwana Y, Miyaji H, Shitara K;  
DR P-PSDB; R33255.  
PT Humanised chimeric antibody prodn. against ganglioside GD3 - for  
PT treating cancers, such as melanoma, neuroblastoma, etc.  
PS Disclosure; Page 27-28; 63pp; English.  
CC This sequence contains the promoter and variable regions of the rat  
CC immunoglobulin heavy (H) chain. This sequence was used in the  
CC construction of humanised chimeric antibody expression vectors. In  
CC these humanised antibodies none of the amino acids of the non-human  
CC animal Ab variable region have been changed.  
SQ Sequence 812 BP; 201 A; 205 C; 186 G; 220 T;

Query Match 71.4%; Score 15; DB 6; Length 812;  
Best Local Similarity 85.7%; Pred. No. 1.16e+01;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 531 acttatgtatgtgtgtggc 551  
|||||  
Qy 1 ACTTCTGATGGGTGAC 21

RESULT 15  
ID Q04729 standard; DNA; 2352 BP.  
AC Q04729;  
DT 12-OCT-1990 (first entry)  
DE Xylene oxygenase gene.

Mar 19 08:22

US-08-612-929-21.mg

13

KW Xylene oxygenase; ds.  
FH Key Location/Qualifier  
FT CDS 27..1136  
FT /\*tag= a  
FT CDS 1286..2338  
FT /\*tag= b  
PN J02119777-A.  
PD 7-MAY-1990.  
PF 28-OCT-1988; 272328.  
PR 28-OCT-1988; JP-272328.  
PA (MITU) Mitsubishi Kasei Corp, (MITS) Mitubishi.  
DR WPI; 90-182380/24.  
DR N-PSDB; R05384 & R05385.  
PT Xylene oxygenase gene - used to create the blue colour of flowering plants.  
PS Claim 2; Page 581; 15pp; Japanese.  
CC Useful in creating the blue colour from flowering plants.  
SQ Sequence 2352 BP; 545 A; 518 C; 629 G; 660 T;

Query Match 71.4%; Score 15; DB 1; Length 2352;  
Best Local Similarity 89.5%; Pred. No. 1.16e+01;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 1506 cttctgctatgggtctgaag 1524

Qy 2 CTTCTGCTATGGGTCTGAG 20

Search completed: Wed Mar 19 08:23:59 1997  
Job time : 15 secs.

\*\*\*\*\*

WATERMAN

(TM)

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MPsrch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed Mar 19 08:27:54 1997; MaePar time 68.40 Seconds  
309,494 Million cell updates/sec

Tabular output not generated.

Title: >US-08-612-929-23  
Description: (1-48) from US08612929.seq  
Perfect Score: 48  
N.A. Sequence: 1 CACATTACTGGCATGATGACAGCGCTATAACCCATCCTGAAGAGC 48  
Comp: GTGTAAATGACCCCTACTACTCTGCGGATATGGCTAGGAGGACTTCGCG

Scoring table: TABLE default  
Gap 10

Nmatch STD : Dbase 0; Query 0

Searched: 630489 seqs, 220513910 bases x 2

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: EST-STS  
1:EST1 2:EST2 3:EST3 4:EST4 5:EST5 6:EST6 7:EST7 8:EST8  
9:EST9 10:EST10 11:EST11 12:EST12 13:EST13 14:EST14  
15:EST15 16:EST16 17:EST17 18:EST18 19:EST19 20:EST20  
21:EST21 22:EST22 23:EST23 24:EST24 25:EST25 26:EST26  
27:EST27 28:EST28 29:EST29 30:EST30 31:EST31 32:EST32  
33:EST33 34:EST34 35:EST35 36:EST36 37:EST37 38:EST38  
39:EST39 40:EST40 41:EST41 42:EST42 43:EST43 44:EST44  
45:EST45 46:EST46 47:EST47 48:EST48 49:EST49 50:EST50  
51:EST51 52:EST52 53:EST53 54:EST54 55:EST55 56:EST56  
57:EST57 58:EST58 59:EST59 60:EST60 61:EST61 62:EST62  
63:EST63 64:EST64 65:EST65 66:EST66 67:EST67 68:EST68  
69:EST69 70:EST70 71:EST71 72:EST72 73:EST73 74:EST74  
75:EST75 76:EST76 77:EST77 78:EST78 79:EST79 80:EST80  
81:EST81 82:EST82 83:EST83 84:EST84 85:EST85 86:EST86  
87:EST87 88:EST88 89:EST89 90:EST90 91:EST91 92:EST92  
93:EST93 94:EST94 95:EST95 96:EST96 97:EST97 98:EST98  
99:EST99  
EST-STS-TWO  
100:EST100 101:EST101 102:EST102 103:EST103 104:EST104  
105:EST105 106:EST106 107:EST107 108:EST108 109:EST109  
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115:EST115 116:EST116 117:EST117 118:EST118 119:EST119  
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Database:

130:STS2 131:STS3 132:STS4 133:STS5 134:STS6 135:STS7  
136:STS8 137:STS9 138:STS10 139:STS11 140:STS12  
141:STS13 142:STS14 143:STS15 144:STS16 145:STS17  
146:STS18 147:STS19 148:STS20 149:STS21 150:STS22  
151:STS23 152:STS24 153:STS25 154:STS26 155:STS27  
156:STS28 157:STS29 158:STS30 159:STS31 160:STS32  
161:STS33 162:STS34 163:STS35 164:STS36 165:STS37  
166:STS38 167:STS39 168:STS40 169:STS41 170:STS42  
171:STS43 172:STS44 173:STS45 174:STS46

Statistics: Mean 7.625; Variance 1.511; scale 5.047

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
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c 2	20	41.7	427	65	yz76f06.sl Homo sapie	4.78e-07
c 3	18	37.5	429	26	yu63d03.sl Homo sapie	2.37e-04
c 4	18	37.5	444	164	zal7b12.sl Homo sapie	2.37e-04
c 5	18	37.5	444	66	zal7b12.sl Homo sapie	2.37e-04
c 6	18	37.5	477	52	Mouse 3'-directed cD	2.37e-04
c 7	17	35.4	389	51	CELI2612 Caenorhabdit	4.51e-03
c 8	17	35.4	434	12	ym47e06.sl Homo sapie	4.51e-03
c 9	17	35.4	455	77	yf47q05.sl Homo sapie	4.51e-03
c 10	17	35.4	461	17	14810 Arabidopsis tha	4.51e-03
c 11	17	35.4	504	90	13443 Arabidopsis tha	4.51e-03
c 12	17	35.4	525	117	ycl4e01.sl Homo sapie	4.51e-03
c 13	16	33.3	167	130	human STS STS1-cSRL-2	7.57e-02
c 14	16	33.3	176	64	ly1330F Homo sapiens	7.57e-02
c 15	16	33.3	182	173	D. melanogaster STS d	7.57e-02
c 16	16	33.3	182	156	D. melanogaster STS d	7.57e-02
c 17	16	33.3	206	2	A. thaliana transcrib	7.57e-02
c 18	16	33.3	211	46	Human fetal brain cDN	7.57e-02
c 19	16	33.3	226	71	Oryza sativa clone pF	7.57e-02
c 20	16	33.3	253	110	EST52070 Homo sapiens	7.57e-02
c 21	16	33.3	266	149	ma55e01.rl Soares mou	7.57e-02
c 22	16	33.3	287	59	yy21b11.rl Homo sapie	7.57e-02
c 23	16	33.3	330	4	C.elegans cDNA clone	7.57e-02
c 24	16	33.3	338	74	C.elegans cDNA clone	7.57e-02
c 25	16	33.3	343	104	EST03336 Homo sapiens	7.57e-02
c 26	16	33.3	343	23	yy94e12.rl Homo sapie	7.57e-02
c 27	16	33.3	360	4	C.elegans cDNA clone	7.57e-02
c 28	16	33.3	360	4	C.elegans cDNA clone	7.57e-02
c 29	16	33.3	360	4	C.elegans cDNA clone	7.57e-02
c 30	16	33.3	362	35	yy60f12.sl Homo sapie	7.57e-02
c 31	16	33.3	410	158	za24b11.rl Homo sapie	7.57e-02
c 32	16	33.3	410	145	za24b11.rl Homo sapie	7.57e-02
c 33	16	33.3	420	73	yy92d06.rl Homo sapie	7.57e-02
c 34	16	33.3	441	55	yy04b09.sl Homo sapie	7.57e-02
c 35	16	33.3	471	56	yx54e07.rl Homo sapie	7.57e-02
c 36	16	33.3	473	159	yy42d02.rl Homo sapie	7.57e-02
c 37	16	33.3	473	141	yy42d02.rl Homo sapie	7.57e-02
c 38	16	33.3	475	63	yy25g02.sl Homo sapie	7.57e-02
c 39	16	33.3	494	57	yy53b12.sl Homo sapie	7.57e-02
c 40	16	33.3	500	26	yy70h04.rl Homo sapie	7.57e-02
c 41	16	33.3	521	10	yl70a10.rl Homo sapie	7.57e-02
c 42	16	33.3	600	114	9871 Arabidopsis tha	7.57e-02

Mar 19 08:27

US-08-612-929-23.rst

3

c 43 16 33.3 610 86 R52751 yg99q06.r1 Homo sapie 7.57e-02  
 44 16 33.3 2881 137 H5MSK1883 human chromosome 7 ST 7.57e-02  
 45 16 33.3 2881 174 H5MSW1883 human chromosome 7 ST 7.57e-02

## ALIGNMENTS

RESULT 1  
 ID HS724291 standard; RNA; EST; 427 BP.  
 AC N62724;  
 DT 02-MAR-1996 (Rel. 47, Created)  
 DT 02-MAR-1996 (Rel. 47, Last updated, Version 1)  
 DE yz76f06.s1 Homo sapiens cDNA clone 288995 3' .  
 KW EST.  
 OS Homo sapiens (human)  
 OC Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;  
 OC Theria; Eutheria; Primates; Haplorhini; Catarrhini; Homidae.  
 RN [1]  
 RP 1-427  
 RA Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M.,  
 RA Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M.,  
 RA Parsons J., Rifkin L., Rohlfing T., Soares M., Tan F.,  
 RA Trevasaki E., Waterston R., Williamson A., Wohlmann P., Wilson R.;  
 RT \*The WashU-Merck EST Project\*;  
 RL Unpublished.  
 CC Contact: Wilson RK WashU-Merck EST Project Washington University  
 CC School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,  
 CC MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email:  
 CC est@watson.wustl.edu Source: IMAGE Consortium, LNL This clone is  
 CC available royalty-free through LNL; contact the IMAGE Consortium  
 CC (info@image.lnl.gov) for further information. NCBI gi: 1210553  
 FH Key Location/Qualifiers  
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 FT 1..427  
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 FT /clone="288995"  
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 NID g1210553  
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 sclerosis 2NHMS3 vector=pT73D (Pharmacia) with a modified  
 polylinker V TYPE: phagemid host=DH10B (ampicillin resistant)  
 Reitel=Not I Rsite2=Eco RI 46 year old male. 1st strand cDNA was  
 primed with a Not I - oligo(dT) primer  
 [5'-TGTTACCAATCTGAAGTGGAGCGCCGCAATTTTTTTTTTTTTTTT-3'],  
 double-stranded cDNA was size selected, ligated to Eco RI adaptors  
 (Pharmacia), digested with Not I and cloned into the Not I and Eco  
 RI sites of a modified pT7 vector (Pharmacia). Library went

Mar 19 08:27

US-08-612-929-23.rst

4

through one round of normalization to a Cot = 5. Library  
 constructed by Bento Soares and M.Fatima Bonaldo. RNA from 4  
 multiple sclerosis lesions from one patient was kindly provided by  
 Dr. Kevin G. Becker (NINDS/NIH).

## ORGANISM

Homo sapiens  
 Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;  
 Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;  
 Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;  
 Eutheria; Archonta; Primates; Catarrhini; Homidae; Homo.

## REFERENCE

## AUTHORS

1 (bases 1 to 427)  
 Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M.,  
 Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M.,  
 Parsons J., Rifkin L., Rohlfing T., Soares M., Tan F.,  
 Trevasaki E., Waterston R., Williamson A., Wohlmann P. and  
 Wilson R.

## TITLE

## JOURNAL

## COMMENT

The WashU-Merck EST Project  
 Unpublished (1995)  
 Contact: Wilson RK  
 WashU-Merck EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 Source: IMAGE Consortium, LNL  
 This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium (info@image.lnl.gov) for further information.

## FEATURES

## source

1..427  
 /organism="Homo sapiens"  
 /clone="288995"  
 /note="human"

BASE COUNT 129 a 76 c 112 g 110 t  
 ORIGIN  
 <1..>427

Query Match 41.7%; Score 20; DB 65; Length 427;  
 Best Local Similarity 79.4%; Pred. No. 4.78e-07;  
 Matches 27; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Db 353 ggatgggtatgctgttcttcataacagtaa 386  
 ||||| ||| ||||| ||||| ||||| |||||

Cp 39 GGATGGGTATAGCGCTTGTCATCATCCAGTAA 6

## RESULT

## LOCUS

## DEFINITION

## ACCESSION

## NID

## KEYWORDS

## SOURCE

3 H64550 429 bp mRNA EST 11-DEC-1995  
 yu63d03.s1 Homo sapiens cDNA clone 238469 3' similar to contains  
 Alu repetitive element; contains THR repetitive element ;  
 H64550  
 q1023290  
 EST.  
 human clone=238469 primer=Promega -21ml3 library=Weizmann Olfactory  
 Epithelium vector=pBluescript SK- host=SOIR cells (kanamycin  
 resistant) Reitel=EcoRI Rsite2=XhoI From 35 year old female. The  
 cDNA was oligo (dT) primed with an XhoI restriction enzyme  
 recognition site and an 18 base poly dT sequence. For the 5' end,  
 the synthesized cDNA termini were treated with T4 DNA polymerase  
 and EcoRI adaptors were ligated to the blunt ends.

## ORGANISM

Homo sapiens  
 Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;  
 Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;  
 Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;



Mar 1908:27

US-08-612-929-23.rst

7

mRNA <1..>444  
 BASE COUNT 101 a 108 c 129 g 105 t 1 others  
 ORIGIN

Query Match 37.5%; Score 18; DB 66; Length 444;  
 Best Local Similarity 75.0%; Pred. No. 2.37e-04;  
 Matches 27; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Db 315 tgggtcagccggtgctccatccctgctacgtgtg 350  
 ||||| |||| |||| ||||| |||| ||||  
 Cp 36 TGGGTATACCGCTTGTCTCATCATCCAGCAATATGTC 1

RESULT 6  
 LOCUS MUSGS00994 477 bp mRNA EST 09-DEC-1995  
 DEFINITION Mouse 3'-directed cDNA, MUSGS00994, clone md0295.  
 ACCESSION D18296  
 NID g1089445  
 KEYWORDS EST(expressed sequence tag); Gene signature (GS); development;  
 transcribed sequence.  
 SOURCE Mus musculus (strain C57BL/6Jsub\_species domesticus, ) decidua  
 tissue (day 6.5-8.5 of gestation) cDNA to mRNA.  
 ORGANISM Mus musculus  
 Eukaryota; Eukaryota; Metazoa; Chordata;  
 Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;  
 Murinae; Mus.

REFERENCE 1 (bases 1 to 477)  
 AUTHORS Kawamoto, S., Okubo, K., Yoshii, J., Katsuki, M. and Matsuura, K.  
 TITLE Analysis of gene expression in mouse embryogenesis by 3'-directed  
 cDNA sequencing  
 JOURNAL Unpublished (1993)  
 COMMENT Submitted (10-Sep-1993) to DDBJ by:  
 Shoko Kawamoto  
 Institute for Cellular and Molecular Biology  
 Osaka University  
 3-1, Yamadaoka  
 Suita, Osaka, 565  
 Japan  
 Phone: 06-879-7992  
 Fax : 06-877-1922  
 Email: shoko@imcb.osaka-u.ac.jp.  
 Location/Qualifiers  
 1..477  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /sub\_species="domesticus"  
 /sequenced\_mol="cDNA to mRNA"  
 /tissue\_type="decidual tissue (day 6.5-8.5 of gestation)"  
 137 a 89 c 95 g 133 t 23 others

BASE COUNT 137 a 89 c 95 g 133 t 23 others  
 ORIGIN

Query Match 37.5%; Score 18; DB 52; Length 477;  
 Best Local Similarity 90.9%; Pred. No. 2.37e-04;  
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 256 tgggtgatgacaaagcgtgta 277  
 ||||| ||||| ||||| ||||  
 Qy 10 TCGGATGATGACAAAGCGCTATA 31

RESULT 7  
 LOCUS M88987 369 bp mRNA EST 16-SEP-1992  
 DEFINITION CEL12G12 Caenorhabditis elegans cDNA clone cm12g12 5'.  
 ACCESSION M88987

Mar 1908:27

US-08-612-929-23.rst

8

NID g275488  
 EST.  
 SOURCE Nematodes clone=cm12g12 library=Chris Martin sorted cDNA library  
 strain=Bristol N2 vector=lambdaphage SHLX2 host=MC1061 Mixed stage  
 hermaphrodite cDNA library. Partially normalized by successively  
 picking groups of clones that didn't hybridize to previously picked  
 clones. Vector: lambdaphage SHLX2 (lipshitz, D.H. et al., Gene  
 88:25-36 (1990)) Host: MC1061.

ORGANISM Caenorhabditis elegans  
 Eukaryota; Animalia; Eumetazoa; Nematoda; Secernentea; Rhabditida;  
 Rhabditina; Rhabditidae; Rhabditidae.

REFERENCE 1 (bases 1 to 389)  
 AUTHORS Waterston, R., Martin, C., Craxton, M., Huynh, C., Coulson, A.,  
 Hillier, L., Durbin, R.K., Green, P., Shownkeen, R., Halloran, N.,  
 Hawkins, T., Wilson, R., Berks, M., Du, Z., Thomas, K., Thierry-Mieg, J.  
 and Sulston, J.  
 TITLE A survey of expressed genes in Caenorhabditis elegans  
 JOURNAL Nature Genet. 1, 114-123 (1992)  
 COMMENT Contact: Waterston R.H. (USA) and Sulston J.E. (UK)  
 (USA) Dept. of Genetics or (UK)  
 (USA) Washington Univ. School of Medicine or (UK) MRC Laboratory of  
 Molecular Biology  
 Box 8232, 4566 Scott Ave., St. Louis, MI 63110, USA, or, Hills  
 Road, Cambridge CB2 2QH, UK  
 Tel: (USA) (314) 3627072 or (UK) (0223) 248011  
 Fax: (USA) (314) 3624137 or (UK) (0223) 402008  
 Email: rwnematode.wustl.edu or jes@mc-lmb.cam.ac.uk.  
 Location/Qualifiers  
 1..389  
 /organism="Caenorhabditis elegans"  
 /clone="cm12g12"  
 /strain="Bristol N2"  
 /note="Nematodes"

BASE COUNT 121 a 63 c 86 g 114 t 5 others  
 ORIGIN

Query Match 35.4%; Score 17; DB 51; Length 389;  
 Best Local Similarity 94.7%; Pred. No. 4.51e-03;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 111 cacattactgtgtatgatg 129  
 ||||| ||||| ||||| |||||  
 Qy 1 CACATTACTGGGATGATG 19

RESULT 8  
 LOCUS H20550 434 bp mRNA EST 03-JUL-1995  
 DEFINITION ym47e06.s1 Homo sapiens cDNA clone 51324 3' similar to gb:M29874  
 CYTOCHROME P450 IIB6 (HUMAN);.  
 ACCESSION H20550  
 NID g889245  
 EST.  
 KEYWORDS EST.  
 SOURCE human clone=51324 library=Soares infant brain 1NIB vector=lafmid BA  
 host=DH10B (ampicillin resistant) primer=Promega -21m13 Rsite=Not  
 I Rsite2=Hind III Whole brain from a 73 days post natal female. 1st  
 strand cDNA was primed with a Not I - oligo(dT) primer [5'  
 AACTGGAAGATTCCGGCCGACGAATTTTTTTTTTTT 3']; double-stranded  
 cDNA was ligated to Hind III adaptors (Pharmacia), digested with  
 Not I and directionally cloned into the Not I and Hind III sites of  
 the Lafmid BA vector. Library went through one round of  
 normalization. Library constructed by Bento Soares and M.Fatima  
 Bonaldo.

ORGANISM Homo sapiens



Db 265 attactgagatggagctcttgctctgtcaccacgggctggagtc 309  
||||| ||||| | | | | | ||||| ||||| |||  
Ov 4 ATTACTGGGATGATCACAAGCGCTATATACCCATCCCTGAACAGC 48





Mar 19 08:27

US-08-612-929-23.rst

15

```
OC Cyclorrhapha; Schizophora; Drosophiloidea; Drosophilidae.
RN [1]
RP 1-182
RA European Drosophila Mapping Consortium;
RT ;
RL Submitted (08-APR-1994) to the EMBL/GenBank/DBJ databases.
RL Michael Ashburner, Department of Genetics, Downing St., Cambridge
RL CB2 3EH, England
RN [2]
RC Updated comments
RA European Drosophila Mapping Consortium;
RT ;
RL Submitted (15-APR-1996) to the EMBL/GenBank/DBJ databases.
RL Michael Ashburner, Department of Genetics, Downing St., Cambridge
RL CB2 3EH, England
CC STS_name = Dm9G3S
CC clone_name = 9G3
CC STS_from_promoter = SP6
CC vector_class = cosmid, Lorient 6
CC origin_of_clone = Oregon-R
CC in_situ_site_primary = 26D
CC in_situ_site_heterochromatin = BH
CC STS_dbSTS_AC = 4932
CC BLAST_program = BLASTN
CC database_searched = EMBL
CC database_version = 45.0 and updates till date_of_search
CC date_of_search = 08-01-1996
CC BLAST_program = BLASTX
CC database_searched = SWISSPROT
CC database_version = 32.0
CC date_of_search = 15-12-1995
FH Key Location/Qualifiers
FH source 1..182
FT /organism="Drosophila melanogaster"
FT /strain="Oregon-R"
FT /clones="9G3"
SQ Sequence 182 BP; 49 A; 35 C; 51 G; 47 T; 0 other;

Query Match 33.3%; Score 16; DB 173; Length 182;
Best Local Similarity 71.1%; Pred. No. 7.57e-02;
Matches 27; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Db 145 ggatggcgaatagatctccattatctcgagtgaatgt 182
||||| ||||| | ||||| |||||
Cp 39 GCATGGCTATACCGCTTGTCATCATCCAGTAATGT 2

Search completed: Wed Mar 19 08:29:11 1997
Job time : 77 secs.
```



DR WPI; 95-123387/16.  
DR P-PSDB; R70191.  
PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived  
PT from high affinity mAbs - useful in treatment of IL-4-mediated  
PT and IgE-mediated allergic conditions  
PS Disclosure; Fig.3; 97pp; English.  
CC A human/mouse chimeric antibody heavy chain variable region was  
CC constructed (given in R70191) that contained the mouse anti-human  
CC IL-4 MAb 3B9 variable region including 3 CDRs (R70198-200) and a  
CC human antibody signal peptide (R70193). The construct was used  
CC for humanized antibody production.  
SQ Sequence 423 BP; 87 A; 115 C; 110 G; 111 T;

Query Match 100.0%; Score 48; DB 14; Length 423;  
Best Local Similarity 100.0%; Pred. No. 2.80e-19;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 214 cacatttactggatgacgaagcgtataaaccatccctgaagc 261  
|||||  
QY 1 CACATTACTGGGATGACGAAGCGCTATAACCCATCCCTCGAAGC 48

## RESULT 2

ID Q83491 standard; cDNA; 483 BP.  
AC Q83491;  
DT 20-SEP-1995 (first entry)  
DE Mouse MAb 3B9 heavy chain.  
KW Chimeric antibody; humanized antibody; antibody engineering;  
KW monoclonal antibody; MAb; Interleukin-4; IL-4; allergy; ds.  
OS Mus sp.  
FH Key Location/Qualifiers  
FT CDS 64..483  
FT /tag= a  
FT sig\_peptide 64..120  
FT /tag= b  
FT mat\_peptide 121..483  
FT /tag= c  
PN W09507301-A.  
PD 16-MAR-1995.  
PE 07-SEP-1994; U10308.  
PR 07-SEP-1993; US-117366.  
PR 14-OCT-1993; US-136783.  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
PA (SMIK ) SMITHKLINE BEECHAM PLC.  
PI Gross MS, Holmes SD, Sylvester DR;  
DR WPI; 95-123387/16.  
DR P-PSDB; R70190.

PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived  
PT from high affinity mAbs - useful in treatment of IL-4-mediated  
PT and IgE-mediated allergic conditions  
PS Disclosure; Fig.2; 97pp; English.  
CC Spleen cells from mice immunized with human IL-4 were used to prepare  
CC hybridomas, which were screened for anti-IL-4 MAb secretion. Only  
CC clone 3B9 was positive. cDNA clones of the 3B9 light and heavy  
CC chains were cloned into pGEM7i+ and transformed into E. coli  
CC DH5-alpha. The clones were sequenced (Q83490-91), and used for  
CC antibody engineering.  
SQ Sequence 483 BP; 108 A; 130 C; 124 G; 121 T;

Query Match 100.0%; Score 48; DB 14; Length 483;  
Best Local Similarity 100.0%; Pred. No. 2.80e-19;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 274 cacatttactggatgacgaagcgtataaaccatccctgaagc 321

QY 1 CACATTACTGGGATGACGAAGCGCTATAACCCATCCCTCGAAGC 48  
|||||

## RESULT 3

ID Q68709 standard; cDNA to mRNA; 366 BP.  
AC Q68709;  
DT 08-FEB-1995 (first entry)  
DE Humanised MAb H-chain coding sequence.  
KW Human; mouse; murine; heavy; light; chain; monoclonal; antibody;  
KW complementarity determining region; CDR; IgG; kappa; IIIB; IIIN; ds.  
OS Chimeric - Mus musculus.  
OS Chimeric - Homo sapiens.  
PN J06141885-A.  
PD 24-MAY-1994.  
PF 05-NOV-1992; 322476.  
PR 05-NOV-1992; JP-322476.  
PA (KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.  
DR WPI; 94-205040/25.  
DR P-PSDB; R54101.  
PT Recombinant anti-HIV monoclonal antibody - capable of  
PT neutralising strains which can not be neutralised by anti-IIIB  
PT and IIIN antibodies  
PS Disclosure; Page 13; 23pp; Japanese.  
CC The sequences given in Q68709-10 encode the heavy and light chains  
CC respectively of the humanised monoclonal antibody (MAb) of the  
CC invention. The antibody has the ability to neutralise human  
CC immunodeficiency virus. The antibody is classified as IgG kappa and  
CC has the sequence RIGPCR or RVGPCR in the principal neutralising  
CC domain. The antibody may be used to neutralise the clinically  
CC separate strains which cannot be neutralised by the neutralising  
CC antibodies against IIIB and IIIN strains.  
SQ Sequence 366 BP; 85 A; 98 C; 84 G; 99 T;

Query Match 87.5%; Score 42; DB 11; Length 366;  
Best Local Similarity 93.8%; Pred. No. 2.82e-15;  
Matches 45; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 154 cacatttactggatgacgaagcgtataaaccatccctgaagc 201  
|||||

QY 1 CACATTACTGGGATGACGAAGCGCTATAACCCATCCCTCGAAGC 48

## RESULT 4

ID Q70612 standard; DNA; 738 BP.  
AC Q70612;  
DT 28-APR-1995 (first entry)  
DE IL-6 binding inhibitor DNA.  
KW Human interleukin-6 binding inhibitor; IL-6; rheumatoid arthritis;  
KW septic shock; multiple myeloma; ss.  
OS Homo sapiens.  
PN EP-617126-A.  
PD 28-SEP-1994.  
PF 16-FEB-1994; 102346.  
PR 17-FEB-1993; JP-028173.  
PA (AJIN ) AJINOMOTO KK.  
PI Hamuro J, Nakazawa H, Shimamura T;  
DR WPI; 94-295777/37.  
DR P-PSDB; R58612.  
PT Polypeptide inhibiting binding of human interleukin-6 (IL-6) to  
PT its receptor - useful for treating autoimmune disease induced  
PT or aggravated by IL-6  
PS Claim 9; Page 19; 26pp; English.  
CC Q70612 codes for human interleukin-6 binding inhibitor, the

CC polypeptide described in R58612. This polypeptide inhibits the  
CC binding of human IL-6 to its receptor, and can therefore be  
CC useful in the treatment of a variety of autoimmune diseases;  
CC specifically in the treatment of rheumatoid arthritis, septic  
CC shock due to bacterial infection and multiple myeloma.  
SQ Sequence 738 BP; 187 A; 189 C; 180 G; 182 T;

	Query Match	87.5%	Score 42;	DB 12;	Length 738;
	Best Local Similarity	93.88;	Pred. No. 2.82e-15;		
	Matches	45;	Conservative	0;	Mismatches 3; Indels
Db	520	cacattttattggatgatgacaaacactataaacccatcccttgaagac	567		
ov	1	CACATTTTACTGGGATGATGACAAAGCGGTATTAACCCATCCCTCGAAGAC	48		

RESULT	5	
ID	T09300 standard; DNA; 360 BP.	
AC	T09300;	
DT	25-JUL-1996 (first entry)	
DE	Murine anti-Protein C MAb HPC-4 VH gamma mature protein coding region.	
KW	Epitope; activation; heavy chain; protein C; vitamin K; plasma protein;	
KW	zymogen; cleavage; mouse; humanised antibody; variable region;	
OS	Light chain; inhibition; anticoagulant; coagulation; tumour; ss.	
PN	Mus musculus.	
PD	W09534652-Al.	
PF	21-DEC-1995.	
PR	09-JUN-1995; U07372.	
PR	10-JUN-1994; US-259321.	
PA	(OKLA-) OKLAHOMA MED RES FOUND.	
PI	Esmon CT, Rezaie A;	
DR	WPI; 96-049681/05.	
DR	P-PSDB; R88109.	
PT	Calcium-binding monoclonal antibody immunoreactive with Protein C -	
PT	inhibits Protein C anticoagulant activation by	
PT	thrombin-thrombomodulin, e.g. for treating tumours	
PS	Claim 4; Page 30; 41pp; English.	

This is the nucleotide sequence encoding the mature protein from the murine anti-protein C monoclonal antibody HPC-4 heavy chain variable region (VH gamma). HPC-4 recognises the activation peptide region (A88106) of the heavy chain of protein C, a vitamin K-dependent plasma protein zymogen. Protein C is activated to activated protein C (APC) by cleavage between the Arg-Leu amino acid contained within the activation peptide sequence. HPC-4 prevents protein C activation to APC by binding to this region. The DNA sequences encoding the variable regions of the heavy and light chains of the antibody (T09299-302) were used to construct humanised antibodies using the PCR primers T09303-9. The humanised antibodies are useful as inhibitors of coagulation and can be used for the treatment of tumours by inhibiting the anticoagulant activity of APC by preventing conversion of protein C to APC.

Sequence 360 BP: 82 A: 91 C: 95 G: 92 T:

Query Match 83.3%; Score 40; DB 19; Length 360;  
Best Local Similarity 91.7%; Pred. No. 5.84e-14;  
Matches 44; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 154 cacatttggtggatgatgacaagcgctataaccaggctcctgaagagc 201  
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Qv 1 CACATTTTACTGGGATCATGACAAGCGCTATACCCATCCCTGAAGAGC 48

RESULT	6
ID	T09299 standard; DNA; 417 BP.
AC	T09299;

DT 25-JUL-1996 (first entry)  
DE Murine anti-Protein C MAb HPC-4 VH gamma coding region.  
KE Epitope; activation; heavy chain; protein C; vitamin K; plasma protein;  
KW zymogen; cleavage; mouse; humanised antibody; variable region;  
KW light chain; inhibition; anticoagulant; coagulation; tumour; ss.  
OS Mus musculus.

Key	Location/Qualifiers
FT sig_peptide	1..57
FT /*tag= a	
FT mat_peptide	58..417
FT /*tag= b	
FT W09534652-Al.	
PD 21-DEC-1995.	
PD 09-JUN-1995; U07372.	
PR 10-JUN-1994; U5-259321.	
PR PA (OKLA-) OKLAHOMA MED RES FOUND.	
PI Esmon CT, Rezaie A;	
PI WPI; 96-049681/05.	
DR P-PSDB; R88107.	
DR Calcium-binding monoclonal antibody immunoreactive with Protein C -	
PT inhibits Protein C anticoagulant activation by	
PT thrombin-thrombomodulin, e.g. for treating tumours	
PT Claim 4; Page 29-30; 41pp; English.	
CC This is the nucleotide sequence encoding the heavy chain variable region	
CC from the murine anti-protein C monoclonal antibody HPC-4 which recognises	
CC the activation peptide region (R88106) of the heavy chain of protein C,	
CC a vitamin K-dependent plasma protein zymogen. Protein C is converted to	
CC activated protein C (APC) by cleavage between the Arg-Leu amino acid	
CC contained within the activation peptide sequence. HPC-4 prevents protein	
CC C activation to APC by binding to this region. The DNA sequences encoding	
CC the variable regions of the heavy and light chains of the antibody	
CC (T09299-302) were used to construct humanised antibodies using the PCR	
CC primers T09303-9. The humanised antibodies are useful as inhibitors of	
CC coagulation and can be used for the treatment of tumours by inhibiting	
CC the anticoagulant activity of APC by preventing conversion of protein C	
CC to APC.	
SQ Sequence	417 BP; 89 A; 108 C; 114 T;

Query Match 83.3%; Score 40; DB 19; Length 417;  
Best Local Similarity 91.7%; Pred. No. 5.84e-14;  
Matches 44; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 211 cacatttggtggatgatgacaagcgctataaaccagtcctgaagagc 258  
||||| ||||||||||||||||||| |||||||  
Ov 1 CACATTTACTGGGATGATGACAAGCGGTATACCCATCCCTGAAGAGC 48

RESULT	7
ID	Q64166 standard; cDNA to mRNA; 429 BP.
AC	Q64166;
DT	29-DEC-1994 (first entry)
DE	Sequence of mouse VH showing the sequences of recombinant
DE	anti-FHV-1 antibody CDRs 1, 2 and 3.
KW	Feline herpes virus; FHV-1; monoclonal antibody; CDR;
KW	complementarity determining region; ss.
OS	Mus musculus.

FH	Key	Location
FT	CDS	1..429
FT	/*tag= a	
FT	misc feature	19
FT	/*tag= b	
FT	/label= MHL341	
FT	misc feature	385..429
FT	/*tag= c	

FN /label= MJH3  
PD W09412661-A.  
PF 25-NOV-1993; JP-341255.  
PR 28-NOV-1992; JP-341255.  
PA (KAGA ) CEMO SERO THERAPEUTIC RES INST.  
PI Kimachi K, Maeda H, Nishiyama K, Tokiyoshi S;  
DR WPI; 94-200288/24.  
DR P-PSDB; R54092.  
PT Feline monoclonal antibody and recombinant antibodies specific  
PT for FHV-1 - for detection, treatment and prevention of FHV-1  
PT infection.  
PS Disclosure; Page 17-18; 53pp; Japanese.  
CC The inventors claim a monoclonal antibody against feline herpes  
CC virus (FHV-1). They also claim a recombinant antibody against FHV-1  
CC and fragments of VH and VL CDR1, CDR2 and CDR3. The antibodies are  
CC used in the detection, treatment and prevention of FHV-1. The  
CC sequences of the CDRs in the VH of the recombinant anti-FHV-1  
CC antibody are given in R54092. The sequences of the CDRs in the VL of  
CC the recombinant anti-FHV-1 antibody are given in R54093. These CDR  
CC sequences are claimed.  
SQ Sequence 429 BP; 84 A; 116 C; 109 G; 120 T;

Query Match 83.3%; Score 40; DB 11; Length 429;  
Best Local Similarity 91.1%; Pred. No. 5.84e-14;  
Matches 44; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 211 cacatttggtggatgataagcgctacagccatctctgaagc 258  
||||| ||||||| ||||||| ||||||| ||||||| |||||||  
Qy 1 CATTACTGGGATGATGACAGCGCTATAACCCATCCCTGAAGC 48

## RESULT 8

ID Q45597 standard; DNA; 423 BP.  
AC Q45597;  
DT 04-DEC-1993 (first entry)  
DE Sequence encoding the VH of antibody B17X2  
KW Variable heavy antibody chain; human subgroup 4 germline; ss.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT CDS 7..423  
FT /\*tag= a  
PN W09312231-A.  
PD 24-JUN-1993.  
PF 13-DEC-1991; W05583.  
PR 13-DEC-1991; W05583.  
PA (DOWC ) DOW CHEM AUSTRALIA LTD.  
PI Johnson KS, Mezes PS, Richard RA;  
DR WPI; 93-214173/26.  
DR P-PSDB; R38315.  
PT New composite antibody binding to tumour associated TAG-72  
PT antigen - includes light chain variable region from human  
PT subgroup 4 germline gene, useful, opt. as conjugate, for  
PT diagnosis or treatment of cancer  
PS Disclosure; Figure 4; 150pp; English.  
CC Cell line B17X2 expresses an antibody utilising a variable light  
CC chain encoded by a gene derived from Hum4 VL and a variable heavy  
CC chain which makes a stable VL and VH combination.  
SQ Sequence 423 BP; 98 A; 120 C; 102 G; 97 T;

Query Match 75.0%; Score 36; DB 7; Length 423;  
Best Local Similarity 89.1%; Pred. No. 2.33e-11;  
Matches 41; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Db 219 cattattggatgataagcgctacagccatctctgaagc 264  
||||| ||||||| ||||||| ||||||| ||||||| |||||||  
Qy 3 CATTACTGGGATGATGACAGCGCTATAACCCATCCCTGAAGC 48

## RESULT 9

ID Q78943 standard; DNA; 613 BP.  
AC Q78943;  
DT 07-AUG-1995 (first entry)  
DE Human immunoglobulin variable heavy chain #5.  
KW Primer; PCR; amplify; human; immunoglobulin; variable; heavy chain;  
KW cosmid; placenta; vector; pJB81; E.coli; mammalian; ds.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT CDS 71..513  
FT /\*tag= a  
FT /product= human immunoglobulin variable heavy chain  
FT intron 117..202  
FT /\*tag= b  
FT misc signal 514..516  
FT /\*tag= c  
FT /note= "miscellaneous signal, does not conform to  
FT terminator or splice site sequence"  
PN W09426895-A.  
PD 24-NOV-1994.  
PF 10-MAY-1993; J00603.  
PR 10-MAY-1993; W0-J00603.  
PA (NIBS ) JAPAN TOBACCO INC.  
PI Honjo T, Matsuda F;  
DR WPI; 95-006791/01.  
DR P-PSDB; R66299.  
PT DNA fragment comprising human immunoglobulin Vh genes - for the  
PT production of human immunoglobulin in mammalian hosts  
PS Disclosure; Page 36-37; 130pp; Japanese.  
CC A series of genes (Q78939-79002) encoding human immunoglobulin variable  
CC heavy chains. The genes were isolated and cloned from a series of cosmid  
CC constructs: Y202; Y103; Y21; Y6; Y24; 3-31; M84; M18 and M131, by PCR  
CC amplification using primers Q78917-38. The genes are subdivided into 5  
CC families of Vh genes. The fragments cover a region of 800 kb. The DNA  
CC fragments were isolated from high molecular weight DNA from human  
CC placenta. The DNA was partially digested with TaqI restriction enzyme.  
CC The fragments were separated by gel electrophoresis and 35-45 kb fractions  
CC were collected. The fragments were ligated with ClaI-digested cosmid  
CC vector pJB81. The ligation products were in vitro packed and infected  
CC into E.coli 490A. The fragments were then subcloned by colony  
CC hybridisation. The Vh genes and the DNA fragments encoding them are  
CC useful in producing human immunoglobulin in mammalian hosts.  
SQ Sequence 613 BP; 139 A; 194 C; 139 G; 141 T;

Query Match 70.8%; Score 34; DB 13; Length 613;  
Best Local Similarity 87.0%; Pred. No. 4.46e-10;  
Matches 40; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Db 369 cattattggatgataagcgctacagccatctctgaagc 414  
||||| ||||||| ||||||| ||||||| ||||||| |||||||  
Qy 3 CATTACTGGGATGATGACAGCGCTATAACCCATCCCTGAAGC 48

## RESULT 10

ID Q75889 standard; cDNA; 418 BP.  
AC Q75889;  
DT 21-AUG-1995 (first entry)  
DE Mouse heavy chain variable region in plasmid pUC-SK2-Vh.  
KW Primer; PCR; amplify; kappa; light chain; variable region; mouse; human;



CC antigenicity due to the use of human derived sequences and low  
 CC antigenicity mouse derived sequences.  
 SQ Sequence 96 BP; 18 A; 24 C; 25 G; 29 T;

Query Match 58.3%; Score 28; DB 13; Length 96;  
 Best Local Similarity 81.8%; Pred. No. 2.52e-06;  
 Matches 36; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Db 41 ttcaaggcagggttagtactatctatcatccaccacaatgtg 84  
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 Cp 44 TTCAGGATGGGTATAGCCCTGTCATCATCCAGTAATATG 1

## RESULT 13

ID Q75917 standard; DNA; 418 BP.  
 AC Q75917;  
 DT 23-AUG-1995 (first entry)  
 DE Anti-human IL-6 chimaeric Ab H chain V region in HEL-RVH-SK2b.  
 KW Primer; PCR; amplify; kappa; light chain; variable region; mouse; human;  
 KW interleukin; antibody; hybridoma; CDR; framework; constant region;  
 KW heavy chain; disorder; antigenicity; ds.  
 OS Synthetic.  
 FH Key Location/Qualifiers  
 FT CDS 1..417  
 FT /\*tag= a  
 FT /note= "Anti-human IL-6 H chain V region"  
 FT sig\_peptide 1..57  
 FT /\*tag= b  
 FT mat\_peptide 58..417  
 FT /\*tag= c  
 PN W09428159-A.  
 PD 08-DEC-1994.  
 PF 30-MAY-1994; J00859.  
 PR 31-MAY-1993; JP-129787.  
 PA (CHUS ) CHUGAI SEIYAKU KK.  
 PA (CHUS ) CHUGAI PHARM CO LTD.  
 PI Hirata Y, Sato K, Tsuchiya M;  
 DR WPI; 95-022828/03.  
 DR P-PSDB; R67659.  
 PT Antibody against IL-6 - useful for the therapy and treatment of  
 PT IL-6 related disorders.  
 PS Claim 21; Page 62-63; 82pp; Japanese.  
 CC The sequence of a recombinant gene encoding the heavy chain variable  
 CC region of a chimaeric antibody against human interleukin-6 (IL-6). The  
 CC sequence is found on the plasmid HEL-RVH-SK2a. This vector and vectors  
 CC Q75914, -5 and -6 express constructs encoding fragments of a chimaeric  
 CC antibody to the human IL-6 comprising (a) a light chain with (i) a  
 CC variable region containing 3 complementarity determining regions (CDR)  
 CC (R77201-3) inserted into several framework regions (FR) (R77204-7) and  
 CC (ii) a human light chain constant region and (b) a heavy chain with (i) a  
 CC variable region containing 3 CDR (R77212-4) inserted into an FR  
 CC (R77215-8) and (ii) a human light chain constant region. The FR of the  
 CC light chain may be mouse derived (Q75888) or from the human antibody REL.  
 CC The heavy chain FR may also be mouse derived (Q75889) or from the human  
 CC antibody DAM. The antibodies can be used in the treatment of IL-6  
 CC related disorders. The antibodies are useful as they have low  
 CC antigenicity due to the use of human derived sequences and low  
 CC antigenicity mouse derived sequences.  
 SQ Sequence 418 BP; 95 A; 116 C; 109 G; 98 T;

Query Match 58.3%; Score 28; DB 13; Length 418;  
 Best Local Similarity 81.8%; Pred. No. 2.52e-06;  
 Matches 36; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Db 211 cacatttggtgaatgatgaagtaactataaccctgcctgaa 254  
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 Qy 1 CACATTTACTGGGATGATGACAGCGCTATATACCCATCCCTGAA 44

## RESULT 14

ID Q75916 standard; DNA; 418 BP.  
 AC Q75916;  
 DT 23-AUG-1995 (first entry)  
 DE Anti-human IL-6 chimaeric Ab H chain V region in HEL-RVH-SK2a.  
 KW Primer; PCR; amplify; kappa; light chain; variable region; mouse; human;  
 KW interleukin; antibody; hybridoma; CDR; framework; constant region;  
 KW heavy chain; disorder; antigenicity; ds.  
 OS Synthetic.  
 FH Key Location/Qualifiers  
 FT CDS 1..417  
 FT /\*tag= a  
 FT /note= "Anti-human IL-6 H chain V region"  
 FT sig\_peptide 1..57  
 FT /\*tag= b  
 FT mat\_peptide 58..417  
 FT /\*tag= c  
 PN W09428159-A.  
 PD 08-DEC-1994.  
 PF 30-MAY-1994; J00859.  
 PR 31-MAY-1993; JP-129787.  
 PA (CHUS ) CHUGAI SEIYAKU KK.  
 PA (CHUS ) CHUGAI PHARM CO LTD.  
 PI Hirata Y, Sato K, Tsuchiya M;  
 DR WPI; 95-022828/03.  
 DR P-PSDB; R67658.  
 PT Antibody against IL-6 - useful for the therapy and treatment of  
 PT IL-6 related disorders.  
 PS Claim 21; Page 60-61; 82pp; Japanese.  
 CC The sequence of a recombinant gene encoding the heavy chain variable  
 CC region of a chimaeric antibody against human interleukin-6 (IL-6). The  
 CC sequence is found on the plasmid HEL-RVH-SK2a. This vector and vectors  
 CC Q75914, -5 and -7 express constructs encoding fragments of a chimaeric  
 CC antibody to the human IL-6 comprising (a) a light chain with (i) a  
 CC variable region containing 3 complementarity determining regions (CDR)  
 CC (R77201-3) inserted into several framework regions (FR) (R77204-7) and  
 CC (ii) a human light chain constant region and (b) a heavy chain with (i) a  
 CC variable region containing 3 CDR (R77212-4) inserted into an FR  
 CC (R77215-8) and (ii) a human light chain constant region. The FR of the  
 CC light chain may be mouse derived (Q75888) or from the human antibody REL.  
 CC The heavy chain FR may also be mouse derived (Q75889) or from the human  
 CC antibody DAM. The antibodies can be used in the treatment of IL-6  
 CC related disorders. The antibodies are useful as they have low  
 CC antigenicity due to the use of human derived sequences and low  
 CC antigenicity mouse derived sequences.  
 SQ Sequence 418 BP; 94 A; 116 C; 110 G; 98 T;

Query Match 58.3%; Score 28; DB 13; Length 418;  
 Best Local Similarity 81.8%; Pred. No. 2.52e-06;  
 Matches 36; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Db 211 cacatttggtgaatgatgaagtaactataaccctgcctgaa 254  
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 Qy 1 CACATTTACTGGGATGATGACAGCGCTATATACCCATCCCTGAA 44

## RESULT 15

ID Q51746 standard; cDNA; 91 BP.  
 AC Q51746;



Db . 13 vhsyyvvvshhsvhhvhvsvvvhhvhvvhvhyhvyy 58  
:: :: :: :: :: :: :: :: :: :: :: ::  
Cp 48 GCTCTTCAGGATGGGTATAGCGCTTGTCATCATCCCAATAATG 3

Search completed: Wed Mar 19 08:27:33 1997  
Job time : 21 secs.

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Mus.

## REFERENCE

## AUTHORS

Young, D.C. and Kearney, J.F.

Sequence analysis and antigen binding characteristics of

immunoglobulins from SCID Ig<sup>+</sup> mice

## JOURNAL

## REFERENCE

2 (bases 1 to 286)

Young, D.C.

Direct Submission

Submitted (17-MAR-1995) David C. Young, University of Texas Health

Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137,

Houston, TX 77030, USA

## FEATURES

## source

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/clone="CB17H-1"

/strain="C57BL/6"

/organism="Mus musculus"

/sub\_species="domesticus"

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/notes="7183 Vh gene family"

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/db\_xref="PID:g780641"

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KGLEWLAHIYDDDKRYNPSIKSLRTISKDFSRNQVFIKITSVDATATY"

## BASE COUNT

67 a 71 c 70 g 72 t

## ORIGIN

Query Match 100.0%; Score 48; DB 65; Length 286;

Best Local Similarity 100.0%; Pred. No. 1.72e-25;

Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 155 cacattactgggatgacagcgctataacccatccctgaagac 202

|||||

QY 1 CACATTTACTGGGATGATGACAGCGCTATAACCCATCCCTGAAGAGC 48

## RESULT

## LOCUS

MM023024

Mus musculus

286 bp DNA

06-MAY-1995

clone CB17H-8, partial cds.

ACCESSION

U23024

NID

g780650

KEYWORDS

house mouse.

SOURCE

Mus musculus

ORGANISM

Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;

Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;

Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;

Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;

Sciurognathi; Myomorpha; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 286)

Young, D.C. and Kearney, J.F.

Sequence analysis and antigen binding characteristics of

immunoglobulins from SCID Ig<sup>+</sup> mice

Int. Immunol. 7 (1995) In press

2 (bases 1 to 286)

Young, D.C.

TITLE Direct Submission

## JOURNAL

Submitted (17-MAR-1995) David C. Young, University of Texas Health

Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137,

Houston, TX 77030, USA

## FEATURES

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/clone="CB17H-8"

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68 a 77 c 69 g 72 t

## ORIGIN

Query Match 100.0%; Score 48; DB 65; Length 286;

Best Local Similarity 100.0%; Pred. No. 1.72e-25;

Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 155 cacattactgggatgacagcgctataacccatccctgaagac 202

|||||

QY 1 CACATTTACTGGGATGATGACAGCGCTATAACCCATCCCTGAAGAGC 48

## RESULT

3

LOCUS

MUSB

306 bp mRNA

14-MAR-1994

Mus musculus immunoglobulin heavy chain (Igh) mRNA, VDJ4 region,

partial cds.

ACCESSION

L22743

NID

g348959

KEYWORDS

Ig heavy chain; diversity region; immunoglobulin; joining region;

variable region.

SOURCE

Mus musculus

ORGANISM

Mus musculus

Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;

Eutheria; Rodentia; Myomorpha; Muridae; Murinae.

REFERENCE

1 (bases 1 to 306)

Sheehan, K.M., Mainville, C.A., Willert, S. and Brodeur, P.H.

The utilization of individual VH exons in the primary repertoire of

adult BALB/c mice

J. Immunol. 151 (10), 5364-5375 (1993)

JOURNAL

94044761

MEDLINE

FEATURES

Location/Qualifiers

1..306

/organism="Mus musculus"

/strain="BALB/cByJ"

/cell\_type="B-lymphocyte"

/dev\_stage="adult"

/sequenced\_mol="cDNA to mRNA"

/sex="female"

/tissue\_type="spleen"

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/gene="Igh"

/map="chromosome 12"

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/map="chromosome 12"

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BASE COUNT 72 a 80 c 75 g 79 t

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Best Local Similarity 100.0%; Pred. No. 1.72e-25;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 97 cacattactgggatgatgacagcgctataaccatccctgaagacg 144  
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Qy 1 CACATTTACTGGGATGATGACAGCGCTATACCCATCCTCGAAGAC 48

RESULT 4 MUSTIGHAEO 328 bp mRNA ROD 14-NOV-1991  
LOCUS Mouse Ig heavy-chain mRNA V region, partial cds. L2-5D2HV.  
ACCESSION M36234  
NID g194851  
KEYWORDS V-region; immunoglobulin heavy chain; processed gene.  
SOURCE Mouse (strain BALB/c), cDNA to mRNA, from hybridoma L2-5D2.  
ORGANISM Mus musculus  
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;  
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.

REFERENCE 1 (bases 1 to 328)  
AUTHORS Kavalier,J., Caton,A.J., Staudt,L.M., Schwartz,D. and Gerhard,W.  
TITLE A set of closely related antibodies dominates the primary antibody response to the antigenic site CB of the A/PR/8/34 influenza virus hemagglutinin

JOURNAL J. Immunol. 145, 2312-2321 (1990)  
MEDLINE 90375932  
COMMENT Draft entry and computer-readable sequence for [J. Immunol. (1990) In press] kindly submitted by J.Kavalier, 06-JUL-1990.

FEATURES  
source Location/Qualifiers  
1..328  
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CDS  
BASE COUNT 76 a 85 c 82 g 83 t 2 others  
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Query Match 100.0%; Score 48; DB 66; Length 328;  
Best Local Similarity 100.0%; Pred. No. 1.72e-25;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 131 cacattactgggatgatgacagcgctataaccatccctgaagacg 178  
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Qy 1 CACATTTACTGGGATGATGACAGCGCTATACCCATCCTCGAAGAC 48  
RESULT 5 MMHCVR4 348 bp RNA ROD 23-FEB-1994  
LOCUS M.musculus (A.SM) mRNA for ASWP1 antibody heavy chain variable region.  
DEFINITION  
ACCESSION X75098  
NID g414167  
KEYWORDS antibody; variable region; VH region.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 348)  
AUTHORS Monestier,M.  
TITLE Direct Submission  
JOURNAL Submitted (09-SEP-1993) to the EMBL/GenBank/DBDJ databases. M. Monestier, Center for Molecular Medicine and Immunology, one Bruce Street, Newark, NJ 07103-2763, USA

REFERENCE 2 (bases 1 to 348)  
AUTHORS Monestier,M., Losman,M.J., Novick,K.E. and Aris,J.P.  
TITLE Molecular analysis of mercury-induced antinuclear antibodies in H-2S mice  
JOURNAL J. Immunol. 152 (2), 667-675 (1994)  
MEDLINE 94110621

FEATURES  
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GFDYWGQGTTLTVS"

V\_region  
BASE COUNT 81 a 95 c 85 g 85 t 2 others  
ORIGIN  
Query Match 100.0%; Score 48; DB 63; Length 348;  
Best Local Similarity 100.0%; Pred. No. 1.72e-25;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 154 cacattactgggatgatgacagcgctataaccatccctgaagacg 201  
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Qy 1 CACATTTACTGGGATGATGACAGCGCTATACCCATCCTCGAAGAC 48

RESULT 6 MMU23007 359 bp mRNA ROD 26-APR-1995  
LOCUS Mus musculus CBI7 SCID immunoglobulin heavy chain V region mRNA, clone 45-4h, partial cds.  
DEFINITION

ACCESSION UZ3007  
NID g780616  
KEYWORDS  
SOURCE house mouse.  
ORGANISM Mus musculus

REFERENCE  
Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;  
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;  
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;  
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;  
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.  
1 (bases 1 to 359)  
Young, D.C. and Kearney, J.F.  
Sequence analysis and antigen binding characteristics of  
immunoglobulins from SCID Ig+ mice  
Int. Immunol. 7 (1995) In press

REFERENCE  
2 (bases 1 to 359)  
Young, D.C.  
Direct Submission  
AUTHORS  
TITLE  
JOURNAL  
SUBMITTED (17-MAR-1995) David C. Young, University of Texas Health  
Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137,  
Houston, TX 77030, USA

FEATURES  
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83 a 97 c 87 g 92 t

BASE COUNT  
ORIGIN

Query Match 100.0%; Score 48; DB 65; Length 359;  
Best Local Similarity 100.0%; Pred. No. 1.72e-25;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 153 cacattactggatgatgacagcgctataaccatccctgaagc 200  
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Qy 1 CACATTTACTGGATGATGACAAAGCGGTATACCCATCCCTGAAGAC 48

RESULT 7  
LOCUS MMHVR3 360 bp RNA ROD 23-FEB-1994  
DEFINITION M.musculus (A.SW) mRNA for ASWB1 antibody heavy chain variable  
region.  
ACCESSION X75097  
NID g414165  
KEYWORDS antibody; variable region; VH region.  
SOURCE house mouse.  
ORGANISM Mus musculus

Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;  
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;  
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;  
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;  
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.  
1 (bases 1 to 360)  
Monestier, M.

TITLE Direct Submission  
JOURNAL Submitted (09-SEP-1993) to the EMBL/GenBank/DBJ databases. M.  
Monestier, Center for Molecular Medicine and Immunology, one Bruce  
Street, Newark, NJ 07103-2763, USA

REFERENCE  
2 (bases 1 to 360)  
Monestier, M., Losman, M.J., Novick, K.E. and Aris, J.P.  
Molecular analysis of mercury-induced antinuclear antibodies in  
H-2S mice  
J. Immunol. 152 (2), 667-675 (1994)

JOURNAL  
MEDLINE 94110621  
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82 a 95 c 89 g 94 t

BASE COUNT  
ORIGIN

Query Match 100.0%; Score 48; DB 63; Length 360;  
Best Local Similarity 100.0%; Pred. No. 1.72e-25;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 154 cacattactggatgatgacagcgctataaccatccctgaagc 201  
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Qy 1 CACATTTACTGGATGATGACAAAGCGGTATACCCATCCCTGAAGAC 48

RESULT 8  
LOCUS MMU22994 360 bp mRNA ROD 09-APR-1996  
DEFINITION Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA,  
clone 45-27h, partial cds.  
ACCESSION U22994  
NID g780590  
KEYWORDS  
SOURCE house mouse.  
ORGANISM Mus musculus

Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;  
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;  
Murinae; Mus.  
1 (bases 1 to 360)  
Young, D. and Kearney, J.F.  
Sequence analysis and antigen binding characteristics of Ig SCID  
Ig+ mice  
Int. Immunol. 7 (5), 807-819 (1995)

JOURNAL  
MEDLINE 96053543  
REFERENCE 2 (bases 1 to 360)  
AUTHORS Young, D.C.  
TITLE Direct Submission  
JOURNAL Submitted (17-MAR-1995) David C. Young, University of Texas Health  
Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137,  
Houston, TX 77030, USA

Mar 19 16:07

US-08-612-929-23.rge

9

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COMMENT  NCBI gi: 780590
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            KGLEWLAHIYWDKDRYNPISIKRLTISKDTSRNQVFIKITSVDTADTATYYCARRVL
            GSSYFDYWGQGTTLTVSS"
BASE COUNT  84 a  95 c  87 g  94 t
ORIGIN

Query Match      100.0%; Score 48; DB 91; Length 360;
Best Local Similarity 100.0%; Pred. No. 1.72e-25;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 154 cacattactgggatgatgacagcgctataaccatccctgaagagc 201
|||||
Qy 1 CACATTTTACTGGGATGATGACAGCGCTATACCCATCCCTGAGAGC 48

RESULT  9
LOCUS    MMU22979      360 bp      mRNA      ROD      26-APR-1995
DEFINITION Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA,
clone 45-12h, partial cds.
ACCESSION U22979
NID       g780560
KEYWORDS  house mouse.
SOURCE    Mus musculus
ORGANISM  Mus musculus
          Eukaryota; Eumetazoa; Bilateria; Chordata; Chordata;
          Metazoa; Eumetazoa; Bilateria; Chordata; Chordata;
          Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata;
          Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
          Sciurognathi; Myomorpha; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 360)
AUTHORS   Young,D.C. and Kearney,J.F.
TITLE      Sequence analysis and antigen binding characteristics of
immunoglobulins from SCID Ig+ mice
JOURNAL    Int. Immunol. 7 (1995) In press
REFERENCE 2 (bases 1 to 360)
AUTHORS   Young,D.C.
TITLE      Direct Submission
JOURNAL    Submitted (17-MAR-1995) David C. Young, University of Texas Health
Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137,
Houston, TX 77030, USA
FEATURES
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            /strain="CB17 SCID"
            /organism="Mus musculus"
            /sub_species="domesticus"
            /cell_type="lymphocyte"
            /tissue_type="spleen"
            <1..>360
            /codon_start=1
CDS
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Mar 19 16:07

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10

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/translation="QVTLKESGPGILQSSQTLSTLTCSEFSGSLSTSCMGVSMIRQPSG
KGLEWLAHIYWDKDRYNPISIKRLTISKDTSRNQVFIKITSVDTADTATYYCARRAL
GSSYFDYWGQGTTLTVSS"
BASE COUNT  84 a  98 c  87 g  91 t
ORIGIN

Query Match      100.0%; Score 48; DB 65; Length 360;
Best Local Similarity 100.0%; Pred. No. 1.72e-25;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 154 cacattactgggatgatgacagcgctataaccatccctgaagagc 201
|||||
Qy 1 CACATTTTACTGGGATGATGACAGCGCTATACCCATCCCTGAGAGC 48

RESULT  10
ID       MM22979      standard; RNA; ROD; 360 BP.
AC       U22979;
DT       29-APR-1995 (Rel. 43, Created)
DE       09-APR-1996 (Rel. 47, Last updated, Version 2)
DE       Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA,
clone 45-12h, partial cds.
KW       Mus musculus (mouse)
OS       Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
OC       Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
RN       [1]
RP       1-360
RA       Young D., Kearney J.F.;
RT       *Sequence analysis and antigen binding characteristics of Ig SCID
RT       Ig+ mice";
RL       Int. Immunol. 7:807-819 (1995).
RN       [2]
RP       1-360
RA       Young D.C.;
RT       ;
RL       Submitted (17-MAR-1995) to the EMBL/GenBank/DBJ databases.
RL       David C. Young, University of Texas Health Science Center, Houston,
RL       Pathology, 6431 Fannin, MSMB 2.137, Houston, TX 77030, USA
CC       NCBI gi: 780560
FH       Key      Location/Qualifiers
FT       1..360
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FT       /strain="CB17 SCID"
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FT       /cell_type="lymphocyte"
FT       /tissue_type="spleen"
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FT       /db_xref="PID:g780561"
FT       /translation="QVTLKESGPGILQSSQTLSTLTCSEFSGSLSTSCMGVSMIRQPSG
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GLEWLAHIYWDKDRYNPISIKRLTISKDTSRNQVFIKITSVDTADTATYYCARRALG
S
SYFDYWGQGTTLTVSS"
SQ       Sequence 360 BP; 84 A; 98 C; 87 G; 91 T; 0 other;
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Best Local Similarity 100.0%; Pred. No. 1.72e-25;
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Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 154 cacatttactggatgacagcgctataaaccatccctgaagagc 201  
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 Qy 1 CACATTACTGGGATGACAAAGCGCTATAACCCATCCCTGAAGAGC 48

RESULT 11  
 ID MM22994 standard; RNA; ROD; 360 BP.  
 AC U22994;  
 DT 29-APR-1995 (Rel. 43, Created)  
 DT 09-APR-1996 (Rel. 47, Last updated, Version 2)  
 DE Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA,  
 DE clone 45-27h, partial cds.  
 KW .  
 OS Mus musculus (mouse)  
 OC Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;  
 OC Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.  
 RN [1]  
 RP 1-360  
 RA Young D., Kearney J.F.;  
 RT "Sequence analysis and antigen binding characteristics of Ig SCID  
 RT Ig+ mice";  
 RL Int. Immunol. 7:807-819(1995).  
 RN [2]  
 RP 1-360  
 RA Young D.C.;

RT ;  
 RL Submitted (17-MAR-1995) to the EMBL/GenBank/DBJ databases.  
 RL David C. Young, University of Texas Health Science Center, Houston,  
 RL Pathology, 6431 Fannin, MSMB 2.137, Houston, TX 77030, USA  
 CC NCBI gi: 780590  
 FH Key Location/Qualifiers

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 FT /strain="CB17 SCID"  
 FT /sub\_species="domesticus"  
 FT /clone="45-27h"  
 FT /cell\_type="lymphocyte"  
 FT /tissue\_type="spleen"  
 FT <1..>360  
 FT /codon\_start=1  
 FT /product="immunoglobulin heavy chain"  
 FT /db\_xref="PID:g780591"  
 FT /translation="QVTLKESGPGILQSSQTLISLTCFSGFSLTSCMGVSHIRP5G  
 K GLEWLAHYWDDDKRNP5IKSLRTISKDTSRNQVFLKITSVDYDTATYYCARRVLG  
 S SYFDYWGQGTTLTVSS"  
 FT Sequence 360 BP; 84 A; 95 C; 87 G; 94 T; 0 other;

Query Match 100.0%; Score 48; DB 12; Length 360;  
 Best Local Similarity 100.0%; Pred. No. 1.72e-25;  
 Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 154 cacatttactggatgacagcgctataaaccatccctgaagagc 201  
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 Qy 1 CACATTACTGGGATGACAAAGCGCTATAACCCATCCCTGAAGAGC 48

RESULT 12  
 ID MM22977 standard; RNA; ROD; 360 BP.  
 AC U22977;

DT 29-APR-1995 (Rel. 43, Created)  
 DT 09-APR-1996 (Rel. 47, Last updated, Version 2)  
 DE Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA,  
 DE clone 45-11h, partial cds.  
 KW .

OS Mus musculus (mouse)  
 OC Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;  
 OC Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.  
 RN [1]  
 RP 1-360

RA Young D., Kearney J.F.;  
 RT "Sequence analysis and antigen binding characteristics of Ig SCID  
 RT Ig+ mice";  
 RL Int. Immunol. 7:807-819(1995).  
 RN [2]  
 RP 1-360

RA Young D.C.;

RT ;  
 RL Submitted (17-MAR-1995) to the EMBL/GenBank/DBJ databases.  
 RL David C. Young, University of Texas Health Science Center, Houston,  
 RL Pathology, 6431 Fannin, MSMB 2.137, Houston, TX 77030, USA  
 CC NCBI gi: 780556  
 FH Key Location/Qualifiers

FT source 1..360  
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 FT /strain="CB17 SCID"  
 FT /sub\_species="domesticus"  
 FT /clone="45-11h"  
 FT /cell\_type="lymphocyte"  
 FT /tissue\_type="spleen"  
 FT <1..>360  
 FT /codon\_start=1  
 FT /product="immunoglobulin heavy chain"  
 FT /db\_xref="PID:g780557"  
 FT /translation="QVTLKESGPGILQSSQTLISLTCFSGFSLTSCMGVSHIRP5G  
 K GLEWLAHYWDDDKRNP5IKSLRTISKDTSRNQVFLKITSVDYDTATYYCARRVLG  
 S SYFDYWGQGTTLTVSS"  
 FT Sequence 360 BP; 84 A; 97 C; 87 G; 92 T; 0 other;

Query Match 100.0%; Score 48; DB 12; Length 360;  
 Best Local Similarity 100.0%; Pred. No. 1.72e-25;  
 Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 154 cacatttactggatgacagcgctataaaccatccctgaagagc 201  
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 Qy 1 CACATTACTGGGATGACAAAGCGCTATAACCCATCCCTGAAGAGC 48

RESULT 13  
 LOCUS MMU22994 360 bp mRNA ROD 26-APR-1995  
 DEFINITION Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA,  
 clone 45-27h, partial cds.

ACCESSION U22994  
 NID g780590  
 KEYWORDS .  
 SOURCE house mouse.  
 ORGANISM Mus musculus

Eukaryota; mitochondrial eukaryotes; Metazoa/Eumycota group;  
 Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;  
 Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;  
 Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;

Sciurognathi; Myomorpha; Muridae; Murinae; Mus.

## REFERENCE

1 (bases 1 to 360)

AUTHORS Young, D.C. and Kearney, J.F.

TITLE Sequence analysis and antigen binding characteristics of

immunoglobulins from SCID Ig+ mice

## JOURNAL

REFERENCE Int. Immunol. 7 (1995) In press

2 (bases 1 to 360)

AUTHORS Young, D.C.

TITLE Direct Submission

## JOURNAL

Submitted (17-MAR-1995) David C. Young, University of Texas Health

Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137,

Houston, TX 77030, USA

## FEATURES

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/clone="45-27h"

/strain="CB17 SCID"

/organism="Mus musculus"

/sub\_species="domesticus"

/cell\_type="lymphocyte"

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/product="immunoglobulin heavy chain"

/db\_xref="PID:g780591"

/translation="QVTIKESGPGILQSSQTLSTCTSFSGSLTSCMGVSNIRQPSG

KGLEMLAHYWDHDKRYNPISIKRLTISKDTSRNQVFIKITSVDTDATATYYCARRVL

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BASE COUNT 84 a 95 c 87 g 94 t

## ORIGIN

Query Match 100.0%; Score 48; DB 65; Length 360;

Best Local Similarity 100.0%; Pred. No. 1.72e-25;

Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 154 cacattactgggatgacacagcgctataaccctccctgaagc 201

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1 CACATTTACTGGGATGATGACACAGCGCTATACCCATCCCTCGAGAGC 48

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## FEATURES

source

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/clone="45-11h"

/strain="CB17 SCID"

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/sub\_species="domesticus"

/cell\_type="lymphocyte"

/tissue\_type="spleen"

<1..>360

/codon\_start=1

/product="immunoglobulin heavy chain"

/db\_xref="PID:g780557"

/translation="QVTIKESGPGILQSSQTLSTCTSFSGSLTSCMGVSNIRQPSG

KGLEMLAHYWDHDKRYNPISIKRLTISKDTSRNQVFIKITSVDTDATATYYCARRVL

GSSYFDYNGQCTTLTVSS"

BASE COUNT 84 a 97 c 87 g 92 t

## ORIGIN

Query Match 100.0%; Score 48; DB 65; Length 360;

Best Local Similarity 100.0%; Pred. No. 1.72e-25;

Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 154 cacattactgggatgacacagcgctataaccctccctgaagc 201

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1 CACATTTACTGGGATGATGACACAGCGCTATACCCATCCCTCGAGAGC 48

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15

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GSSYFDYWGQGTTLTVSS"

BASE COUNT 84 a 97 c 87 g 92 t  
ORIGIN

Query Match 100.0%; Score 48; DB 91; Length 360;  
Best Local Similarity 100.0%; Pred. No. 1.72e-25;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 154 cacattactgggatgacagcgctataaccatccctgaagc 201  
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Qy 1 CACATTTACTGGATGATGACAGCGCTATTAACCCATCCCTGAAGC 48  
GSSYFDYWGQGTTLTVSS"

RESULT 16  
LOCUS MMU22979 360 bp mRNA ROD 09-APR-1996  
DEFINITION Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA,  
clone 45-12h, partial cds.

ACCESSION U22979  
NID g780560

KEYWORDS house mouse.  
SOURCE Mus musculus  
ORGANISM Mus musculus  
Eukaryotae; Mitochondrial eukaryotes; Metazoa; Chordata;  
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;  
Murinae; Mus.

REFERENCE 1 (bases 1 to 360)  
AUTHORS Young, D. and Kearney, J.F.  
TITLE Sequence analysis and antigen binding characteristics of Ig SCID  
Ig<sup>+</sup> mice  
JOURNAL Int. Immunol. 7 (5), 807-819 (1995)  
MEDLINE 96053543

REFERENCE 2 (bases 1 to 360)  
AUTHORS Young, D.C.  
TITLE Direct Submission  
JOURNAL Submitted (17-MAR-1995) David C. Young, University of Texas Health  
Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137,  
Houston, TX 77030, USA

COMMENT NCBI gi: 780560  
FEATURES Location/Qualifiers  
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/tissue\_type="spleen"  
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KGLELAHYWDDDKYNPISLSRLTISKDSRNQVFIKITSVDTADTATYYCARRAL  
GSSYFDYWGQGTTLTVSS"

BASE COUNT 84 a 98 c 87 g 91 t  
ORIGIN

Query Match 100.0%; Score 48; DB 91; Length 360;  
Best Local Similarity 100.0%; Pred. No. 1.72e-25;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Mar 19 16:07

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16

Db 154 cacattactgggatgacagcgctataaccatccctgaagc 201  
|||||  
Qy 1 CACATTTACTGGATGATGACAGCGCTATTAACCCATCCCTGAAGC 48

RESULT 17  
LOCUS MM1GMSMJ 366 bp RNA ROD 03-APR-1995  
DEFINITION Mouse mRNA for variable region of IgM heavy immunoglobulin chain.  
ACCESSION X53097  
NID g52368  
KEYWORDS autoantibody; Ig heavy chain; variable region.  
SOURCE house mouse.  
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 366)  
AUTHORS Carmack, C.E.  
TITLE Direct Submission  
JOURNAL Submitted (16-MAY-1990) to the EMBL/GenBank/DBJ databases. Carmack  
C.E., Medical Biology Institute, 11077 North Torrey Pines Road, La  
Jolla California 92037 USA

REFERENCE 2 (bases 21 to 366)  
AUTHORS Hayakawa, K., Carmack, C.E., Hyman, R. and Hardy, R.R.  
TITLE Natural autoantibodies to thymocytes: origin, VH genes, fine  
specificities, and the role of Thy-1 glycoprotein  
JOURNAL J. Exp. Med. 172 (3), 869-878 (1990)  
MEDLINE 90354788

FEATURES Location/Qualifiers  
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/organism="Mus musculus"  
/strain="SM/J"  
/tissue\_type="spleen"  
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/cell\_line="1-6C10 hybridoma (with SP2/0)"  
/chromosome="12"  
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1..21  
/note="leader (7 AA)"  
sig\_peptide  
<1..>366  
CDS  
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/db\_xref="PID:g762983"

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misc\_feature 22..108  
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misc\_feature 109..132  
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J\_segment 337..366  
/note="joining (2) region (10 AA)"

BASE COUNT 85 a 98 c 93 g 90 t  
ORIGIN

Query Match 100.0%; Score 48; DB 64; Length 366;

Mar 19 16:07

US-08-612-929-23.rgc

17

Best Local Similarity 100.0%; Pred. No. 1.72e-25;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 175 cacattactgggatgatgacagcgctataaccatccctgaagagc 222  
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Qy 1 CACATTTACTGGGATGATGACAGCGGCTATACCCATCCCTGAGAGC 48

RESULT 18  
LOCUS S75897 438 bp mRNA ROD 14-JUN-1995  
DEFINITION Ig VH=IgG heavy chain variable region [mice, Ric45.14.U1 hybridoma,  
secondary variant DMK, mRNA Partial, 438 nt].  
ACCESSION S75897  
NID g861529  
KEYWORDS  
SOURCE mice Ric45.14.U1 hybridoma secondary variant DMK.  
ORGANISM Mus sp.  
Unclassified.  
REFERENCE 1 (bases 1 to 438)  
AUTHORS Kobrin,B.J., Schiff,C., Zivion,D., Scharff,M.D. and Spira,G.  
TITLE In vitro activation of a nonproductive immunoglobulin allele by a  
single base pair insertion  
JOURNAL Hybridoma 13 (4), 257-261 (1994)  
MEDLINE 95104873  
REMARK GenBank staff at the National Library of Medicine created this  
entry [NCBI gibbsq 161740] from the original journal article.  
This sequence comes from Fig. 2.  
COMMENT Insertion of a single A converts nonproductive allele to productive  
one.

FEATURES Location/Qualifiers  
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307..438  
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/note="Method: conceptual translation supplied by author.  
This sequence comes from Fig. 3."  
/codon\_start=1  
/product="IgG heavy chain variable region"  
/db\_xref="PID:g861530"  
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BASE COUNT 100 a 131 c 99 g 108 t  
ORIGIN

Query Match 100.0%; Score 48; DB 70; Length 438;  
Best Local Similarity 100.0%; Pred. No. 1.72e-25;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 163 cacattactgggatgatgacagcgctataaccatccctgaagagc 210  
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Qy 1 CACATTTACTGGGATGATGACAGCGGCTATACCCATCCCTGAGAGC 48

Search completed: Wed Mar 19 16:08:57 1997  
Job time : 104 secs.



Mar 19 08:30

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3

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c 44 15 45.5 686 154 W23231 81A2 Human retina CDN 2.02e-01
c 45 15 45.5 981 169 MM1627 ma74d12.r1 Soares mou 2.02e-01
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ALIGNMENTS

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RESULT 1
ID HS941327 standard; RNA; EST; 136 BP.
AC W19941;
DT 05-MAY-1996 (Rel. 47, Created)
DT 05-MAY-1996 (Rel. 47, Last updated, Version 1)
DE z642h04.r1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone
DE 306295 5' similar to SW:PPCT BOVIN P02720
DE PHOSPHATIDYLCHOLINE-TRANSFER PROTEIN. [1] ;.
KW EST.
OS Homo sapiens (human)
OC Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
OC Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominoidea;
RN [1]
RP 1-136
RA Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M.,
RA Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M.,
RA Parsons J., Rifkin L., Rohlfing T., Soares M., Tan F.,
RA Trevasakis E., Waterston R., Williamson A., Wohlmann P., Wilson R.;
RT "The WashU-Merck EST Project";
RL Unpublished.
CC Contact: Wilson RK WashU-Merck EST Project Washington University
CC School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,
CC MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email:
CC est@watson.wustl.edu This clone is available royalty-free through
CC LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for
CC further information. Trace considered overall poor quality Possible
CC reversed clone: similarity on wrong strand Seq primer: mob.REGA+ET
CC High quality sequence stop: 1. NCBI gi: 1296114
FH Key Location/Qualifiers
FH source
FT 1..136
FT /organism="Homo sapiens"
FT /note="Vector: pT7T3D (Pharmacia) with a modified
FT polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
FT was primed with a Not I - oligo(dT) primer [5'-
FT TCTTACCAATCTGAAGTGGCGCGCCGACCAATTTTTTTTTTTTTTTTTT
FT T-3'] , double-stranded cDNA was size selected, ligated to
FT Eco RI adapters (Pharmacia), digested with Not I and clone
FT
FT into the Not I and Eco RI sites of a modified pT7T3 vector
FT (Pharmacia) . Library went through one round of
FT normalization to a Cot = 5. Library constructed by Bento
FT Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid
FT adenomas was kindly provided by Dr. Stephen Marx, National
FT Institute of Diabetes and Digestive and Kidney Diseases,
FT NIH."
FT /clone="306295"
FT /clone_lib="Soares parathyroid tumor NbHPA"
FT /dev_stage="adult"
FT /lab_host="DH10B (ampicillin resistant)"
FT mRNA
FT <1..>136
SQ Sequence 136 BP; 44 A; 28 C; 33 G; 28 T; 3 other;
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Query Match 54.5%; Score 18; DB 166; Length 136;  
Best Local Similarity 95.0%; Pred. No. 3.36e-05;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Mar 19 08:30

US-08-612-929-25.rst

4

```
Db 48 gagagactgggtctactgg 67
|||||
Qy 2 GAGACTGTGTCTACTGG 21
```

```
RESULT 2
LOCUS W19941 136 bp mRNA 03-MAY-1996
DEFINITION z642h04.r1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone
306295 5' similar to SW:PPCT BOVIN P02720
PHOSPHATIDYLCHOLINE-TRANSFER PROTEIN. [1] ;.
ACCESSION W19941
NID g1296114
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 136)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevasakis,E., Waterston,R., Williamson,A., Wohlmann,P. and
Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT
Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: mob.REGA+ET
High quality sequence stop: 1.
```

```
NCBI gi: 1296114
Location/Qualifiers
1..136
/organism="Homo sapiens"
/note="Vector: pT7T3D (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer
[5'-
TCTTACCAATCTGAAGTGGCGCGCCGACCAATTTTTTTTTTTTTTTTTT
T-3'] , double-stranded cDNA was size selected, ligated to
Eco RI adapters (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of a modified pT7T3
vector (Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid
adenomas was kindly provided by Dr. Stephen Marx, National
Institute of Diabetes and Digestive and Kidney Diseases,
NIH."
/clone="306295"
/clone_lib="Soares parathyroid tumor NbHPA"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
<1..>136
mRNA
BASE COUNT 44 a 28 c 33 g 28 t 3 others
```

Mar 19 08:30

US-08-612-929-25.rst

5

## ORIGIN

Query Match 54.5%; Score 18; DB 153; Length 136;  
Best Local Similarity 95.0%; Pred. No. 3.36e-05;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 48 gagagactgtgtctactgg 67  
|||||  
Qy 2 GAGAGACTGTGTCTACTGG 21

## RESULT 3

LOCUS W04200 491 bp mRNA EST 22-APR-1996  
DEFINITION za57q09.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone  
296704 5' similar to SH:PPCT\_BOVIN P02720  
PHOSPHATIDYLCHOLINE-TRANSFER PROTEIN. [1] ;.

## ACCESSION W04200

NID g1276109

KEYWORDS EST.

SOURCE human.

## ORGANISM Homo sapiens

Eukaryotae; mitochondrion eukaryotes; Metazoa; Chordata;  
Vertebrata; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 491)

AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,  
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,  
Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and  
Wilson, R.

TITLE The WashU-Merck EST Project

JOURNAL Unpublished (1995)

## COMMENT

Contact: Wilson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone is available royalty-free through LNL ; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Seq primer: ETPrimer  
High quality sequence stop: 449.

NCBI gi: 1276109

Location/Qualifiers

## FEATURES

source

1..491  
/organism="Homo sapiens"  
/note="Organ: Liver and Spleen; Vector: pTT3D (Pharmacia)  
with a modified polylinker; Site\_1: Pac I; Site\_2: Eco RI;  
1st strand cDNA was primed with a Pac I - oligo(dT) primer  
[5' AACTGGAAGAAATTAAGATCTTTTCTTTTCTTTT 3'],  
double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Pac I and cloned into the Pac I  
and Eco RI sites of the modified pTT3 vector. Library  
went through one round of normalization. Library  
constructed by Bento Soares and M.Fatima Bonaldo."  
/clone="296704"

/clone\_lib="Soares fetal liver spleen INFLS"

/sex="male"

/dev stage="20 week-post conception fetus"

/lab host="DH10B (ampicillin resistant)"

&lt;1..&gt;491

mRNA

BASE COUNT 131 a 113 c 142 g 102 t 3 others

Mar 19 08:30

US-08-612-929-25.rst

6

## ORIGIN

Query Match 54.5%; Score 18; DB 147; Length 491;  
Best Local Similarity 95.0%; Pred. No. 3.36e-05;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 2 gagagactgtgtctactgg 21  
|||||  
Qy 2 GAGAGACTGTGTCTACTGG 21

## RESULT 4

ID HSW04200 standard; RNA; EST; 491 BP.  
AC W04200;  
DT 30-APR-1996 (Rel. 47, Created)  
DT 30-APR-1996 (Rel. 47, Last updated, Version 1)  
DE za57q09.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone  
296704 5' similar to SH:PPCT\_BOVIN P02720  
DE PHOSPHATIDYLCHOLINE-TRANSFER PROTEIN. [1] ;.

KW EST.

OS Homo sapiens (human)

OC Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;

OC Theria; Eutheria; Primates; Haplorhini; Catarrhini; Homidae.

RN [1]

RP 1-491

RA Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,

RA Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,

RA Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,

RA Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P., Wilson, R.;

RT "The WashU-Merck EST Project";

RL Unpublished.

CC Contact: Wilson RK WashU-Merck EST Project Washington University  
School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,  
MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email:  
est@watson.wustl.edu This clone is available royalty-free through  
LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for  
further information. Seq primer: ETPrimer High quality sequence  
stop: 449. NCBI gi: 1276109

FH Key

FH Location/Qualifiers

FT source

1..491

/organism="Homo sapiens"

/note="Organ: Liver and Spleen; Vector: pTT3D (Pharmacia)

with a modified polylinker; Site\_1: Pac I; Site\_2: Eco RI;

1st strand cDNA was primed with a Pac I - oligo(dT) primer

[5' AACTGGAAGAAATTAAGATCTTTTCTTTTCTTTT 3'],

double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Pac I and cloned into the Pac I

and Eco RI sites of the modified pTT3 vector. Library was

through one round of normalization. Library constructed by

Bento Soares and M.Fatima Bonaldo."

/clone="296704"

/clone\_lib="Soares fetal liver spleen INFLS"

/sex="male"

/dev stage="20 week-post conception fetus"

/lab host="DH10B (ampicillin resistant)"

&lt;1..&gt;491

FT mRNA

SQ Sequence 491 BP; 131 A; 113 C; 142 G; 102 T; 3 other;

Query Match 54.5%; Score 18; DB 168; Length 491;

Best Local Similarity 95.0%; Pred. No. 3.36e-05;

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Mar 19 08:30

US-08-612-929-25.fst

7

Db 2 gagagactgtgtctactgg 21  
|||||  
Oy 2 GAGAGACTGTGTCTACTGG 21

RESULT 5  
LOCUS HS2482C1 332 bp DNA STS 28-NOV-1994  
DEFINITION H. sapiens (D19S225) DNA segment containing (CA) repeat; clone  
AFW2482c1; single read.

ACCESSION 217126  
NID g23751  
KEYWORDS CA repeat; dinucleotide repeat; CT repeat; microsatellite DNA;  
microsatellite marker; repeat polymorphism.

SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Eumetazoa; Bilateria; Chordata; Metazoa; Eumetazoa; Bilateria; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Tetrapoda; Amniota; Mammalia; Theria; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 332)  
Weissenbach, J.  
Direct Submission  
Submitted (05-OCT-1992) to the EMBL/GenBank/DBJ databases.  
Genethon, B.P. 60, 91002 Evry Cedex France. E-mail: Jean.Weissenbach@genethon.fr

REFERENCE 2 (bases 1 to 332)  
Weissenbach, J., Gyapay, G., Dib, C., Vignal, A., Morissette, J., Millasseau, P., Vaysseix, G. and Lathrop, M.  
A second-generation linkage map of the human genome [see comments]  
Nature 359 (6398), 794-801 (1992)

REFERENCE 3 (bases 1 to 332)  
Gyapay, G., Morissette, J., Vignal, A., Dib, C., Fizames, C., Millasseau, P., Marc, S., Bernardi, G., Lathrop, M. and Weissenbach, J.  
The 1993-94 Genethon human genetic linkage map [see comments]  
Nature Genet. 7 (2 Spec No), 246-339 (1994)

JOURNAL Nature Genet. 7 (2 Spec No), 246-339 (1994)  
MEDLINE 95004593

COMMENT cloning vector is M13mp18;  
full automatic.

FEATURES  
source  
Location/Qualifiers  
1..332  
/organism="Homo sapiens"  
/cell\_line="CEPH 134702"  
/clone\_lib="genomic DNA"  
/chromosome="19"

BASE COUNT 97 a 89 c 49 g 97 t  
ORIGIN

Query Match 51.5%; Score 17; DB 135; Length 332;  
Best Local Similarity 87.0%; Pred. No. 6.87e-04;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 232 catctaagcaccagtcgaacaca 254  
|||||  
Cp 31 CATCGAGTACCAGTAGAACA 9

RESULT 6  
LOCUS H03526 395 bp mRNA EST 20-JUN-1995  
DEFINITION yj37c07.r1 Homo sapiens cDNA clone 150924 5'.  
ACCESSION H03526  
NID g866459  
KEYWORDS EST.

Mar 19 08:30

US-08-612-929-25.fst

8

SOURCE human clone=150924 library=Soares placenta Nb2HP vector=p7T73D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) primer=M13Rp1 Rsite1-Not I Rsite2-Eco RI Female placenta obtained at birth (full term). 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'  
AACTGGAAGATTCCGCCGCGAGGAATTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p7T73 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM Homo sapiens  
Eukaryota; Eumetazoa; Bilateria; Chordata; Metazoa; Eumetazoa; Bilateria; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcophaga; Chordata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 395)  
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevisan, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.  
The WashU-Merck EST Project  
Unpublished (1995)

TITLE The WashU-Merck EST Project  
JOURNAL  
COMMENT

Contact: Wilson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.edu  
High quality sequence stops: 314  
Source: IMAGE Consortium, LINL  
This clone is available royalty-free through LINL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES  
source  
Location/Qualifiers  
1..395  
/organism="Homo sapiens"  
/clone="150924"  
/note="human"

BASE COUNT 81 a 95 c 79 g 139 t 1 others  
ORIGIN

Query Match 51.5%; Score 17; DB 7; Length 395;  
Best Local Similarity 90.5%; Pred. No. 6.87e-04;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 254 aagaccagttcaacagtc 274  
|||||  
Cp 26 AAGTACCAGTAGAACAAGTC 6

RESULT 7  
LOCUS H33284 280 bp mRNA EST 08-SEP-1995  
DEFINITION EST109132 Rattus sp. cDNA 5' end.  
ACCESSION H33284  
NID g978701  
KEYWORDS EST.  
SOURCE rat primer=M13 Reverse library=Rat PC-12 cells, NGF-treated (9 days) vector=pBluescript SK- Rsite1-EcoRI Rsite2-XhoI poly(A) + RNA was purified from 9-day NGF treated PC12 cells. cDNA was constructed using an oligo-dT primer and directionally cloned using the Lambda ZAP II Vector Kit by Stratagene.

ORGANISM Rattus sp.

Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Rattus.

## REFERENCE

AUTHORS Lee, N.H., Weinstock, K.G., Kirkness, E.F., Earle-Hughes, J.A., Fuldner, R.A., Marmaras, S., Glodek, A., Cocayne, J.D., Adams, M.D., Kerlavage, A.R., Fraser, C.M. and Venter, J.C.

## TITLE

Comparative expressed sequence tag analysis of differential gene expression profiles in PC-12 cells before and after nerve growth factor treatment

## JOURNAL

Proc. Natl. Acad. Sci. USA 92, 8303-8307 (1995)

## COMMENT

Contact: Lee NH  
The Institute for Genomic Research  
932 Clopper Rd, Gaithersburg, MD 20878  
Tel: 3018699056  
Fax: 3018699423  
Email: nhlee@tigr.org  
For clone availability please contact the TIGR Database (tdbinfo@tdb.tigr.org)

## FEATURES

source Location/Qualifiers  
1..280  
/organism="Rattus sp."  
/note="rat"

mRNA  
BASE COUNT 75 a 68 c 62 g 73 t 2 others  
ORIGIN  
1..280  
/note="rat"

Query Match 48.5%; Score 16; DB 16; Length 280;  
Best Local Similarity 90.0%; Pred. No. 1.25e-02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 80 agtaccagtcacaccacgctc 99  
||||||||| |

Cp 25 AGTACCAGTAGACACACTC 6

## RESULT

ID M42722 standard; RNA; EST; 361 BP.

AC W12272;

DT 29-APR-1996 (Rel. 47, Created)

DT 29-APR-1996 (Rel. 47, Last updated, Version 1)

DE ma05hl2.rl Soares mouse p3NMF19.5 Mus musculus cDNA 5'.

KW EST.

OS Mus musculus (mouse)

OC Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;

OC Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.

RN [1]

RP 1-361

RA Marra M., Hillier L., Allen M., Bowles M., Dietrich N.,

RA Dubuque T., Geisel S., Kucaba T., Lacy M., Le M., Martin J.,

RA Morris M., Schellenberg K., Steptoe M., Tan F., Underwood K.,

RA Moore B., Theising B., Wylie T., Lennon G., Soares B., Wilson R.,

RA Waterston R.;

RT "The WashU-HHMI Mouse EST Project";

RL Unpublished.

CC Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project

CC Washington University School of Medicinep 4444 Forest Park Parkway,

CC Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810

CC Email: mouseest@watson.wustl.edu This clone is available

CC royalty-free through LNL ; contact the IMAGE Consortium

CC (info@image.llnl.gov) for further information. Putative full length

CC read Seq primer: mob.REGA+ET. NCBI gi: 1282961

FH Key

Location/Qualifiers

FH source  
FT 1..361  
/organism="Mus musculus"

FT /note="Vector: pT7T3D (Pharmacia) with a modified  
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA  
was primed with a Not I - oligo(dT) primer [5'  
TCTTACCAATCTGAAGTGGAGCGCGCATTTTTTTTTTTT 3'],  
double-stranded cDNA was size selected, ligated to Eco RI  
adapters (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of a modified pT7T3 vector  
(Pharmacia). Library went through one round of  
normalization to a Cot = 5. Library constructed by Bento  
Soares and M.Fatima Bonaldo."

FT /clone\_lib="Soares mouse p3NMF19.5"

FT /dev\_stage="19 weeks"

FT /lab\_host="DH10B (ampicillin resistant)"

FT mRNA  
<1..>361

SQ Sequence 361 BP; 89 A; 77 C; 104 G; 91 T; 0 other;

Query Match 48.5%; Score 16; DB 169; Length 361;

Best Local Similarity 90.0%; Pred. No. 1.25e-02;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 225 cgaagtacctgcagaacaca 244  
||||||||| |

Cp 28 CGAAGTACCAGTAGACACA 9

## RESULT

LOCUS W12272 361 bp mRNA EST 26-APR-1996  
DEFINITION ma05hl2.rl Soares mouse p3NMF19.5 Mus musculus cDNA 5'.

ACCESSION W12272

NTID g1282961

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;

Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;

Murinae; Mus.

REFERENCE 1 (bases 1 to 361)

AUTHORS

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,

Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,

Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,

Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and

Waterston, R.

TITLE The WashU-HHMI Mouse EST Project

JOURNAL Unpublished (1996)

COMMENT

Contact: Marra M/Mouse EST Project

WashU-HHMI Mouse EST Project

Washington University School of Medicinep

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LNL ; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Putative full length read

Seq primer: mob.REGA+ET.

NCBI gi: 1282961

FEATURES

source

Location/Qualifiers

1..361

/organism="Mus musculus"

Otsuka Pharmaceutical CO., Ltd  
463-10 Kagasuno Kawauchi-cho  
Tokushima, Tokushima  
771-01  
Japan  
Phone: 0896-65-2888  
Fax : 0896-37-1035.  
Location/Qualifiers  
1..487  
source  
FEATURES  
/clone\_lib="human fetal brain"  
/dev stage="Fetus"

RESULT	12
LOCUS	HUM533E03B
DEFINITION	Human placenta cDNA 5'-end GEN-533E03.
ACCESSION	D79180
EST	
13-DEC-1995	



NID g1181053  
KEYWORDS EST(expressed sequence tag); Human placenta.  
SOURCE Homo sapiens placenta cDNA to mRNA, clone lib:human placenta polyA+.  
ORGANISM Homo sapiens  
Eukaryota; Eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE 1 (bases 1 to 207)  
AUTHORS Fujiwara, T.  
TITLE Direct Submission  
JOURNAL Submitted (07-NOV-1995) to the DDBJ/EMBL/GenBank databases. Tsutomu Fujiwara, Otsuka GEN Research Institute, Otsuka Pharmaceutical Co., Ltd, 463-10 Kagasuno Kawauchi-cho, Tokushima, Tokushima 771-01, Japan  
REFERENCE 2 (bases 1 to 207)  
AUTHORS Fujiwara, T., Hirano, H., Katagiri, T., Kawai, A., Kuga, Y., Nagata, M., Okuno, S., Ozaki, K., Shimizu, F., Shimada, Y., Shinomiya, H., Takaichi, A., Takeda, S., Watanabe, F., Takahashi, E., Hirai, Y., Maekawa, H., Shin, S. and Nakamura, Y.  
TITLE Large-scale sequencing project at Otsuka GEN Research Institute  
JOURNAL Unpublished (1995)  
COMMENT Submitted (7-Nov-1995) to DDBJ by:  
Tsutomu Fujiwara  
Otsuka GEN Research Institute  
Otsuka Pharmaceutical Co., Ltd  
463-10 Kagasuno Kawauchi-cho  
Tokushima, Tokushima 771-01  
Japan  
Phone: 0886-65-2888  
Fax : 0886-37-1035.  
FEATURES  
source 1..207  
/clone lib="human placenta polyA+"  
/organism="Homo sapiens"  
/sequenced\_mol="cDNA to mRNA"  
/tissue\_type="placenta"  
BASE COUNT 52 a 41 c 42 g 72 t  
ORIGIN  
Query Match 45.5%; Score 15; DB 49; Length 207;  
Best Local Similarity 89.5%; Pred. No. 2.02e-01;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Db 54 agtacaagttagaccacagt 72  
||||| ||||||| |||||||  
Cp 25 AGTACCAGTAGACACAGT 7  
RESULT 13  
ID BT641 standard; DNA; STS; 213 BP.  
AC G18641;  
DT 13-MAR-1996 (Rel. 47, Created)  
DT 13-MAR-1996 (Rel. 47, Last updated, Version 1)  
DE cow STS BMS1242.  
KW primer; sequence tagged site; STS sequence.  
OS Bos taurus (cattle)  
OC Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;  
OC Theria; Eutheria; Artiodactyla; Ruminantia; Pecora; Bovidae.  
RN [1]  
RP 1-213  
RA Stone R.T., Pulido J.C., Duyk G.M., Kappes S.M., Keele J.W.,  
RA Beattie C.W.;  
RT \*A small-insert bovine genomic library highly enriched for

RT microsatellite repeat sequences\*;  
RL Mamm. Genome 6:714-724(1995).  
CC Contact: Roger Stone U.S. Meat Animal Research Center U.S. Dept. of Agriculture - Agricultural Research Service P.O. Box 166, Clay Center, NE 68933 Tel: (402) 762-4166 Fax: (402) 762-4173 Primer A: AGTGTGATCAACACGGCAG Primer B: AGTCACTGTCAGTGTTC STS size: 107.  
CC NCBI gi: 1223098  
FH Key Location/Qualifiers  
FH source 1..213  
FT /organism="Bos taurus"  
FT /note="cow"  
FT STS 84..190  
FT primer\_bind 84..103  
FT primer\_bind complement(171..190)  
SQ Sequence 213 BP; 41 A; 41 C; 64 G; 67 T; 0 other;  
Query Match 45.5%; Score 15; DB 173; Length 213;  
Best Local Similarity 94.1%; Pred. No. 2.02e-01;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Db 196 gtagaacacattctctc 212  
||||| ||||||| |||||||  
Cp 18 GTAGACACAGTCTCTC 2  
RESULT 14  
LOCUS G18641 213 bp DNA STS 12-MAR-1996  
DEFINITION cow STS BMS1242.  
ACCESSION G18641  
NID g1223098  
KEYWORDS STS sequence; primer; sequence tagged site.  
SOURCE cow.  
ORGANISM Bos taurus  
REFERENCE 1 (bases 1 to 213)  
AUTHORS Stone, R.T., Pulido, J.C., Duyk, G.M., Kappes, S.M., Keele, J.W. and Beattie, C.W.  
TITLE A small-insert bovine genomic library highly enriched for microsatellite repeat sequences  
JOURNAL Mamm. Genome 6 (10), 714-724 (1995)  
MEDLINE 96116960  
COMMENT Contact: Roger Stone  
U.S. Meat Animal Research Center  
U.S. Dept. of Agriculture - Agricultural Research Service  
P.O. Box 166, Clay Center, NE 68933  
Tel: (402) 762-4166  
Fax: (402) 762-4173  
Primer A: AGTGTGATCAACACGGCAG  
Primer B: AGTCACTGTCAGTGTTC  
STS size: 107.  
FEATURES  
source 1..213  
Location/Qualifiers  
/organism="Bos taurus"  
/note="cow"  
STS 84..190  
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primer\_bind complement(171..190)  
BASE COUNT 41 a 41 c 64 g 67 t  
ORIGIN  
Query Match 45.5%; Score 15; DB 135; Length 213;

91

Db 74 t g t c t a c t g g t t c t c t a t g 94  
|| || || || || || || || || || || ||  
Qy 11 T G T C T A C T G G T A C T T C G A T G 31





Query Match	63.6%;	Score 21;	DB 9;	Length 91;	
Best Local Similarity	0.0%;	Pred. No. 3.54e-02;			
Matches	0;	Conservative 26;	Mismatches 5;	Indels 0;	Gaps 0;

Db	18	vvhvvshhshvhhvhhvshvvvvhhvhhv 48
		::::::::: : ::::: : :::::
Qy	1	AGAGAGACTGTTCTTACTGCTACTTCGATG 31

RESULT	5	
ID	Q83500	standard; DNA; 120 BP.
AC	Q83500;	
DT	20-SEP-1995	(first entry)
DE	Heavy chain variable region fragment.	
KW	Humanized antibody; antibody engineering; monoclonal antibody;	
KW	MAb; interleukin-4; IL-4; allergy; heavy chain; ss.	
OS	Synthetic.	
PN	W09507301-A.	
PD	16-MAR-1995.	
PF	07-SEP-1994;	U10308.
PR	07-SEP-1993;	US-117366.
PR	14-OCT-1993;	US-136783.
PA	(SMIK ) SMITHKLINE BEECHAM CORP.	
PA	(SMIK ) SMITHKLINE BEECHAM PLC.	
PI	Gross MS, Holmes SD, Sylvester DR;	
DR	WPI; 95-123387/16.	
PT	Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived	
PT	from high affinity mAbs - useful in treatment of IL-4-mediated	
PT	and IgE-mediated allergic conditions	
PS	Example 3; Page 62; 9pp; English.	
CC	A humanized antibody was designed to contain mouse CDRs (from	
CC	anti-IL-4 MAb 3B9 MAb) within a human antibody framework. A	
CC	synthetic heavy chain was made using the oligonucleotides given	
CC	in Q83498-502 and amplified by PCR using the primers given in	
CC	Q83503-04. The construct was ligated into vector pCD, along	
CC	with a signal sequence (Q83494) and an IgG1 human constant	
CC	region. The CDR gene regions of a pre-existing light chain	
CC	framework were replaced with synthetic IL-4 CDR genes constructed	
CC	from oligonucleotides given in Q83505-08 (CDR1), Q83509-10 (CDR2),	
CC	and Q83511-12 (CDR3). The synthetic VL (Q73986) was ligated into	
CC	the vector. The anti-IL4 engineered antibody was expressed in	
CC	COS and CHO cells.	
SQ	Sequence 120 BP;	20 A; 39 C; 29 G; 32 T;

Query Match	63.6%;	Score 21;	DB 14;	Length 120;	
Best Local Similarity	86.2%;	Pred. No. 3.54e-02;			
Matches	25;	Conservative 0;	Mismatches 4;	Indels 0;	Gaps 0;

Query Match 63.6%; Score 21; DB 14; Length 120;  
Best Local Similarity 86.2%; Pred. No. 3.54e-02;  
Matches 25; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

[illegible]

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FT /*tag= a 1.57
FT sig_peptide
FT /*tag= b
FT mat_peptide 58..423
FT /*tag= c
PN W09507301-A.
PD 16-MAR-1995.
PF 07-SEP-1994; U10308.
PR 07-SEP-1993; US-117366.
PS 14-OCT-1993; US-136783.
PA (SMIK ) SMITHKLINE BEECHAM CORP.
PA (SMIK ) SMITHKLINE BEECHAM PLC.
PI Gross MS, Holmes SD, Sylvestre DR;
DR WPI; 95-123387/16.
DR P-PSDB; R70192.
PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived
PT from high affinity mAbs - useful in treatment of IL-4-mediated
PT and IgE-mediated allergic conditions
PS Disclosure; Fig.4; 97pp; English.
CC A humanized antibody heavy chain variable region and signal
CC sequence is given in R70192. The signal sequence is also
CC provided in R70193. The CDR sequences of the construct are
CC identical to the native CDRs of mouse anti-human IL-4 MAb
CC 3B9 (R70198-200).
SQ Sequence 423 BP; 84 A; 131 C; 102 G; 106 T;

Query Match 63.6%; Score 21; DB 14; Length 423;
Best Local Similarity 86.2%; Pred.No. 3,54e-02;
Matches 25; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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**Db**      361    gaacgcgttttctactggtactcgacgt    389  
         || | | | | | | | | | | | |  
**Qy**      4    GAGACTGTGTTCTACTGGTACTTCGATGT    32

RESULT	7	Q51555 standard; DNA; 417 BP.
ID		
AC	Q51555;	
DT	25-MAY-1994 (first entry)	
DE	PB1.3/Humanised heavy chain-C signal peptide and variable region DNA.	
DE	Human; Immunoglobulin; constant; region; humanised; p-selectin; light;	
KW	blocking; antibody; heavy; chain; variable; murine; thrombotic disease;	
KW	monoclonal; PB1.3; CDR; complementarity determining region; leukocyte;	
KW	expression vector; coexpression; pHCW-1748RIA-gammaCI-dhfr; epitope;	
KW	pHCW-1748RIA-KR-neo; PB1.3/Humanised version A; vascular endothelium;	
KW	pHCW-1747CH-gammaCI-neo; pHCW-1747-CL-KR-neo; PB1.3 chimera;	
KW	acute lung injury; ischaemia reperfusion injury; inflammation; ss.	
OS	Chimera Mus musculus.	
OS	Chimera Homo sapiens.	
PN	W09321956-A.	
PD	11-NOV-1993.	
PF	04-MAY-1993; U04274.	
PR	05-MAY-1992; US-880196.	
PA	(CYTE-) CYTEL CORP.	
PI	Chestnut RW, Paulson JC, Polley MJ;	
DR	WPI; 93-368423/46.	
DR	P-PSDB; R43693.	
PT	Anti-p-selectin antibody for ischaemia acute lung injury treatment -	
PT	useful to treat inflammation and pathological conditions of	
PT	intercellular adhesion by competitive inhibition assays	
PS	Example 10; Fig 17; 82pp; English.	
CC	The sequences given in Q51551-55 encode the heavy and light chains of	
CC	the PB1.3/Humanised p-selectin blocking antibody of the invention.	
CC	The sequences given in Q51549-50 which encode the heavy and light	

CC chain variable region sequences of the murine monoclonal antibody  
 CC PBL1.3 and the sequences given in Q51547-48 which encode human  
 CC immunoglobulin constant regions were used in the production of this  
 CC antibody. The CDRs from PBL1.3 heavy and light chains were substituted  
 CC for the CDRs of human heavy and light chains. The humanised variable  
 CC regions were inserted into expression vectors. By coexpression of  
 CC appropriate combinations of heavy and light chains, several humanised  
 CC antibodies can be expressed. Coexpression of pHCMV-1748RHA-gamma1C1-  
 CC dhfr and pHCMV-1748RIA-KR-neo gives rise to the PBL1.3/Humanised  
 CC version A. Coexpression of pHCMV-1747CH-gamma1C1-neo and pHCMV-1747-  
 CC C1-K3-neo gives rise to the PBL1.3 chimera. These humanised antibodies  
 CC selectively bind epitopes on P-selectin and block adhesion of  
 CC leukocytes to the vascular endothelium. They may be used to treat  
 CC inflammatory and thrombotic diseases and other pathological conditions  
 CC involving P-selectin and antibodies to it, esp. acute lung injury and  
 CC ischaemia reperfusion injury.  
 SQ Sequence 417 BP; 95 A; 101 C; 119 G; 102 T;

Query Match 60.6%; Score 20; DB 9; Length 417;  
 Best Local Similarity 95.5%; Pred. No. 1.20e-01;  
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 363 gttcgaactgtacttcgatgac 384

QY 12 GTTCTACTGGTACTTCGATGTC 33  
 ||||| ||||| ||||| ||||| |||||

#### RESULT 8

ID Q73023 standard; cDNA; 417 BP.  
 AC Q73023;  
 DT 12-JUN-1995 (first entry)  
 DE CY1748RHA VH region.  
 KW P-selectin; CY1748RHA; light chain; heavy chain; variable region;  
 KW VI; VH; complementarity determining region; CDR;  
 KW antibody engineering; humanized antibody; leukocyte adhesion;  
 KW transplacental rejection; autoimmune disease; therapeutic; diagnostic;  
 KW monoclonal antibody; Mab; COS; ss.  
 OS Homo sapiens.

FH Key Location/Qualifiers

FT CDS 1..417

FT /tag= a

FT sig\_peptide 1..57

FT /tag= b

FT mat\_peptide 58..417

FT /tag= c

PN M09425067-A.

PD 10-NOV-1994.

PF 04-MAY-1994; U04935.

PR 04-MAY-1993; WO-U04272.

PR 05-MAY-1993; US-057292.

PR 25-FEB-1994; US-202047.

PA (CYTE-) CYTEL CORP.

PI Bayer R, Bendig MM, Chesnut RW, Jones ST, Krieglner M;

PI Nunn M, Paulson JC, Perez C, Polley MJ, Saldanha JW;

DR WPI; 94-357916/44.

DR P-PSDB; R62678.

PT Blocking antibodies against P-selectin - used to treat

PT inflammation and inhibit leukocyte adhesion to platelets and/or

PT activated vascular endothelium

PS Disclosure; Fig. 11; 138pp; English.

CC Human Mab DEN VI and human Mab 21/28'CL VH regions were selected

CC as fragments to join the corresponding CDRs of mouse anti-P-selectin

CC Mab PBL1.3 (ATCC HB 11041) for construction of humanized antibodies.

CC 3 Versions of the VH region (CY1748RHA, CY1748RHB, CY1748RHC) were

CC designed (given in R62678-80, respectively) and 4 versions of the VL  
 CC region (CY1748RLA, CY1748RLB, CY1748RLC, CY1748RLD) (R62674-77).  
 CC Humanized antibodies were expressed in COS cells. The preferred  
 CC construct was formed from CY1748RHB and CY1748RLD.

SQ Sequence 417 BP; 94 A; 102 C; 119 G; 102 T;

Query Match 60.6%; Score 20; DB 12; Length 417;  
 Best Local Similarity 95.5%; Pred. No. 1.20e-01;  
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 363 gttcgaactgtacttcgatgac 384

QY 12 GTTCTACTGGTACTTCGATGTC 33  
 ||||| ||||| ||||| ||||| |||||

#### RESULT 9

ID Q73025 standard; cDNA; 417 BP.  
 AC Q73025;  
 DT 12-JUN-1995 (first entry)  
 DE CY1748RHC VH region.  
 KW P-selectin; CY1748RHC; light chain; heavy chain; variable region;  
 KW VI; VH; complementarity determining region; CDR;  
 KW antibody engineering; humanized antibody; leukocyte adhesion;  
 KW transplacental rejection; autoimmune disease; therapeutic; diagnostic;  
 KW monoclonal antibody; Mab; COS; ss.  
 OS Homo sapiens.

FH Key Location/Qualifiers

FT CDS 1..417

FT /tag= a

FT sig\_peptide 1..57

FT /tag= b

FT mat\_peptide 58..417

FT /tag= c

PN M09425067-A.

PD 10-NOV-1994.

PF 04-MAY-1994; U04935.

PR 04-MAY-1993; WO-U04272.

PR 05-MAY-1993; US-057292.

PR 25-FEB-1994; US-202047.

PA (CYTE-) CYTEL CORP.

PI Bayer R, Bendig MM, Chesnut RW, Jones ST, Krieglner M;

PI Nunn M, Paulson JC, Perez C, Polley MJ, Saldanha JW;

DR WPI; 94-357916/44.

DR P-PSDB; R62680.

PT Blocking antibodies against P-selectin - used to treat

PT inflammation and inhibit leukocyte adhesion to platelets and/or

PT activated vascular endothelium

PS Disclosure; Fig. 13; 138pp; English.

CC Human Mab DEN VI and human Mab 21/28'CL VH regions were selected

CC as fragments to join the corresponding CDRs of mouse anti-P-selectin

CC Mab PBL1.3 (ATCC HB 11041) for construction of humanized antibodies.

CC 3 Versions of the VH region (CY1748RHA, CY1748RHB, CY1748RHC) were

CC designed (given in R62678-80, respectively) and 4 versions of the VL

CC region (CY1748RLA, CY1748RLB, CY1748RLC, CY1748RLD) (R62674-77).

CC Humanized antibodies were expressed in COS cells. The preferred

CC construct was formed from CY1748RHB and CY1748RLD.

SQ Sequence 417 BP; 95 A; 101 C; 119 G; 102 T;

Query Match 60.6%; Score 20; DB 12; Length 417;

Best Local Similarity 95.5%; Pred. No. 1.20e-01;

Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 363 gttcgaactgtacttcgatgac 384

||||| ||||| ||||| ||||| |||||

QY 12 GTTCTACTGGTACTTCGATGTC 33

## RESULT 10

ID Q73024 standard; cDNA; 417 BP.  
AC Q73024;  
DT 12-JUN-1995 (first entry)  
DE CY1748RHB VH region.  
KW P-selectin; CY1748RHB; light chain; heavy chain; variable region;  
KW VL; VH; complementarity determining region; CDR;  
KW antibody engineering; humanized antibody; leukocyte adhesion;  
KW transplant rejection; autoimmune disease; therapeutic; diagnostic;  
KW monoclonal antibody; Mab; COS; ss.  
OS Homo sapiens. Location/Qualifiers  
FH Key 1..417  
FT CDS /\*tag= a  
FT sig\_peptide 1..57  
FT /\*tag= b  
FT mat\_peptide 58..417  
FT /\*tag= c  
PN W09425067-A.  
PD 10-NOV-1994.  
PF 04-MAY-1994; U04935.  
PR 04-MAY-1993; W0-004272.  
PR 05-MAY-1993; US-057292.  
PR 25-FEB-1994; US-202047.  
PA (CYTE-) CYTEL CORP.  
PI Bayer R, Bendig MM, Chesnut RW, Jones ST, Krieglner M;  
PI Nunn M, Paulson JC, Perez C, Polley MJ, Saldanha JW;  
DR WP1; 94-357916/44.  
DR P-PSDB; R62679.  
PT Blocking antibodies against P-selectin - used to treat  
PT inflammation and inhibit leukocyte adhesion to platelets and/or  
PT activated vascular endothelium  
PS Disclosure; Fig. 12; 138pp; English.  
CC Human Mab DEN VL and human Mab 21/28'CL VH regions were selected  
CC as fragments to join the corresponding CDRs of mouse anti-P-selectin  
CC Mab PBL.3 (ATCC HB 11041) for construction of humanized antibodies.  
CC 3 Versions of the VH region (CY1748RHA, CY1748RHB, CY1748RHC) were  
CC designed (given in R62678-80, respectively) and 4 versions of the VL  
CC region (CY1748RLA, CY1748RLB, CY1748RLC, CY1748RLD) (R62674-77).  
CC Humanized antibodies were expressed in COS cells. The preferred  
CC construct was formed from CY1748RHB and CY1748RLD.  
SQ Sequence 417 BP; 94 A; 102 C; 118 G; 103 T;

Query Match 60.6%; Score 20; DB 12; Length 417;  
Best Local Similarity 95.5%; Pred. No. 1.20e-01;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 363 gttcgaactggtacttcgagtgc 384

||||| ||||||| ||||||| |||||||

QY 12 GTTCTACTGGTACTTCGATGTC 33

## RESULT 11

ID Q51551 standard; DNA; 417 BP.  
AC Q51551;  
DT 25-MAY-1994 (first entry)  
DE PBL.3/Humanised heavy chain signal peptide and variable region DNA.  
KW Human; immunoglobulin; constant; region; humanised; P-selectin; light;  
KW blocking; antibody; heavy; chain; variable; murine; thrombotic disease;  
KW monoclonal; PBL.3; CDR; complementarity determining region; leukocyte;  
KW expression vector; coexpression; pHCMV-1748RHA-gamma1CI-dhfr; epitope;

KW pHCMV-1748RLA-KR-neo; PBL.3/Humanised version A; vascular endothelium;  
KW pHCMV-1747CH-gamma1CI-neo; pHCMV-1747-CL-KR-neo; PBL.3 chimera;  
KW acute lung injury; ischaemia reperfusion injury; inflammation; ss.  
OS Chimera Mus musculus.  
OS Chimera Homo sapiens.  
PN W09321956-A.  
PD 11-NOV-1993.  
PF 04-MAY-1993; U04274.  
PR 05-MAY-1992; US-880196.  
PA (CYTE-) CYTEL CORP.  
PI Chestnut RW, Paulson JC, Polley MJ;  
DR WP1; 93-368423/46.  
DR P-PSDB; R43689.  
PT Anti-P-selectin antibody for ischaemia acute lung injury treatment -  
PT useful to treat inflammation and pathological conditions of  
PT intercellular adhesion by competitive inhibition assays  
PS Example 10; Fig 13; 82pp; English.  
CC The sequences given in Q51551-55 encode the heavy and light chains of  
CC the PBL.3/Humanised P-selectin blocking antibody of the invention.  
CC The sequences given in Q51549-50 which encode the heavy and light  
CC chain variable region sequences of the murine monoclonal antibody  
CC PBL.3 and the sequences given in Q51547-48 which encode human  
CC immunoglobulin constant regions were used in the production of this  
CC antibody. The CDRs from PBL.3 heavy and light chains were substituted  
CC for the CDRs of human heavy and light chains. The humanised variable  
CC regions were inserted into expression vectors. By coexpression of  
CC appropriate combinations of heavy and light chains, several humanised  
CC antibodies can be expressed. Coexpression of pHCMV-1748RHA-gamma1CI-  
CC dhfr and pHCMV-1748RLA-KR-neo gives rise to the PBL.3/Humanised  
CC version A. Coexpression of pHCMV-1747CH-gamma1CI-neo and pHCMV-1747-  
CC CL-KR-neo gives rise to the PBL.3 chimera. These humanised antibodies  
CC selectively bind epitopes on P-selectin and block adhesion of  
CC leukocytes to the vascular endothelium. They may be used to treat  
CC inflammatory and thrombotic diseases and other pathological conditions  
CC involving P-selectin and antibodies to it, esp. acute lung injury and  
CC ischaemia reperfusion injury.  
SQ Sequence 417 BP; 94 A; 101 C; 119 G; 103 T;

Query Match 60.6%; Score 20; DB 9; Length 417;  
Best Local Similarity 95.5%; Pred. No. 1.20e-01;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 363 gttcgaactggtacttcgagtgc 384

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QY 12 GTTCTACTGGTACTTCGATGTC 33

## RESULT 12

ID Q78738 standard; DNA; 30 BP.  
AC Q78738;  
DT 18-JUL-1995 (first entry)  
DE Murine anti-human atherosclerotic plaque Mab 22D3 VH CDR3 DNA.  
KW Atherosclerosis; atherosclerotic plaque; anti-hydroxysteroid antibody;  
KW murine monoclonal antibody; heavy chain variable region; CDR3;  
KW complementarity determining region; imaging; plaque ablation; ds.  
OS Mus musculus.  
FH Key Location/Qualifiers  
FT misc RNA 1..30  
FT /\*tag= a  
FT /product= CDR3  
PN W09425053-A.  
PD 10-NOV-1994.  
PF 26-APR-1994; U04641.  
PR 26-APR-1993; US-053451.

21

PA	(FARH ) HOECHST AG.
PI	Habermann P, Seed B, Stengelin S, Uhlmann E, Ulmer W;
PR	WPI; 93-235119/29.
DR	Fusion proteins for prodn. of e.g. pro-insulin - comprise gene
PT	for desired protein and oligo-nucleotide(s) encoding ballast
PT	protein
PS	Claim 9; Column 30; 22pp; English.
CC	This preferred mixed oligonucleotide encodes a ballast constituent
CC	and is inserted between a regulatory region and the structural gene
CC	encoding a desired protein, esp. pro-insulin. The short ballast
CC	component improves protease resistance of the fusion protein while
CC	still allowing the desired protein to adopt its correct conformation
CC	prior to cleavage of the ballast constituent.
SQ	Sequence 39 BP; 1 A; 11 C; 1 G; 1 T;

Query Match	57.6%;	Score 19;	DB 7;	Length 39;
Best Local Similarity	28.0%;	Pred. No. 4.02e-01;		
Matches	7;	Conservative 15;	Mismatches 3;	Indels 0;
Gaps	0;			

RESULT	14
ID	Q04593 standard; DNA; 318 BP.
AC	Q04593;
DT	28-SEP-1990 (first entry)
DE	Sequence encoding region of human carcinoembrionic heavy chain antigen (CEA).
DE	antigen (CEA).
KW	Carcinoembrionic antigen; CEA; Chelate-specific antigen; CEA;
KW	tumor; cancer; serum sickness.

DT 28-SEP-1990 (first entry)  
DE Sequence encoding region of human carcinoembryonic heavy chain  
DE antigen (CEA).  
DE Carcinoembryonic antigen; CEA; Chelate-specific antigen; CHA;  
KW tumor; cancer; serum sickness.

OS	<i>Homo sapiens</i> .
PN	EP-369566-A.
PD	23-MAY-1990.
PF	8-MAR-1989; 302313.
PR	17-NOV-1988; US-274105; EP-302313.
PA	(HYBR-) Hybritech Inc.
PI	Johnson MJ, Phelps JL;
DR	WPI; 90-157695/21.
DR	P-PSDB; R04937.
PT	Bifunctional chimeric antibodies -
PT	having variable regions which recognise different antigens and
PT	metal chelates and human constant regions.
PS	Claim 2; Page 24; 40pp; English.
CC	Gene encodes portion of CEA heavy chain antigen, useful in
CC	generating chimeric monoclonal antibody binding to CEA at a tumour
CC	site and a metal chelate bonded to say a toxin or other drug.
SC	Sequence 318 BP: 74 A; 86 G; 83 G; 75 T;

Query Match	57.6%;	Score 19;	DB 1;	Length 318;
Best Local Similarity	100.0%;	Pred. No. 4, 02e-01;		
Matches	19;	Conservative	0;	Mismatches 0;
		Indels	0;	Gaps 0;
Db	264	ctactggtacttcgatgctc	282	
Qy	15	CTACTGCTACTTCGATGTC	33	
RESULT	15			
ID	T12813	standard;	cDNA;	364 BP.
	AC	T12813;		
DT	10-OCT-1996	(first entry)		
DE	Murine antibody ZCE-025	heavy chain variable region	cDNA.	



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13

KW Heavy chain; variable region; murine; tumour antigen; antibody;  
KW ZCE-025; construction; CDR switched variable light chain region;  
KW kappa-body fragment; in vitro; diagnosis; therapy;  
KW naked antibody; radioimmunotherapy; radioimmunodiagnosics;  
KW radioimmunometric assays; ELISA; immunohistochemical;  
KW complementarity determining region; ss.

OS Mus musculus.

FH Key Location/Qualifiers  
FT mat\_peptide 1..363

FT /\*tag= a

PN M09606625-A1.

PD 07-MAR-1996.

PF 25-AUG-1995; U10791.

PR 26-AUG-1994; US-296625.

PA (ELIL ) LILLY & CO ELL.

PI ILL CR, Ludwig JR, Rathnachalam R;

DR WPI; 96-160137/16.

DR P-PSDB; R88846.

PT Recombinant antibody comprising CDR-switched light chain variable  
PT region - having VL domain framework and VH domain CDRs, useful in  
PT radioimmunotherapy, ELISA assays, etc.

PS Example 1; Page 61; 162pp; English.

CC The present sequence encodes the heavy chain variable (HL) region  
CC of the murine anti-ZCE-025 tumour antigen antibody (Ab), ZCE-025,  
CC which was used in the construction of a CDR switched light chain  
CC variable (VL) region (CSVL) Ab, or kappa-body fragment. A CSVL  
CC comprises at least 1 VL region with 3 CDR, where 1 or more of the

CC CDR is derived from the corresponding CDR of a VH region of 1  
CC (donor) Ab, and 4 framework (FW) regions where 1 or more of the  
CC regions is derived from the corresponding FW region(s) from the VL  
CC region of the same or different (acceptor) Ab.

CC The CSVL Ab, or kappa-body fragment can be used in in vitro and  
CC in vivo diagnostic and therapeutic applications, including naked Ab  
CC therapy, radioimmunotherapy (i.e. when fused to a chelating peptide  
CC incorporating Yttrium-90 as the therapeutic radioion), in vivo  
CC radioimmunodiagnosics, in vitro radioimmunometric assays, ELISA  
CC and immunohistochemical applications.

SQ Sequence 364 BP; 85 A; 91 C; 101 G; 87 T;

Query Match 57.6%; Score 19; DB 22; Length 364;

Best Local Similarity 100.0%; Pred. No. 4.02e-01;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 312 ctactgttacttcgatgtc 330

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Qy 15 CTACTGCTACTTCGATGTC 33

Search completed: Wed Mar 19 08:31:07 1997

Job time : 15 secs.



Mar 19:08:28

US-08-612-929-25.fgc

3

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Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
Murinae; Mus.
REFERENCE
AUTHORS      Caton,A.J., Swartzentruber,J.R., Kuhl,A.L., Carding,S.R. and
              Stark,S.E.
TITLE         Activation and negative selection of functionally distinct subsets
              of antibody-secreting cells by influenza hemagglutinin as a viral
              and a neo-self antigen
JOURNAL       J. Exp. Med. 183 (1), 13-26 (1996)
MEDLINE       96136744
REFERENCE     2 (bases 1 to 324)
              Swartzentruber,J.R.
AUTHORS       Direct Submission
TITLE         Submitted (10-OCT-1995) Jennifer R. Swartzentruber, The Wistar
              Institute, 3601 Spruce St., Philadelphia, PA 19104, USA
JOURNAL       Location/Qualifiers
FEATURES      source
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              /isolate="h920-293"
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              /db_xref="PID:g1127629"
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              TTVTVS"
BASE COUNT   77 a 84 c 85 g 78 t
ORIGIN
Query Match      69.7%; Score 23; DB 65; Length 324;
Best Local Similarity 84.8%; Pred. No. 9.34e-04;
Matches 28; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Db 262 agagagattctctactgtactgtactgtc 294
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Qy 1 AGAGAGACTGCTGTTCTACTGCTACTTCGATGTC 33
RESULT 2
ID MM37857 standard; RNA; ROD; 324 BP.
AC U37857;
DT 23-DEC-1995 (Rel. 46, Created)
DT 20-MAR-1996 (Rel. 47, Last updated, Version 2)
DE Mus musculus rearranged immunoglobulin heavy chain variable region
DE mRNA, partial cds.
KW Mus musculus (mouse)
OS Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
OC Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
RN [1]
RP 1-324
RA Caton A.J., Swartzentruber J.R., Kuhl A.L., Carding S.R.,
RA Stark S.E.;
RT "Activation and negative selection of functionally distinct
RT subsets of antibody-secreting cells by influenza hemagglutinin as
RT a viral and a neo-self antigen";
RL J. Exp. Med. 183:13-26(1996).
RN [2]
RP 1-324
RA Swartzentruber J.R.;
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Mar 19:08:28

US-08-612-929-25.fgc

4

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; Submitted (10-OCT-1995) to the EMBL/GenBank/DBJ databases.
RL Jennifer R. Swartzentruber, The Wistar Institute, 3601 Spruce St.,
RL Philadelphia, PA 19104, USA
CC NCBI gi: 1127628 Location/Qualifiers
FH Key
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FT /isolate="h920-293"
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FT /cell_type="B-lymphocyte"
FT <1..>324
FT /codon_start=1
FT /product="rearranged immunoglobulin heavy chain variable
FT region"
FT /db_xref="PID:g1127629"
FT /translation="LVKPGASVKLSCKASGYFTSYINWIKORPQGQLEWIGRIAPG
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FT VTWS"
SQ Sequence 324 BP; 77 A; 84 C; 85 G; 78 T; 0 other;
Query Match      69.7%; Score 23; DB 12; Length 324;
Best Local Similarity 84.8%; Pred. No. 9.34e-04;
Matches 28; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Db 262 agagagattctctactgtactgtactgtc 294
||||| | | | | | | | | | | | | | | | | |
Qy 1 AGAGAGACTGCTGTTCTACTGCTACTTCGATGTC 33
RESULT 3
LOCUS MUSIHC 414 bp mRNA ROD 05-MAY-1995
DEFINITION Mus musculus immunoglobulin heavy chain mRNA, 5' end of cds.
ACCESSION L41877
NID g798802
KEYWORDS immunoglobulin heavy chain.
SOURCE Mus musculus (strain BALB/c, sub_species domesticus) cDNA to mRNA.
ORGANISM Mus musculus
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE 1 (bases 1 to 414)
AUTHORS Asakura,K., Miller,D.J., Pogulis,R.J., Pease,L.R. and Rodriguez,M.
TITLE Oligodendrocyte-specific O1, O4, and HNK-1 monoclonal antibodies
are encoded by germline immunoglobulin genes
JOURNAL DNA (1995) In press
FEATURES      Location/Qualifiers
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Mar 19 08:28

US-08-612-929-25.fge

5

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mat_peptide      /codon start=1
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BASE COUNT      99 a   97 c  117 g  101 t
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Matches 28; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Db 349 agagggccaggttctactgtactgtatgc 381
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QY 1 AGAGAGACTGCTTCTACTGCTACTTCGATGC 33

RESULT 4
LOCUS S67978 53 bp mRNA ROD 15-MAR-1994
DEFINITION Ig VH81X=Ig heavy chain VDJ region [mice, BALB/c, liver, mRNA
Partial, 53 nt].
ACCESSION S67978
NID 9460843
KEYWORDS
SOURCE mice liver BALB/c.
ORGANISM Mus sp.
Unclassified.
REFERENCE 1 (bases 1 to 53)
AUTHORS Chukwuocha,R.U. and Feeney,A.J.
TITLE Role of homology-directed recombination: predominantly productive
rearrangements of VH81X in newborns but not in adults
JOURNAL Mol. Immunol. 30 (16), 1473-1479 (1993)
MEDLINE 94049838
REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI gibbsq 142175] from the original journal article.
This sequence comes from Fig. 3.
FEATURES
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Location/Qualifiers
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/notes="Description: Ig heavy chain VDJ region"
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BASE COUNT 12 a 16 c 11 g 14 t
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Best Local Similarity 100.0%; Pred. No. 2.52e-02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 33 ttctactgtactgtatgc 53
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QY 13 TTCTACTGCTACTTCGATGC 33

RESULT 5
LOCUS MUSIGHAVRN 339 bp mRNA ROD 27-APR-1995
DEFINITION Mouse mRNA for IgH variable region.
ACCESSION D25498
NID 9624903
KEYWORDS IgH variable region.
SOURCE Mus musculus (strain BALB/c) cell-line hybridoma 1F7 (library:
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Mar 19 08:28

US-08-612-929-25.fge

6

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lambda HL) cDNA to mRNA, clone 1F7802.
Mus musculus
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE 1 (bases 1 to 339)
AUTHORS Chin,I.-S., Lin,C.-P. and Tseng,T.-C.
TITLE Molecular cloning and expression of Anti-aflatoxin B1 monoclonal
antibody fragment in E.coli
JOURNAL Unpublished (1993)
COMMENT Submitted (24-Nov-1993) to DDBJ by:
Tsung-Che Tseng
Phone: 7899590 x424
Email: BOCHAW@TNAS886.BITNET
Fax: 7827954.
FEATURES
source
Location/Qualifiers
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/organism="Mus musculus"
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/sequenced_mol="cDNA to mRNA"
/clone_lib="lambda HL"
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Best Local Similarity 81.8%; Pred. No. 2.52e-02;
Matches 27; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Db 274 agatgtattacgggtactgtactgtatgc 306
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QY 1 AGAGAGACTGCTTCTACTGCTACTTCGATGC 33

RESULT 6
LOCUS MMIG03 532 bp DNA ROD 29-JAN-1994
DEFINITION Part of mouse gene for immunoglobulin heavy chain J segments.
ACCESSION V00759
NID g51578
KEYWORDS germ line; immunoglobulin.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 532)
AUTHORS Early,P., Huang,H., Davis,M., Calame,K. and Hood,L.
TITLE An immunoglobulin heavy chain variable region gene is generated
from three segments of DNA: VH, D and JH
JOURNAL Cell 19 (4), 981-992 (1980)
MEDLINE 80199926
COMMENT KST MMU.IGHC.GL.2.
FEATURES
source
Location/Qualifiers
1..532
/organism="Mus musculus"
163..213
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482..526
/note="reading frame (JOINING SEGMENT H315)"
BASE COUNT 126 a 118 c 148 g 140 t
ORIGIN
Query Match 63.6%; Score 21; DB 64; Length 532;
Best Local Similarity 95.7%; Pred. No. 2.52e-02;
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Mar 19 08:28

US-08-612-929-25.rge

7

Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 158 tgtgctactgtacttcgatgtc 180  
|||||  
Qy 11 TGTCTACTGCTACTTCGATGTC 33

RESULT 7  
ID MMIG03  
AC V00759;  
DT 09-JUN-1982 (Rel. 01, Created)  
DT 07-MAY-1996 (Rel. 47, Last updated, Version 7)  
DE Part of mouse gene for immunoglobulin heavy chain J segments.  
KW germ line; immunoglobulin.  
OS Mus musculus (mouse)  
OC Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;  
OC Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.  
RN [1]  
RX 1-532  
RX MEDLINE; 80199926.  
RA Early P., Huang H., Davis M., Calame K., Hood L.;  
RT "An immunoglobulin heavy chain variable region gene is generated  
RT from three segments of DNA: VH, D and JH";  
RL Cell 19:981-992(1980).  
DR IMG7/LIGM; V00759; Release 3.0.  
CC KST MWI.IGHC.GL.2  
FH Key Location/Qualifiers

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FT 163..213  
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FT 482..526  
FT /note="reading frame (JOINING SEGMENT H315)"  
FT /db\_xref="PID:e6310"  
FT /translation="YFYDWGQGTTLTVSS"  
FT  
SQ Sequence 532 BP; 126 A; 118 C; 148 G; 140 T; 0 other;

Query Match 63.6%; Score 21; DB 12; Length 532;  
Best Local Similarity 95.7%; Pred. No. 2.52e-02;  
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 158 tgtgctactgtacttcgatgtc 180  
|||||  
Qy 11 TGTCTACTGCTACTTCGATGTC 33

RESULT 8  
LOCUS MMC57IG 1338 bp DNA ROD 09-DEC-1992  
DEFINITION M.musculus (C57BL/10) DNA for Igh-J locus.  
ACCESSION X63167  
NID g50243  
KEYWORDS immunoglobulin heavy chain J locus.  
SOURCE house mouse.  
ORGANISM Mus musculus

Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;  
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;  
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;  
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;  
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 1338)  
AUTHORS Solin,M.

Mar 19 08:28

US-08-612-929-25.rge

8

TITLE Direct Submission  
JOURNAL Submitted (11-NOV-1991) to the EMBL/GenBank/DBJ databases. M.  
Solin, Dept. of Bacteriology and Immunology, University of Finland,  
Haartmaninkatu 3, SF-00290 Helsinki, FINLAND

REFERENCE 2 (bases 1 to 1338)  
AUTHORS Solin,M.L. and Kaartinen,M.  
TITLE Allelic polymorphism of mouse Igh-J locus, which encodes  
immunoglobulin heavy chain joining (JH) segments

JOURNAL Immunogenetics 36 (5), 306-313 (1992)

MEDLINE 92355114

FEATURES Location/Qualifiers  
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/note="JH4"

BASE COUNT 308 a 293 c 356 g 371 t 10 others  
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Best Local Similarity 95.7%; Pred. No. 2.52e-02;  
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Db 6 tgtgctactgtacttcgatgtc 28  
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Qy 11 TGTCTACTGCTACTTCGATGTC 33

RESULT 9  
LOCUS MMSJLIG 1338 bp DNA ROD 09-DEC-1992  
DEFINITION M.musculus (SJL) DNA for Igh-J locus.  
ACCESSION X63175  
NID q54100  
KEYWORDS immunoglobulin heavy chain J locus.  
SOURCE house mouse.  
ORGANISM Mus musculus

Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;  
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;  
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;  
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;  
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 1338)  
AUTHORS Solin,M.

TITLE Direct Submission  
JOURNAL Submitted (11-NOV-1991) to the EMBL/GenBank/DBJ databases. M.  
Solin, Dept. of Bacteriology and Immunology, University of Finland,  
Haartmaninkatu 3, SF-00290 Helsinki, FINLAND

REFERENCE 2 (bases 1 to 1338)  
AUTHORS Solin,M.L. and Kaartinen,M.  
TITLE Allelic polymorphism of mouse Igh-J locus, which encodes  
immunoglobulin heavy chain joining (JH) segments

JOURNAL Immunogenetics 36 (5), 306-313 (1992)

MEDLINE 92355114

FEATURES Location/Qualifiers  
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Mar 19 08:28

US-08-612-929-25.rge

9

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misc_feature 330..374
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misc_feature 710..757
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Best Local Similarity 95.7%; Pred. No. 2.52e-02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 6 tgtgtactgttacttcgatgctc 28
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Qy 11 TGTCTACTGGTACTTCGATGTC 33
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RESULT 10
LOCUS MMC581G 1338 bp DNA ROD 09-DEC-1992
DEFINITION M.musculus (C58) DNA for Igh-J locus.
ACCESSION X63168
NID g50244
KEYWORDS immunoglobulin heavy chain J locus.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1338)
AUTHORS Solin,M.
TITLE Direct Submission
JOURNAL Submitted (11-NOV-1991) to the EMBL/GenBank/DBJ databases. M.
Haartmaninkatu 3, SF-00290 Helsinki, FINLAND
REFERENCE 2 (bases 1 to 1338)
AUTHORS Solin,M.L. and Kaartinen,M.
TITLE Allelic polymorphism of mouse Igh-J locus, which encodes
immunoglobulin heavy chain joining (JH) segments
JOURNAL Immunogenetics 36 (5), 306-313 (1992)
MEDLINE 92355114
FEATURES
Location/Qualifiers
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Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy 11 TGTCTACTGGTACTTCGATGTC 33
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LOCUS MMRFIG 1339 bp DNA ROD 09-DEC-1992
DEFINITION M.musculus (RF) DNA for Igh-J locus.
ACCESSION X63173
NID g53978
KEYWORDS immunoglobulin heavy chain J locus.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1339)
AUTHORS Solin,M.
TITLE Direct Submission
JOURNAL Submitted (11-NOV-1991) to the EMBL/GenBank/DBJ databases. M.
Haartmaninkatu 3, SF-00290 Helsinki, FINLAND
REFERENCE 2 (bases 1 to 1339)
AUTHORS Solin,M.L. and Kaartinen,M.
TITLE Allelic polymorphism of mouse Igh-J locus, which encodes
immunoglobulin heavy chain joining (JH) segments
JOURNAL Immunogenetics 36 (5), 306-313 (1992)
MEDLINE 92355114
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Location/Qualifiers
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/notes="JH4"
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Best Local Similarity 95.7%; Pred. No. 2.52e-02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Mar 19 08:28

US-08-612-929-25.rge

10

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Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 5 tgtgtactgttacttcgatgctc 27
|||||
Qy 11 TGTCTACTGGTACTTCGATGTC 33
|||||
RESULT 11
LOCUS MMRFIG 1339 bp DNA ROD 09-DEC-1992
DEFINITION M.musculus (RF) DNA for Igh-J locus.
ACCESSION X63173
NID g53978
KEYWORDS immunoglobulin heavy chain J locus.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1339)
AUTHORS Solin,M.
TITLE Direct Submission
JOURNAL Submitted (11-NOV-1991) to the EMBL/GenBank/DBJ databases. M.
Haartmaninkatu 3, SF-00290 Helsinki, FINLAND
REFERENCE 2 (bases 1 to 1339)
AUTHORS Solin,M.L. and Kaartinen,M.
TITLE Allelic polymorphism of mouse Igh-J locus, which encodes
immunoglobulin heavy chain joining (JH) segments
JOURNAL Immunogenetics 36 (5), 306-313 (1992)
MEDLINE 92355114
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Location/Qualifiers
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misc_feature 710..757
/notes="JH2"
misc_feature 1279..1329
/notes="JH3"
misc_feature 1279..1329
/notes="JH4"
BASE COUNT 313 a 292 c 358 g 372 t 4 others
ORIGIN
Query Match 63.6%; Score 21; DB 64; Length 1339;
Best Local Similarity 95.7%; Pred. No. 2.52e-02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 6 tgtgtactgttacttcgatgctc 28
|||||
Qy 11 TGTCTACTGGTACTTCGATGTC 33
|||||
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Mar 19 08:28

US-08-612-999-25.fge

11

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RESULT 12
LOCUS MMBALB1G 1339 bp DNA ROD 09-DEC-1992
DEFINITION M.musculus (Balb/c) DNA for Igh-J locus.
ACCESSION X63166 S41804
NID g50121
KEYWORDS immunoglobulin heavy chain J locus.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1339)
AUTHORS Solin,M.
TITLE Direct Submission
JOURNAL Submitted (11-NOV-1991) to the EMBL/GenBank/DBJ databases. M.
Solin, Dept. of Bacteriology and Immunology, University of Finland,
Haartmaninkatu 3, SF-00290 Helsinki, FINLAND
REFERENCE 2 (bases 1 to 1339)
AUTHORS Solin,M.L. and Kaartinen,M.
TITLE Allelic polymorphism of mouse Igh-J locus, which encodes
immunoglobulin heavy chain joining (JH) segments
JOURNAL Immunogenetics 36 (5), 306-313 (1992)
MEDLINE 92355114
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source Location/Qualifiers
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BASE COUNT 313 a 292 c 359 g 375 t
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Best Local Similarity 95.7%; Pred. No. 2.52e-02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 6 ttgtctactgtacttcgatgctc 28
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Qy 11 TGTCTACTGGTACTTCGATGTC 33

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LOCUS MMCE1G 1339 bp DNA ROD 09-DEC-1992
DEFINITION M.musculus (CE) DNA for Igh-J locus.
ACCESSION X63170
NID g50380
KEYWORDS immunoglobulin heavy chain J locus.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
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Mar 19 08:28

US-08-612-999-25.fge

12

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Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1339)
AUTHORS Solin,M.
TITLE Direct Submission
JOURNAL Submitted (11-NOV-1991) to the EMBL/GenBank/DBJ databases. M.
Solin, Dept. of Bacteriology and Immunology, University of Finland,
Haartmaninkatu 3, SF-00290 Helsinki, FINLAND
REFERENCE 2 (bases 1 to 1339)
AUTHORS Solin,M.L. and Kaartinen,M.
TITLE Allelic polymorphism of mouse Igh-J locus, which encodes
immunoglobulin heavy chain joining (JH) segments
JOURNAL Immunogenetics 36 (5), 306-313 (1992)
MEDLINE 92355114
FEATURES
source Location/Qualifiers
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/organism="Mus musculus"
/germline
/strain="CE"
/tissue type="liver"
/chromosome="12"
misc_feature 11..61
/note="JH1"
misc_feature 330..374
/note="JH2"
misc_feature 710..757
/note="JH3"
misc_feature 1279..1329
/note="JH4"
BASE COUNT 312 a 293 c 359 g 374 t 1 others
ORIGIN
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Best Local Similarity 95.7%; Pred. No. 2.52e-02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 6 ttgtctactgtacttcgatgctc 28
||| ||||||||||||||||||
Qy 11 TGTCTACTGGTACTTCGATGTC 33

RESULT 14
LOCUS MMCBA1G 1339 bp DNA ROD 09-DEC-1992
DEFINITION M.musculus (CBA) DNA for Igh-J locus.
ACCESSION X63169
NID g50309
KEYWORDS immunoglobulin heavy chain J locus.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1339)
AUTHORS Solin,M.
TITLE Direct Submission
JOURNAL Submitted (11-NOV-1991) to the EMBL/GenBank/DBJ databases. M.
Solin, Dept. of Bacteriology and Immunology, University of Finland,
Haartmaninkatu 3, SF-00290 Helsinki, FINLAND
REFERENCE 2 (bases 1 to 1339)
AUTHORS Solin,M.L. and Kaartinen,M.
TITLE Allelic polymorphism of mouse Igh-J locus, which encodes
immunoglobulin heavy chain joining (JH) segments
```

Mar 19 08:28

US-08-612-929-25.rge

13

JOURNAL Immunogenetics 36 (5), 306-313 (1992)

MEDLINE 92355114

FEATURES

source

Location/Qualifiers

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/organism="Mus musculus"

/germline

/strain="CBA"

/tissue\_type="liver"

/chromosome="12"

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/note="JH1"

330..374

/note="JH2"

710..757

/note="JH3"

1279..1329

/note="JH4"

BASE COUNT 313 a 291 c 358 g 371 t 6 others

ORIGIN

Query Match 63.6%; Score 21; DB 63; Length 1339;

Best Local Similarity 95.7%; Pred. No. 2.52e-02;

Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 6 tgtgtactgtacttcgatgtc 28

|||||

Qy 11 TGTCTACTGGTACTTCGATGTC 33

RESULT 15

LOCUS

MMDBA2IG 1339 bp DNA ROD 09-DEC-1992

DEFINITION M.musculus (DBA2) DNA for Igh-J locus.

ACCESSION X63171

NID g50670

KEYWORDS immunoglobulin heavy chain J locus.

SOURCE house mouse.

ORGANISM

Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;

Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;

Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;

Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;

Sciurognathi; Myomorpha; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 1339)

AUTHORS Solin,M.

TITLE Direct Submission

JOURNAL Submitted (11-NOV-1991) to the EMBL/GenBank/DBJ databases. M.

Solin, Dept. of Bacteriology and Immunology, University of Finland,

Haartmaninkatu 3, SF-00290 Helsinki, FINLAND

REFERENCE 2 (bases 1 to 1339)

AUTHORS Solin,M.L. and Kaartinen,M.

TITLE Allelic polymorphism of mouse Igh-J locus, which encodes

immunoglobulin heavy chain joining (JH) segments

JOURNAL Immunogenetics 36 (5), 306-313 (1992)

MEDLINE 92355114

FEATURES

source

1..1339

/organism="Mus musculus"

/germline

/strain="DBA/2"

/tissue\_type="liver"

/chromosome="12"

11..61

/note="JH1"

330..374

misc\_feature

misc\_feature

Mar 19 08:28

US-08-612-929-25.rge

14

/note="JH2"

710..757

/note="JH3"

misc\_feature

misc\_feature

1279..1329

/note="JH4"

BASE COUNT 313 a 291 c 359 g 374 t 2 others

ORIGIN

Query Match 63.6%; Score 21; DB 63; Length 1339;

Best Local Similarity 95.7%; Pred. No. 2.52e-02;

Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 6 tgtgtactgtacttcgatgtc 28

|||||

Qy 11 TGTCTACTGGTACTTCGATGTC 33

Search completed: Wed Mar 19 08:30:34 1997

Job time : 63 secs.



Mar 19 08:33

US-08-612-929-27.jst

1

\*\*\*\*\*  
[A sequence of vertical bars and slashes representing a barcode or alignment visualization]  
\*\*\*\*\* (TM)

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MPerch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed Mar 19 08:34:49 1997; MasPar time 59.81 Seconds  
199.100 Million cell updates/sec

Tabular output not generated.

Title: >US-08-612-929-27  
Description: (1-27) from US08612929.seq  
Perfect Score: 27  
N.A. Sequence: 1 CAGCAAGTAATGAGTCTCCGAGG 27  
Comp: GTGCTTTCATTACTCTAGGAGGCTCC

Scoring table: TABLE default  
Gap 10

Nmatch STD : Dbase 0; Query 0

Searched: 630489 seqs, 220513910 bases x 2

Post-processing: Minimum Match 0\$  
Listing first 45 summaries

Database: EST-STS  
1:EST1 2:EST2 3:EST3 4:EST4 5:EST5 6:EST6 7:EST7 8:EST8  
9:EST9 10:EST10 11:EST11 12:EST12 13:EST13 14:EST14  
15:EST15 16:EST16 17:EST17 18:EST18 19:EST19 20:EST20  
21:EST21 22:EST22 23:EST23 24:EST24 25:EST25 26:EST26  
27:EST27 28:EST28 29:EST29 30:EST30 31:EST31 32:EST32  
33:EST33 34:EST34 35:EST35 36:EST36 37:EST37 38:EST38  
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57:EST57 58:EST58 59:EST59 60:EST60 61:EST61 62:EST62  
63:EST63 64:EST64 65:EST65 66:EST66 67:EST67 68:EST68  
69:EST69 70:EST70 71:EST71 72:EST72 73:EST73 74:EST74  
75:EST75 76:EST76 77:EST77 78:EST78 79:EST79 80:EST80  
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93:EST93 94:EST94 95:EST95 96:EST96 97:EST97 98:EST98  
99:EST99  
EST-STS-TWO  
100:EST100 101:EST101 102:EST102 103:EST103 104:EST104  
105:EST105 106:EST106 107:EST107 108:EST108 109:EST109  
110:EST110 111:EST111 112:EST112 113:EST113 114:EST114  
115:EST115 116:EST116 117:EST117 118:EST118 119:EST119  
120:EST120 121:EST121 122:EST122 123:EST123 124:EST124  
125:EST125 126:EST126 127:EST127 128:EST128 129:EST129

Mar 19 08:33

US-08-612-929-27.jst

2

130:STS2 131:STS3 132:STS4 133:STS5 134:STS6 135:STS7  
136:STS8 137:STS9 138:STS10 139:STS11 140:STS12  
141:STS13 142:STS14 143:STS15 144:STS16 145:STS17  
146:STS18 147:STS19 148:STS20 149:STS21 150:STS22  
151:STS23 152:STS24 153:STS25 154:STS26 155:STS27  
156:STS28 157:STS29 158:STS30 159:STS31 160:STS32  
161:STS33 162:STS34 163:STS35 164:STS36 165:STS37  
166:STS38 167:STS39 168:STS40 169:STS41 170:STS42  
171:STS43 172:STS44 173:STS45

Statistics: Mean 6.970; Variance 1.339; scale 5.205

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	17	63.0	314	124	T84399	Yd45g03.rl Homo sapie 1.34e-04
2	16	59.3	374	99	R95278	SW31C0175SK Onchocerc 2.98e-03
3	16	59.3	408	30	H77752	yu23g11.rl Homo sapie 2.98e-03
4	16	59.3	482	128	T98290	ye59g06.sl Homo sapie 2.98e-03
5	16	59.3	522	78	R21547	yh19h02.sl Homo sapie 2.98e-03
6	15	55.6	179	91	R69241	yi44c03.sl Homo sapie 5.84e-02
7	15	55.6	215	61	N49151	yy84b12.rl Homo sapie 5.84e-02
8	15	55.6	236	61	N48736	yy55d11.rl Homo sapie 5.84e-02
9	15	55.6	329	149	W12396	ma67g11.rl Soares mou 5.84e-02
10	15	55.6	329	170	MM3966	ma67g11.rl Soares mou 5.84e-02
11	15	55.6	336	101	RICC10026A	Rice cDNA, partial se 5.84e-02
12	15	55.6	349	27	H69879	yr88h01.sl Homo sapie 5.84e-02
13	15	55.6	358	95	R82708	yj20e08.rl Homo sapie 5.84e-02
14	15	55.6	361	143	T26512	AB284F11R Homo sapien 5.84e-02
15	15	55.6	361	162	HS51288	AB284F11R Homo sapien 5.84e-02
16	15	55.6	361	108	T26512	AB284F11R Homo sapien 5.84e-02
17	15	55.6	368	46	HSPD03654	H.sapiens mitochondri 5.84e-02
18	15	55.6	368	168	HSPD03654	H.sapiens mitochondri 5.84e-02
19	15	55.6	368	155	HSPD03654	H.sapiens mitochondri 5.84e-02
20	15	55.6	372	168	HSPD04181	H.sapiens mitochondri 5.84e-02
21	15	55.6	372	46	HSPD04181	H.sapiens mitochondri 5.84e-02
22	15	55.6	372	155	HSPD04181	H.sapiens mitochondri 5.84e-02
23	15	55.6	412	100	R97220	yq62ell.sl Homo sapie 5.84e-02
24	15	55.6	423	168	HSPD03830	H.sapiens mitochondri 5.84e-02
25	15	55.6	423	46	HSPD03830	H.sapiens mitochondri 5.84e-02
26	15	55.6	423	155	HSPD03830	H.sapiens mitochondri 5.84e-02
27	15	55.6	433	119	T67165	ya53b07.sl Homo sapie 5.84e-02
28	15	55.6	437	105	T08817	EST07609 Homo sapiens 5.84e-02
29	15	55.6	455	148	MM4343	ma63a01.rl Soares mou 5.84e-02
30	15	55.6	455	170	MM4343	ma63a01.rl Soares mou 5.84e-02
31	15	55.6	560	36	H98114	yx09e10.sl Homo sapie 5.84e-02
32	14	51.9	204	105	T11763	All190F Homo sapiens c 9.87e-01
33	14	51.9	233	155	HSPD03312	H.sapiens mitochondri 9.87e-01
34	14	51.9	276	155	HSPD00476	H.sapiens mitochondri 9.87e-01
35	14	51.9	295	110	T31970	EST41705 Homo sapiens 9.87e-01
36	14	51.9	381	96	R83635	yql2d09.rl Homo sapie 9.87e-01
37	14	51.9	387	32	H86202	yt03a08.rl Homo sapie 9.87e-01
38	14	51.9	398	168	HSPD03891	H.sapiens mitochondri 9.87e-01
39	14	51.9	401	158	HS098347	J2301F Homo sapiens c. 9.87e-01
40	14	51.9	416	47	HUM119D10B	Human fetal brain cDN 9.87e-01
41	14	51.9	420	168	HSPD04138	H.sapiens mitochondri 9.87e-01
42	14	51.9	429	74	R10676	yf31h11.rl Homo sapie 9.87e-01

	c	43	14	51.9	455	116	T5980	y35h05.r1	Homo sapie	9.87e-01
	c	44	14	51.9	477	162	H3465335	zb33c06.r1	Soares par	9.87e-01
	c	45	14	51.9	482	167	H3959328	zb37e10.r1	Soares par	9.87e-01

## ALIGNMENTS

RESULT	1				
LOCUS	T84399	314 bp	mRNA	EST	
DEFINITION	y445q03.ri Homo sapiens cDNA clone 111220 5'.				
ACCESSION	T84399				
	NID	g712687			
KEYWORDS	EST.				

SOURCE

human clone=111220 library=Soares fetal liver spleen 1NFLS vector=pT73D (Pharmacia) with a modified polyLinker host=DH10B (ampicillin resistant) primer=M13RPI Rsite1=Pac I Rsite2=Eco RI Liver and spleen from a 20 week-post conception male fetus. 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5' AACTGGACGATTAATTAAGACGCTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fátima Bonaldo.

## ORGANISM

Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

## REFERENCE

**AUTHORS** Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and Willson, R.

**TITLE** The WashU-Merck EST Project

JOURNAL Unpublished (1995)

**COMMENT**

Contact: Wilson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810

Email: [est@watson.wustl.edu](mailto:est@watson.wustl.edu)  
 High quality sequence stops: 207

Source: IMAGE Consortium I.I.N.I.

This clone is available royalty-free through LNL ; contact the  
 Source: IMAGE Consortium  
 IMAGE Consortium (info@image.lnl.gov) for further information.

## FEATURES

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source
1.314
/organism="Homo sapiens"
/clone="111220"
/note="human"
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BASE COUNT	90 a	55 c	74 g	91 t	4 others
ORIGIN					

Query Match 63.0%; Score 17; DB 124; Length 314;  
Best Local Similarity 87.0%; Pred. No. 1.34e-04;  
Matches 20: Conservative 0; Mismatches 3; Index

Db 282 aatgaatactcattacttaacta 304

Cp 23 GGAGGATCCTCATTTACTTTCCTG

## RESULT

2

LOCUS	R95278	374 bp	mRNA	EST	31-JAN-1996
DEFINITION	SW3IC0175SK Onchocerca volvulus cDNA clone SW3IC0175 5'.				
ACCESSION	R95278				
NID	g975434				
KEYWORDS	EST.				

**SOURCE**

infective larva cDNA (SAM94WL-Ov13) strain-Sierra Leone vector-lambda UniZap XR host-XL1-Blue MRF<sup>+</sup> Reitel-EcoR I Reite2-Xho I Cutaneous filarial nematode parasite of humans. mRNA was prepared from third stage infective larvae of *Onchocerca volvulus* isolated from mosquitoes 10 days after infection and converted to double stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNase I. The library had 1.8 x 10<sup>5</sup> independent recombinants and average insert size was 900 base pairs. The library was constructed by Wenhong Lu. The library is available from Dr. S.A. Williams. email [williams@smith.smith.edu](mailto:williams@smith.smith.edu).

## ORGANISM

Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group; Metazoa; Eumetazoa; Bilateria; Pseudocoelomata; Nematoda; Secernentea; Spirurida; Spirulina; Filarioidea; Onchocercidae; Onchocercinae; Onchocerca.

## REFERENCE

**AUTHORS** Blaxter, M.L., Ragha-

**TITLE** Genes expressed in *Brugia malayi* infected  
**JOURNAL** Mol. Biochem. Parasitol. (1996) In press

## COMMENT

Contact: Steven A. Williams  
Molecular Parasitology  
Smith College Department of Biological Sciences  
Department of Biological Sciences, Clark Science Center, Smith  
College, Northampton, MA, 01063, USA

Tel: 4135853826

**Fax: 4135853786**  
**Email: swilliams@smith.smith.edu**  
**similar to myosin binding protein.**

## FEATURES

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source      1..374  
            /organism="Onchocerca volvulus"  
            /clone="SW3IC0175"  
            /strain="Sierra Leone"  
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mRNA       125 a   70 c   80 g   96 t   3 others  
BASE COUNT  
ORIGIN
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Query Match	59.3%;	Score 16;	DB 99;	Length 374;
Best Local Similarity	86.4%;	Pred. No. 2.98e-03;		
Matches	19;	Conservative	0;	Mismatches 3;
				Indels 0;
				Gaps 0;

Db 160 ctcggaqaatcctcatatctt 181

[illegible]

26 CTCGAGGATCCTCACTT 5

### RESULT 3

LOCUS	H77752	408 bp	mRNA	EST	09-NOV-1995
DEFINITION	yu33g11.r1 Homo sapiens cDNA clone 234692 5'.				
ACCESSION	H77752				
NID	q1055841				
KEYWORDS	EST.				
SOURCE	Human clone=234692 primer=M3RP1 library=Soares fetal liver spleen INFLS vector=pFT73D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) Raite1=Pac I Raite2=Eco RI Liver and spleen from a 20 week-post conception male fetus; 1st strand				

cDNA was primed with a Pac I - oligo(dT) primer [5' AACTGAGAGATTAAATGAATCTTTTCTTTTCTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pTT3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo.

## ORGANISM

Homo sapiens

Eucaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomi; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 (bases 1 to 408)

## AUTHORS

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevisakis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.

## TITLE

The WashU-Merck EST Project

## JOURNAL

Unpublished (1995)

## COMMENT

Contact: Wilson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence stops: 281

Source: IMAGE Consortium, L1NL

This clone is available royalty-free through L1NL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

## FEATURES

source

1..408

/organism="Homo sapiens"

/clone="234692"

/note="human"

&lt;1..&gt;408

## BASE COUNT

116 a 50 c 85 g 154 t 3 others

## ORIGIN

Query Match

Best Local Similarity 59.3%; Score 16; DB 30; Length 408;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 155 ggaggatcctcatttaatt 172

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Cp 23 GGAGATCCTCATTACTT 6

## RESULT

4

## LOCUS

T98290 482 bp mRNA EST 31-MAR-1995

DEFINITION ye59q06.s1 Homo sapiens cDNA clone 122074 3' similar to contains

Alu repetitive element;.

## ACCESSION

T98290

## NID

q748027

## KEYWORDS

EST.

## SOURCE

human clone=122074 library=Soares fetal liver spleen INFLS vector=pTT3D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) primer=-21ml3 Rsite1=Pac I Rsite2=Eco RI Liver and spleen from a 20 week-post conception male fetus. 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5' AACTGAGAGATTAAATGAATCTTTTCTTTTCTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pTT3

vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo.

## ORGANISM

Homo sapiens

Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 (bases 1 to 482)

## AUTHORS

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevisakis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.

## TITLE

The WashU-Merck EST Project

## JOURNAL

Unpublished (1995)

## COMMENT

Contact: Wilson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence stops: 288

Source: IMAGE Consortium, L1NL

This clone is available royalty-free through L1NL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

## FEATURES

source

1..482

/organism="Homo sapiens"

/clone="122074"

/note="human"

## BASE COUNT

119 a 89 c 142 g 123 t 9 others

## ORIGIN

Query Match 59.3%; Score 16; DB 128; Length 482;

Best Local Similarity 90.0%; Pred. No. 2.98e-03;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 166 caacacagtaatgagatcc 185

|||||

Qy 1 CAGCAAGTAATGAGATCC 20

## RESULT

5

## LOCUS

R21547 522 bp mRNA EST 18-APR-1995

DEFINITION yH19h02.s1 Homo sapiens cDNA clone 130227 3'.

## ACCESSION

R21547

## NID

q776328

## KEYWORDS

EST.

## SOURCE

human clone=130227 library=Soares placenta Nb2HP vector=pTT3D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) primer=-21ml3 Rsite1=Not I Rsite2=Eco RI Female placenta obtained at birth (full term). 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' AACTGGAAGATTCGGCGCGCAGGAATTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTT3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo.

## ORGANISM

Homo sapiens

Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 (bases 1 to 522)

## AUTHORS

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,

Mar 19 08:33

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7

Parsons,J., Rifkin,L., Rohlfling,T., Soares,M., Tan,F.,  
Trevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and  
Wilson,R.

TITLE  
JOURNAL  
COMMENT

COMMENT

Contact: Wilson RK

WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.wustl.edu

High quality sequence stops: 433  
Source: IMAGE Consortium, LLNL

This clone is available royalty-free through LLNL ; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES

Location/Qualifiers  
1..522  
/organism="Homo sapiens"  
/clone="130227"  
/note="human"

BASE COUNT 136 a 122 c 117 g 143 t 4 others  
ORIGIN

Query Match 59.3%; Score 16; DB 78; Length 522;  
Best Local Similarity 82.6%; Pred. No. 2.98e-03;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 469 cctccaggtcagcattacttt 491

Cp 27 CCTCGGAGGATCCTCATTACTTT 5

RESULT 6

LOCUS R69241 179 bp mRNA EST 01-JUN-1995  
DEFINITION Y144C03.s1 Homo sapiens cDNA clone 142084 5' similar to gb:U01120  
GLUCOSE-6-PHOSPHATASE (HUMAN); contains Alu repetitive element;.  
R69241  
ACCESSION  
NID g842758  
KEYWORDS EST.

human clone=142084 library=Soares placenta Nb2HP vector=pT7T3D  
(Pharmacia) with a modified polylinker host=DH10B (ampicillin  
resistant) primer=M13R1 Rsite1=Not I Rsite2=Eco RI Female placenta  
obtained at birth (full term). 1st strand cDNA was primed with a  
Not I - oligo(dT) primer [5'

AACTGAGAAATTCGGCGCGGAGGAATTTTTTTTTTTTTTTTTTTT 3'], double-stranded  
cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not  
I and cloned into the Not I and Eco RI sites of the modified pT7T3  
vector. Library went through one round of normalization. Library  
constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM

Homo sapiens  
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;  
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;  
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;  
Eutheria; Archonta; Primates; Catarrhini; Homidae; Homo.

REFERENCE

AUTHORS  
1 (bases 1 to 179)  
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,  
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,  
Parsons,J., Rifkin,L., Rohlfling,T., Soares,M., Tan,F.,  
Trevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and  
Wilson,R.

TITLE

JOURNAL

Unpublished (1995)

Mar 19 08:33

US-08-612-929-27.rst

8

COMMENT

Contact: Wilson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.wustl.edu  
Source: IMAGE Consortium, LLNL  
This clone is available royalty-free through LLNL ; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Putative full length read.

FEATURES

Location/Qualifiers  
1..179  
/organism="Homo sapiens"  
/clone="142084"  
/note="human"

BASE COUNT 34 a 40 c 41 g 64 t  
ORIGIN

Query Match 55.6%; Score 15; DB 91; Length 179;  
Best Local Similarity 80.0%; Pred. No. 5.84e-02;  
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Db 45 cctcagtgatcctcataactctgc 69

Cp 27 CCTCGGAGGATCCTCATTACTTGC 3

RESULT 7

LOCUS N49151 215 bp mRNA EST 14-FEB-1996  
DEFINITION Y946b12.r1 Homo sapiens cDNA clone 280223 5'.  
ACCESSION N49151  
NID g1190317  
KEYWORDS EST.

SOURCE  
2NBHSP vector=pT7T3D (Pharmacia) with a modified polylinker  
V\_TYPE: phagemid host=DH10B (ampicillin resistant) Rsite1=Not I  
Rsite2=Eco RI 46 year old male. 1st strand cDNA was primed with a  
Not I - oligo(dT) primer

[5'-TCTTACCAATCTGAAGTCGAGCGCGCAATTTTTTTTTTTTTTTT-3'],  
double-stranded cDNA was size selected, ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not I and Eco  
RI sites of a modified pT7T vector (Pharmacia). Library went  
through one round of normalization to a Cot = 5. Library  
constructed by Bento Soares and M.Fatima Bonaldo. RNA from 4  
multiple sclerosis lesions from one patient was kindly provided by  
Dr. Kevin G. Becker (NINDS/NIH).

ORGANISM

Homo sapiens  
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;  
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;  
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;  
Eutheria; Archonta; Primates; Catarrhini; Homidae; Homo.

REFERENCE

AUTHORS  
1 (bases 1 to 215)  
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,  
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,  
Parsons,J., Rifkin,L., Rohlfling,T., Soares,M., Tan,F.,  
Trevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and  
Wilson,R.

TITLE

JOURNAL

Unpublished (1995)

COMMENT

Contact: Wilson RK

WashU-Merck EST Project

Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800  
Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence stops: 193

Source: IMAGE Consortium, L1NL

This clone is available royalty-free through L1NL ; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.

## FEATURES

source

1..215  
/organism="Homo sapiens"  
/clone="280223"  
/note="human"

<1..>215

BASE COUNT 43 a 43 c 46 g 80 t 3 others  
ORIGIN

Query Match 55.6%; Score 15; DB 61; Length 215;  
Best Local Similarity 85.7%; Pred. No. 5.84e-02;

Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 151 agtatcctcattgcttgcgtg 171

|| ||||| |||||

Cp 21 AGGATCCTCATTTACTTTGCTG 1

## RESULT

8

LOCUS N48736 236 bp mRNA EST 14-FEB-1996

DEFINITION yy55d11.r1 Homo sapiens cDNA clone 277461 5'.

ACCESSION N48736

NID g1189902

KEYWORDS EST.

SOURCE

human clone=277461 primer=T7 library=Soares multiple sclerosis  
2NDHSP vector-pTT3D (Pharmacia) with a modified polylinker  
V TYPE: phagemid host=DH10B (ampicillin resistant) Reitel-Not I  
Rsite2=Eco RI A6 year old male. 1st strand cDNA was primed with a  
Not I - oligo(dT) primer

[5'-GCTTACCAATCTGAAGTGGGCGCGCATTTTTTTTTTTTTTTT-3'],

double-stranded cDNA was size selected, ligated to Eco RI adapters  
(Pharmacia), digested with Not I and cloned into the Not I and Eco  
RI sites of a modified pTT vector (Pharmacia). Library went  
through one round of normalization to a Cot = 5. Library

constructed by Bento Soares and M.Fatima Bonaldo. RNA from 4  
multiple sclerosis lesions from one patient was kindly provided by

Dr. Kevin G. Becker (NINDS/NIH).

## ORGANISM

Homo sapiens

Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata;  
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;  
Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;  
Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 236)

## REFERENCE

AUTHORS

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,  
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,  
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,  
Trevasakis,E., Waterston,R., Williamson,A., Wohlmann,P. and  
Wilson,R.

TITLE The WashU-Merck EST Project

JOURNAL Unpublished (1995)

COMMENT

Contact: Wilson RK

WashU-Merck EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800  
Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence stops: 193

Source: IMAGE Consortium, L1NL

This clone is available royalty-free through L1NL ; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.

## FEATURES

source

1..236  
/organism="Homo sapiens"  
/clone="277461"  
/note="human"

<1..>236

BASE COUNT 51 a 44 c 50 g 87 t 4 others  
ORIGIN

Query Match 55.6%; Score 15; DB 61; Length 236;  
Best Local Similarity 85.7%; Pred. No. 5.84e-02;

Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 168 agtatcctcattgcttgcgtg 188

|| ||||| |||||

Cp 21 AGGATCCTCATTTACTTTGCTG 1

## RESULT

9

LOCUS W12396 329 bp mRNA EST 26-APR-1996

DEFINITION ma67q11.r1 Soares mouse p3NWF19.5 Mus musculus cDNA 5'.

ACCESSION W12396

NID g1286526

KEYWORDS EST.

SOURCE house mouse.

ORGANISM

Mus musculus  
Eukaryota; mitochondrial eukaryotes; Metazoa; Chordata;  
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;  
Murinae; Mus.

1 (bases 1 to 329)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,  
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,  
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,  
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and  
Waterston,R.

The WashU-HHMI Mouse EST Project

Unpublished (1996)

## COMMENT

Contact: Marra M/Mouse EST Project

WashU-HHMI Mouse EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through L1NL ; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Putative full length read

Seq primer: ETPrimer

High quality sequence stop: 321.

NCBI gi: 1286526

Location/Qualifiers

source

1..329

/organism="Mus musculus"

/note="Vector: pT73D (Pharmacia) with a modified  
polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA

Mar 19 08:33

US-08-612-929-27.rst

11

was primed with a Not I - oligo(dT) primer [5'  
 TCTTACCAATCTGAAGTCGAGCGCGCCGCAATTTTTTTTTTTT 3' ],  
 double-stranded cDNA was size selected, ligated to Eco RI  
 adapters (Pharmacia), digested with Not I and cloned into  
 the Not I and Eco RI sites of a modified pT7T3 vector  
 (Pharmacia). Library went through one round of  
 normalization to a Cot = 5. Library constructed by Bento  
 Soares and M.Fatima Bonaldo.\*  
 /clone\_lib="Soares mouse p3NMF19.5"  
 /dev\_stage="19 weeks"  
 /lab\_host="DH10B (ampicillin resistant)"  
 <1..>329

mRNA 79 a 87 c 68 g 95 t  
 BASE COUNT  
 ORIGIN

Query Match 55.6%; Score 15; DB 149; Length 329;  
 Best Local Similarity 85.7%; Pred. No. 5.84e-02;  
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 181 gcagagcattgagatcctcc 201

||||| | | | | | | | | | | | | | |

Qy 3 GCAGAGTAATGAGGATCTCC 23

RESULT 10

ID MM3966 standard; RNA; EST; 329 BP.

AC W12396;

DT 29-APR-1996 (Rel. 47, Created)

DT 29-APR-1996 (Rel. 47, Last updated, Version 1)

DE ma67g11.r1 Soares mouse p3NMF19.5 Mus musculus cDNA 5'.

KW EST.

OS Mus musculus (mouse)

OC Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;

OC Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.

RN [1]

RP 1-329

RA Marra M., Hillier L., Allen M., Bowles M., Dietrich N.,

RA Dubuque T., Geisel S., Kucaba T., Lacy M., Le M., Martin J.,

RA Morris M., Schellenberg K., Steptoe M., Tan F., Underwood K.,

RA Moore B., Theising B., Wylie T., Lennon G., Soares B., Wilson R.,

RA Waterston R.;

RT "The WashU-HHMI Mouse EST Project";

RL Unpublished.

CC Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project

CC Washington University School of Medicine# 4444 Forest Park Parkway,

CC Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810

CC Email: mouseest@wustl.edu This clone is available

CC royalty-free through INL; contact the IMAGE Consortium

CC (info@image.llnl.gov) for further information. Putative full length

CC read Seq primer: ETPRimer High quality sequence stop: 321. NCBI gi:

CC 1286526

FH Key Location/Qualifiers

FH source

FT 1..329

FT /organism="Mus musculus"

FT /notes="Vector: pT7T3D (Pharmacia) with a modified

FT polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA

FT was primed with a Not I - oligo(dT) primer [5'

FT TCTTACCAATCTGAAGTCGAGCGCGCCGCAATTTTTTTTTTTT 3' ],

FT double-stranded cDNA was size selected, ligated to Eco RI

FT adapters (Pharmacia), digested with Not I and cloned into

FT the Not I and Eco RI sites of a modified pT7T3 vector

FT (Pharmacia). Library went through one round of

FT normalization to a Cot = 5. Library constructed by Bento

FT

Mar 19 08:33

US-08-612-929-27.rst

12

FT Soares and M.Fatima Bonaldo.\*  
 FT /clone\_lib="Soares mouse p3NMF19.5"  
 FT /dev\_stage="19 weeks"  
 FT /lab\_host="DH10B (ampicillin resistant)"  
 FT mRNA <1..>329

SQ Sequence 329 BP; 79 A; 87 C; 68 G; 95 T; 0 other;

Query Match 55.6%; Score 15; DB 170; Length 329;  
 Best Local Similarity 85.7%; Pred. No. 5.84e-02;  
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 181 gcagagcattgagatcctcc 201  
 ||||| | | | | | | | | | | | | | | |

Qy 3 GCAGAGTAATGAGGATCTCC 23

RESULT 11  
 LOCUS RICC10026A 336 bp mRNA EST 25-MAY-1995  
 DEFINITION Rice cDNA, partial sequence (C10026\_1A).  
 ACCESSION D21897

NID g426041

KEYWORDS EST(expressed sequence tag).

SOURCE Oryza sativa (strain Nipponbare, ) Callus Callus cDNA to mRNA.

ORGANISM Oryza sativa

Eukaryota; mitochondrial eukaryotes; Chlorophyta/Embryophyta

group; Charophyta/Embryophyta group; Embryophyta; Magnoliophyta;

Liliopsida; Commelinidae; Poales; Poaceae; Oryza.

REFERENCE 1 (bases 1 to 336)

AUTHORS Minobe,Y. and Sasaki,T.

TITLE Rice cDNA from callus

JOURNAL Unpublished (1993)

COMMENT Submitted (2-NOV-1993) to DDBJ by:

Yuzo Minobe

Dept. Rice Genome Research Program

National Institute of Agrobiological Resources

Kannondai 2-1-2

Tsukuba, Ibaraki

Japan

Phone: 0298-38-7441

Fax: 0298-38-7468

PROJECT = 'RGP'.

Location/Qualifiers

1..336

/organism="Oryza sativa"

/strain="Nipponbare"

/dev\_stage="Callus"

/sequenced\_mol="cDNA to mRNA"

/tissue\_type="Callus"

BASE COUNT 101 a 68 c 80 g 86 t 1 others

ORIGIN

Query Match 55.6%; Score 15; DB 101; Length 336;  
 Best Local Similarity 85.7%; Pred. No. 5.84e-02;  
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 53 aaggaatgagatcaccag 73

||||| | | | | | | | | | | | | | |

Qy 6 AAGTAATGAGGATCTCCGAG 26

RESULT 12

LOCUS H69879 349 bp mRNA EST 24-OCT-1995

DEFINITION yr88h01.s1 Homo sapiens cDNA clone 212401 3'.

ACCESSION H69879

Mar 19 08:33

US-08-612-929-27.rst

13

NID q1040085  
KEYWORDS EST.  
SOURCE human clones-212401 primer=Promega -21ml3 library=Soares fetal liver spleen INFLS vector=pTT73D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) Reitel=Pac I Rsite2=Eco RI Liver cDNA was primed with a Pac I - oligo(dT) primer [5' AACTCGAAGATTTATTTAGATCTTTTTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pTT73 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM

Homo sapiens  
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 349)  
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.

TITLE The WashU-Merck EST Project  
JOURNAL Unpublished (1995)  
COMMENT

Contact: Wilson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810

Email: est@watson.wustl.edu  
High quality sequence stops: 323  
Source: IMAGE Consortium, LNL

This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES

source  
1..349  
/organism="Homo sapiens"  
/clone="212401"  
/note="human"

BASE COUNT

mRNA  
99 a 62 c 91 g 96 t 1 others

ORIGIN

Query Match 55.6%; Score 15; DB 27; Length 349;  
Best Local Similarity 85.7%; Pred. No. 5.84e-07;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 175 aggaagttatgaagatcctc 195

|| ||||| ||||| ||||| |||||

Qy 2 ACCAAAGTATGAGGATCTCT 22

RESULT 13

LOCUS R82708 358 bp mRNA EST 14-JUN-1995  
DEFINITION yj20e08.r1 Homo sapiens cDNA clone 149318 5' similar to contains MER22 repetitive element ;.

ACCESSION

R82708

NID

q862099

KEYWORDS

EST.

SOURCE human clone=149318 library=Soares placenta Nb2HP vector=pTT73D (Pharmacia) with a modified polylinker host=DH10B (ampicillin

Mar 19 08:33

US-08-612-929-27.rst

14

resistant) primer=M13RP1 Rsite1=Not I Rsite2=Eco RI Female placenta obtained at birth (full term). 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' AACTCGAAGATTTCCGCCGCCAGGATTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTT73 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM

Homo sapiens  
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 358)

AUTHORS

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.

TITLE The WashU-Merck EST Project

JOURNAL

Unpublished (1995)

COMMENT

Contact: Wilson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence stops: 284

Source: IMAGE Consortium, LNL

This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES

source

1..358  
/organism="Homo sapiens"  
/clone="149318"  
/note="human"

BASE COUNT 68 a 123 c 65 g 101 t 1 others

ORIGIN

Query Match 55.6%; Score 15; DB 95; Length 358;  
Best Local Similarity 80.0%; Pred. No. 5.84e-02;  
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Db 229 agcaaaagtcagaaatgctccag 253

||||||| ||||| || ||||| ||

Qy 2 ACCAAAGTATGAGGATCTCCGAG 26

RESULT 14

LOCUS T26512 361 bp mRNA EST 15-APR-1996

DEFINITION AB284F11R Homo sapiens cDNA clone LLAB284F11 5'.

ACCESSION

T26512

NID

q773829

KEYWORDS

EST.

SOURCE human clone=LLAB284F11 primer=M13 Reverse library=Infant brain,

LIML array of Dr. M. Soares INIB vector=Infmid BA Reitel=HindIII

Rsite2=NotI Normalized infant brain cDNA library made by Dr. M.

Soares (Columbia University), oligo-dT primed and directionally

cloned between HindIII (5') and NotI (3') sites.

ORGANISM

Homo sapiens  
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;

Mar 19 08:33

US-08-612-929-27.fst

15

Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 361)

Authors: Ghiso, N.S., Eveleth, G.G., Lieuallen, K. and Lennon, G.G.

Title: Chromosomal assignment of 20 cDNAs using flow-sorted spot-blot stamps

Journal: Genomics 28 (3), 570-572 (1995)

Medline: 96039272

Comment:

Contact: Greg G. Lennon

Human Genome Center, L-452

Lawrence Livermore National Laboratory

Livermore CA 94550

Tel: 510 422 8361

Fax: 510 422 2282

Email: info@image.llnl.gov.

NCBI gi: 773829

Location/Qualifiers

1..361

/organism="Homo sapiens"

/clone="LLAB284F11"

/note="human"

<1..>361

BASE COUNT 101 a 124 c 39 g 94 t 3 others

ORIGIN

Query Match 55.6%; Score 15; DB 143; Length 361;

Best Local Similarity 89.5%; Pred. No. 5.84e-02;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 286 gatcctcattactattctg 304

|||||

Cp 19 GATCCTCATTACTTTGCTG 1

RESULT 15

ID H51288 standard; RNA; EST; 361 BP.

AC T26512;

DT 23-APR-1995 (Rel. 43, Created)

DT 18-APR-1996 (Rel. 47, Last updated, Version 3)

DE AB284F11R Homo sapiens cDNA clone LLAB284F11 5'.

KW EST.

OS Homo sapiens (human)

OC Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;

OC Theria; Eutheria; Primates; Haplorhini; Catarrhini; Homnidae.

RN [1]

RP 1-361

RA Ghiso N.S., Eveleth G.G., Lieuallen K., Lennon G.G.;

RT "Chromosomal assignment of 20 cDNAs using flow-sorted spot-blot

stamps";

RL Genomics 28:570-572 (1995).

CC Contact: Greg G. Lennon Human Genome Center, L-452 Lawrence

CC Livermore National Laboratory Livermore CA 94550 Tel: 510 422 8361

CC Fax: 510 422 2282 Email: info@image.llnl.gov. NCBI gi: 773829

FH Key Location/Qualifiers

FH

source 1..361

/organism="Homo sapiens"

/clone="LLAB284F11"

/note="human"

<1..>361

FT mRNA

FT Sequence 361 BP; 101 A; 124 C; 39 G; 94 T; 3 other;

Mar 19 08:33

US-08-612-929-27.fst

16

Query Match 55.6%; Score 15; DB 162; Length 361; Best Local Similarity 89.5%; Pred. No. 5.84e-02; Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 286 gatcctcattactattctg 304

|||||

Cp 19 GATCCTCATTACTTTGCTG 1

Search completed: Wed Mar 19 08:35:56 1997

Job time : 67 secs.





CC anti-IL-4 Mab 3B9 Mab) within a human antibody framework. A  
 CC synthetic heavy chain was made using the oligonucleotides given  
 CC in Q83498-502 and amplified by PCR using the primers given in  
 CC Q83503-04. The construct was ligated into vector pCD, along  
 CC with a signal sequence (Q83494) and an IgG1 human constant  
 CC region. The CDR gene regions of a pre-existing light chain  
 CC framework were replaced with synthetic IL-4 CDR genes constructed  
 CC from oligonucleotides given in Q83505-08 (CDR1), Q83509-10 (CDR2),  
 CC and Q83511-12 (CDR3). The synthetic VL (Q73986) was ligated into  
 CC the vector. The anti-IL4 engineered antibody was expressed in  
 CC COS and CHO cells.  
 SQ Sequence 51 BP; 14 A; 11 C; 16 G; 10 T;

Query Match 100.0%; Score 27; DB 14; Length 51;  
 Best Local Similarity 100.0%; Pred. No. 2.07e-06;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 11 cagcaagtaagatgagatcctcgagg 37  
 |||||  
 Qy 1 CAGCAAGTAAGTACGATCCTCGAGG 27

## RESULT 2

ID Q83512 standard; DNA; 53 BP.  
 AC Q83512;  
 DT 20-SEP-1995 (first entry)  
 DE IL-4 CDR3 gene fragment.  
 KW Humanized antibody; antibody engineering; monoclonal antibody;  
 KW Mab; interleukin-4; IL-4; allergy; heavy chain; CDR;  
 KW complementarity determining region; ss.  
 OS Synthetic.  
 PN W09507301-A.  
 PD 16-MAR-1995.  
 PF 07-SEP-1994; U10308.  
 PR 07-SEP-1993; US-117366.  
 PR 14-OCT-1993; US-136783.  
 PA (SMIK ) SMITHKLINE BEECHAM CORP.  
 PA (SMIK ) SMITHKLINE BEECHAM PLC.  
 PI Gross M5, Holmes SD, Sylvester DR;  
 DR WPI; 95-123387/16.  
 PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived  
 PT from high affinity mAbs - useful in treatment of IL-4-mediated  
 PT and IgE-mediated allergic conditions  
 PS Example 3; Page 28; 97pp; English.

CC A humanized antibody was designed to contain mouse CDRs (from  
 CC anti-IL-4 Mab 3B9 Mab) within a human antibody framework. A  
 CC synthetic heavy chain was made using the oligonucleotides given  
 CC in Q83498-502 and amplified by PCR using the primers given in  
 CC Q83503-04. The construct was ligated into vector pCD, along  
 CC with a signal sequence (Q83494) and an IgG1 human constant  
 CC region. The CDR gene regions of a pre-existing light chain  
 CC framework were replaced with synthetic IL-4 CDR genes constructed  
 CC from oligonucleotides given in Q83505-08 (CDR1), Q83509-10 (CDR2),  
 CC and Q83511-12 (CDR3). The synthetic VL (Q73986) was ligated into  
 CC the vector. The anti-IL4 engineered antibody was expressed in  
 CC COS and CHO cells.  
 SQ Sequence 53 BP; 9 A; 17 C; 12 G; 15 T;

Query Match 100.0%; Score 27; DB 14; Length 53;  
 Best Local Similarity 100.0%; Pred. No. 2.07e-06;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 19 cctcgaggatcctcattctgtg 45  
 |||||

Cp 27 CCTCGAGATCCTCATTCTGTC 1

## RESULT 3

ID Q73986 standard; cDNA; 393 BP.  
 AC Q73986;  
 DT 20-SEP-1995 (first entry)  
 DE Humanized antibody 3B9 light chain.  
 KW Humanized antibody; antibody engineering; monoclonal antibody;  
 KW Mab; interleukin-4; IL-4; allergy; ds.  
 OS Homo sapiens.

FH Key Location/Qualifiers  
 FT CDS 1..393

FT /tag= a  
 FT sig\_peptide 1..60  
 FT /tag= b  
 FT mat\_peptide 61..393  
 FT /tag= c

PN W09507301-A.

PD 16-MAR-1995.

PF 07-SEP-1994; U10308.

PR 07-SEP-1993; US-117366.

PR 14-OCT-1993; US-136783.

PA (SMIK ) SMITHKLINE BEECHAM CORP.

PA (SMIK ) SMITHKLINE BEECHAM PLC.

PI Gross M5, Holmes SD, Sylvester DR;

DR WPI; 95-123387/16.

DR P-PSDB; R75355.

PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived  
 PT from high affinity mAbs - useful in treatment of IL-4-mediated  
 PT and IgE-mediated allergic conditions

PS Disclosure; Fig.5; 97pp; English.

CC A humanized antibody light chain variable region and signal  
 CC sequence is given in R75355. The signal sequence is also

CC provided in R70194. The sequences of the first 2 CDRs

CC are identical to mouse anti-human IL-4 Mab 3B9 light chain

CC CDRs (given in R70195-96), but the third (R70201) differs

CC by a single amino acid from the native mouse CDR (R70197).

SQ Sequence 393 BP; 97 A; 96 C; 108 G; 92 T;

Query Match 100.0%; Score 27; DB 14; Length 393;  
 Best Local Similarity 100.0%; Pred. No. 2.07e-06;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 334 cagcaagtaagatgagatcctcgagg 360

|||||  
 Qy 1 CAGCAAGTAAGTACGATCCTCGAGG 27

## RESULT 4

ID Q83520 standard; cDNA; 393 BP.

AC Q83520;

DT 20-SEP-1995 (first entry)

DE Humanized antibody 3B9 light chain.

KW Humanized antibody; antibody engineering; monoclonal antibody;

KW Mab; interleukin-4; IL-4; allergy; ds.

OS Homo sapiens.

FH Key Location/Qualifiers

FT CDS 1..393

FT /tag= a

PN W09507301-A.

PD 16-MAR-1995.

PF 07-SEP-1994; U10308.

PR 07-SEP-1993; US-117366.

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5

PR 14-OCT-1993; US-136783.  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
PI Gross MS, Holmes SD, Sylvester DR;  
DR WPI; 95-123387/16.  
DR P-PSD9; R70202.  
PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived from high affinity mAbs - useful in treatment of IL-4-mediated PT and IgE-mediated allergic conditions  
PS Disclosure; Page 71-72; 97pp; English.  
CC A humanized antibody light chain variable region and signal CC sequence is given in R75355. The signal sequence is also CC provided in R70194. The sequences of the 3 CDRs CC are identical to mouse anti-human IL-4 MAb 3B9 light chain CC CDRs (given in R70195-97).  
SQ Sequence 393 BP; 97 A; 98 C; 105 G; 93 T;  
Query Match 92.6%; Score 25; DB 14; Length 393;  
Best Local Similarity 100.0%; Pred. No. 3.58e-05;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 334 cagcaagaatgagatcctccga 358  
|||||  
Qy 1 CAGCAAGTATGAGGATCCTCCGA 25  
RESULT 5  
ID Q83490 standard; cDNA; 396 BP.  
AC Q83490;  
DT 20-SEP-1995 (first entry)  
DE Mouse MAb 3B9 light chain.  
KW Chimeric antibody; humanized antibody; antibody engineering;  
KW monoclonal antibody; MAb; interleukin-4; IL-4; allergy; ds.  
OS Mus sp.  
FH Key Location/Qualifiers  
FT CDS 1..396  
FT /tag= a  
FT sig\_peptide 1..60  
FT /tag= b  
FT mat\_peptide 61..396  
FT /tag= c  
PN W09507301-A.  
PD 16-MAR-1995.  
PF 07-SEP-1994; U10308.  
PR 07-SEP-1993; US-117366.  
PR 14-OCT-1993; US-136783.  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
PI (SMIK ) SMITHKLINE BEECHAM PLC.  
PI Gross MS, Holmes SD, Sylvester DR;  
DR WPI; 95-123387/16.  
DR P-PSD9; R70189.  
PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived from high affinity mAbs - useful in treatment of IL-4-mediated PT and IgE-mediated allergic conditions  
PS Disclosure; Fig.1; 97pp; English.  
CC Spleen cells from mice immunized with human IL-4 were used to prepare CC hybridomas, which were screened for anti-IL-4 MAb secretion. Only CC clone 3B9 was positive. cDNA clones of the 3B9 light and heavy CC chains were cloned into pGEM7f+ and transformed into E. coli CC DH5-alpha. The clones were sequenced (Q83490-91), and used for CC antibody engineering.  
SQ Sequence 396 BP; 99 A; 103 C; 103 G; 91 T;

Query Match 92.6%; Score 25; DB 14; Length 396;

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US-08-612-929-27.rmg

6

Best Local Similarity 100.0%; Pred. No. 3.58e-05;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 337 cagcaagaatgagatcctccga 361  
|||||  
Qy 1 CAGCAAGTATGAGGATCCTCCGA 25  
RESULT 6  
ID Q55014 standard; DNA; 99 BP.  
AC Q55014;  
DT 06-JUL-1994 (first entry)  
DE Humanised Ab 60.3 VL oligonucleotide.  
KW Monoclonal antibody; MAb; heavy chain; light chain;  
KW constant region; variable region; amplification; primer;  
KW polymerase chain reaction; PCR; chimera; Ig;  
KW immunoglobulin; humanised antibody; leucocyte; integrin; ss.  
OS Synthetic.  
PN EP-578515-A.  
PD 12-JAN-1994.  
PF 24-MAY-1993; 401328.  
PR 26-MAY-1992; US-888233.  
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
PI Rajorath J, Harris LJ, Heiao K, Ku-Chuan H;  
DR WPI; 94-010334/02.  
PT Humanised monoclonal antibodies prepn. - using comparative model PT building, by computer database searching  
PS Disclosure; Fig 3; 68pp; English.  
CC A humanised monoclonal antibody corresponding to the murine anti-CD18 CC antibody 60.3 was prepared. The variable (V) region sequences from CC both the heavy (H) and light (L) chains were determined from cDNA CC (amplified by PCR), and spliced onto human constant (C) regions, CC resulting in a chimeric 60.3 Ab (IgG1, kappa). The chimeric Ab was CC expressed in tissue culture (Aq8.653 mouse myeloma cells, detected CC by ELISA), and examined in binding assays. The results from CC competition and inhibition assays showed that the chimeric Ab was CC as effective as the murine 60.3 MAb. The deduced murine VH and VL CC protein sequences were compared to the protein sequence data base, CC and two human Ig protein sequences were selected to be used as CC templates. A murine 60.3 Fv was modeled according to the deduced CC VH and VL protein sequences. Based on the 60.3 Fv model and the two CC human template sequences selected from the protein data base, a CC humanised Fv was modeled. Construction of the humanised 60.3 was CC done by piecing 5 pairs of complementary oligonucleotides together CC (spanning the entire V region) to form the VH and VL. These were CC then attached onto vectors containing genes for appropriate C regions CC to form humanised Ab (IgG1, kappa). The humanised proteins were again CC expressed in Aq8.653 cells and binding assays were done. FACS analyses CC indicated that the humanised Ab recognised cells expressing CD18.  
CC About a dozen of the humanised 60.3 Ab master wells were transferred CC and assayed for Ig.  
SQ Sequence 99 BP; 26 A; 28 C; 19 G; 26 T;

Query Match 85.2%; Score 23; DB 9; Length 99;  
Best Local Similarity 96.0%; Pred. No. 5.85e-04;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 66 tcgagagatcctcattctgtctg 90  
|||||  
Qp 25 TCCGAGGATCCTCACTACTTCTCTG 1

RESULT 7

ID Q55000 standard; DNA; 334 BP.

AC Q55002;  
 DT 06-JUL-1994 (first entry)  
 DE Humanised anti-CD18 Ab 60.3 light chain.  
 KW Monoclonal antibody; Mab; heavy chain; light chain;  
 KW constant region; variable region; amplification; primer;  
 KW polymerase chain reaction; PCR; chimera; Ig;  
 KW immunoglobulin; humanised antibody; leucocyte; integrin; ss.  
 OS Chimeric; Homo sapiens.  
 PN EP-578515-A.  
 PD 12-JAN-1994.  
 PF 24-MAY-1993; 401328.  
 PR 26-MAY-1992; US-888233.  
 PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
 PI Bajorath J, Harris LJ, Heiao K, Ku-Chuan H;  
 DR WPI; 94-010334/02.  
 DR P-PSDB; R47492.  
 PT Humanised monoclonal antibodies prepn. - using comparative model  
 PT building, by computer database searching  
 PS Disclosure; Page 18-19; 68pp; English.  
 CC A humanised monoclonal antibody corresponding to the murine anti-CD18  
 CC antibody 60.3 was prepared. The variable (V) region sequences from  
 CC both the heavy (H) and light (L) chains were determined from cDNA  
 CC (amplified by PCR), and spliced onto human constant (C) regions,  
 CC resulting in a chimeric 60.3 Ab (IgG1, kappa). The chimeric Ab was  
 CC expressed in tissue culture (Aq8.653 mouse myeloma cells, detected  
 CC by ELISA), and examined in binding assays. The results from  
 CC competition and inhibition assays showed that the chimeric Ab was  
 CC as effective as the murine 60.3 Mab. The deduced murine VH and VL  
 CC protein sequences were compared to the protein sequence data base,  
 CC and two human Ig protein sequences were selected to be used as  
 CC templates. A murine 60.3 Fv was modeled according to the deduced  
 CC VH and VL protein sequences. Based on the 60.3 Fv model and the two  
 CC human template sequences selected from the protein data base, a  
 CC humanised Fv was modeled. Construction of the humanised 60.3 was  
 CC done by piecing 5 pairs of complementary oligonucleotides together  
 CC (spanning the entire V region) to form the VH and VL. These were  
 CC then attached onto vectors containing genes for appropriate C regions  
 CC to form humanised Ab (IgG1, kappa). The humanised proteins were again  
 CC expressed in Aq8.653 cells and binding assays were done. FACS analyses  
 CC indicated that the humanised Ab recognised cells expressing CD18.  
 CC About a dozen of the humanised 60.3 Ab master wells were transferred  
 CC and assayed for Ig.  
 SQ Sequence 334 BP; 90 A; 79 C; 80 G; 85 T;

Query Match 85.2%; Score 23; DB 9; Length 334;  
 Best Local Similarity 96.0%; Pred. No. 5.85e-04;  
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 277 cagcaagtaagtgcggtctctcgga 301  
 |||||  
 QY 1 CAGCAAGTAAGTGCAGGATCTCTCGGA 25

RESULT 8  
 ID Q55002 standard; DNA; 334 BP.  
 AC Q55002;  
 DT 06-JUL-1994 (first entry)  
 DE Murine anti-CD18 Ab 60.3 light chain.  
 KW Monoclonal antibody; Mab; heavy chain; light chain;  
 KW constant region; variable region; amplification; primer;  
 KW polymerase chain reaction; PCR; chimera; Ig;  
 KW immunoglobulin; humanised antibody; leucocyte; integrin; ss.  
 OS Mus sp.

PN EP-578515-A.  
 PD 12-JAN-1994.  
 PF 24-MAY-1993; 401328.  
 PR 26-MAY-1992; US-888233.  
 PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
 PI Bajorath J, Harris LJ, Heiao K, Ku-Chuan H;  
 DR WPI; 94-010334/02.  
 DR P-PSDB; R47494.  
 PT Humanised monoclonal antibodies prepn. - using comparative model  
 PT building, by computer database searching  
 PS Disclosure; Page 21; 68pp; English.  
 CC A humanised monoclonal antibody corresponding to the murine anti-CD18  
 CC antibody 60.3 was prepared. The variable (V) region sequences from  
 CC both the heavy (H) and light (L) chains were determined from cDNA  
 CC (amplified by PCR), and spliced onto human constant (C) regions,  
 CC resulting in a chimeric 60.3 Ab (IgG1, kappa). The chimeric Ab was  
 CC expressed in tissue culture (Aq8.653 mouse myeloma cells, detected  
 CC by ELISA), and examined in binding assays. The results from  
 CC competition and inhibition assays showed that the chimeric Ab was  
 CC as effective as the murine 60.3 Mab. The deduced murine VH and VL  
 CC protein sequences were compared to the protein sequence data base,  
 CC and two human Ig protein sequences were selected to be used as  
 CC templates. A murine 60.3 Fv was modeled according to the deduced  
 CC VH and VL protein sequences. Based on the 60.3 Fv model and the two  
 CC human template sequences selected from the protein data base, a  
 CC humanised Fv was modeled. Construction of the humanised 60.3 was  
 CC done by piecing 5 pairs of complementary oligonucleotides together  
 CC (spanning the entire V region) to form the VH and VL. These were  
 CC then attached onto vectors containing genes for appropriate C regions  
 CC to form humanised Ab (IgG1, kappa). The humanised proteins were again  
 CC expressed in Aq8.653 cells and binding assays were done. FACS analyses  
 CC indicated that the humanised Ab recognised cells expressing CD18.  
 CC About a dozen of the humanised 60.3 Ab master wells were transferred  
 CC and assayed for Ig.  
 SQ Sequence 334 BP; 88 A; 85 C; 81 G; 80 T;

Query Match 85.2%; Score 23; DB 9; Length 334;  
 Best Local Similarity 96.0%; Pred. No. 5.85e-04;  
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 277 cagcaagtaagtgcggtctctcgga 301  
 |||||  
 QY 1 CAGCAAGTAAGTGCAGGATCTCTCGGA 25

RESULT 9  
 ID Q30757 standard; cDNA; 393 BP.  
 AC Q30757;  
 DT 30-MAR-1993 (first entry)  
 DE p64-k4.  
 KW Human; antibody; interleukin-6; receptor; IL-6R; light chain; L; H;  
 KW heavy chain; variable region; mouse; monoclonal; hybridoma; AUK64-7;  
 KW plasmid; p64-k4; p64-h2; ss.  
 OS Synthetic.  
 FH Key Location/Qualifiers  
 FT sig\_peptide 1..60  
 FT /tag= a  
 FT mat\_peptide 61..393  
 FT /tag= b  
 PN W09219759-A.  
 PD 12-NOV-1992.  
 PE 24-APR-1992; J00544.  
 PR 25-APR-1991; JP-095476.  
 PR 19-FEB-1992; JP-032084.

PA (CHUS ) CHUGAI SEIYAKU KK.  
 PI Bendig MM, Jones ST, Saldanha JW, Sato K, Tsuchiya M;  
 DR WPI; 92-398882/48.  
 DR P-PSDB; R29008.  
 PT Reconstituted human antibody to human interleukin-6 receptor -  
 PT has low antigenicity and contains mouse V-region complementarity  
 PT determining regions  
 PS Disclosure; Page 124-125; 207pp; Japanese.  
 CC The sequences given in Q30757-58 were used in example to illustrate  
 CC the production of a human antibody which recognises human  
 CC interleukin-6 receptor (IL-6R). The antibody comprises light (L)  
 CC chain and heavy (H) chain variable regions which were derived from a  
 CC mouse monoclonal antibody produced from the hybridoma AUK64-7 which  
 CC contained the plasmids p64-k4 and p64-h2.  
 SQ Sequence 393 BP; 93 A; 101 C; 100 G; 99 T;

Query Match 85.2%; Score 23; DB 5; Length 393;  
 Best Local Similarity 100.0%; Pred. No. 5.85e-04;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 337 cagcaaaagtgaagatcctcc 359  
 |||||  
 QY 1 CAGCAAAAGTAATGAGGATCCTCC 23

RESULT 10  
 ID Q36609 standard; DNA; 393 BP.  
 AC Q36609;  
 DT 02-JUN-1993 (first entry)  
 DE Anti-CD4 antibody MF 3.10 light chain variable region.  
 KW immunosuppression; tissue transplantation; graft; L chain; V region;  
 KW T-helper cell inhibition; transplant rejection; MAb;  
 KW interleukin-2 receptor; ss.  
 FH Key Location/Qualifiers  
 FT sig peptide 1..60  
 FT /\*tag= a  
 FT mat\_peptide 61..393  
 FT /\*tag= b  
 FT /note= "JL region begins at position 361"  
 PN DE4143214-A.  
 PD 28-JAN-1993.  
 PF 30-DEC-1991; 143214.  
 PR 25-JUL-1991; DE-124759.  
 PR 30-DEC-1991; DE-143214.  
 PA (BOEF ) BOEHRINGER MANNHEIM GMBH.  
 PI Kaluza B, Riethmuller G, Scheuer W, Weidle U;  
 DR WPI; 93-037582/05.  
 DR P-PSDB; R32123.  
 PT Synergistic antibody compsn. for use as immunosuppressant -  
 PT comprises monoclonal anti-CD4 antibodies and monoclonal anti-IL2R  
 PT alpha- or anti-IL2R beta antibodies  
 PS Claim 5; Page 11; 18pp; German.  
 CC This sequence encodes the light chain variable region of a preferred  
 CC anti-CD4 monoclonal antibody for use in the claimed synergistic  
 CC composition. Mab MT 3.10 is deposited as clone 3.101/sB10 (ECACC  
 CC 90090702). The anti-CD4 antibody is used with at least one anti-IL2R  
 CC alpha or beta antibody. Individually the antibodies are strongly  
 CC inhibiting and when used together their immunosuppressive properties  
 CC are improved; they synergistically inhibit T-helper cell  
 CC proliferation to effectively inhibit transplant rejection at low  
 CC doses without significantly reducing the general immune response.  
 CC See Q36607-Q36616.  
 SQ Sequence 393 BP; 100 A; 105 C; 98 G; 90 T;

Query Match 85.2%; Score 23; DB 6; Length 393;  
 Best Local Similarity 96.0%; Pred. No. 5.85e-04;  
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 337 cagcaaaagtgaagatcctccga 361  
 |||||  
 QY 1 CAGCAAAAGTAATGAGGATCCTCCGA 25

RESULT 11  
 ID Q51746 standard; cDNA; 91 BP.  
 AC Q51746;  
 DT 31-MAY-1994 (first entry)  
 DE Oligonucleotide probe MK14-A  
 KW Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;  
 KW ss.  
 OS Synthetic.  
 PN EP-571911-A.  
 PD 01-DEC-1993.  
 PF 24-MAY-1993; 108325.  
 PR 26-MAY-1992; US-889651.  
 PA (BECT ) BECTON DICKINSON CO.  
 PI Shank DD, Spears PA;  
 DR WPI; 93-378844/48.  
 PT New oligonucleotide probes specific for Mycobacteria - used for  
 PT detection and amplification of Mycobacteria nucleic acid in  
 PT samples  
 PS Claim 3; Page 14; 23pp; English.  
 CC Oligonucleotide probe MK14-A consists of nucleotides 5-95 of MK14  
 CC (Q51735). It hybridized to all spp. of mycobacteria tested, but  
 CC cross reacted to a few non-mycobacterial spp. The probe may  
 CC be useful as an initial screen for mycobacterial infection.  
 CC See also Q51735-45 and Q51747-59.  
 SQ Sequence 91 BP; 5 A; 17 G; 15 G; 4 T;

Query Match 81.5%; Score 22; DB 9; Length 91;  
 Best Local Similarity 0.0%; Pred. No. 2.31e-03;  
 Matches 0; Conservative 22; Mismatches 0; Indels 0; Gaps 0;

Db 34 hvhsvvvvhhvhhvhhvhh 55  
 :  
 Cp 27 CCTCGGAGGATCCTCATTACT 6

RESULT 12  
 ID Q12684 standard; DNA; 336 BP.  
 AC Q12684;  
 DT 01-OCT-1991 (first entry)  
 DE Murine IB4 light chain-2 variable region.  
 KW Monoclonal antibody; complementarity determining region; CDR;  
 KW integrin; hybridoma IB4; protein REI; Gal/Rei; Ig; ss.  
 PN EP-438312-A.  
 PN EP-440351-A.  
 PD 24-JUL-1991.  
 PF 17-JAN-1991; 300367.  
 PR 19-JAN-1990; US-467692.  
 PR 20-DEC-1990; US-627421.  
 PA (MERI ) MERCK & CO INC.  
 PI Law WF, Mark GE, Schmidt JA, Singer II;  
 DR WPI; 91-216985/30.  
 DR P-PSDB; R13089.  
 PT New recombinant immunoglobulin(s) reactive with leukocyte CD18  
 PT antigen - comprise human heavy chain framework and murine  
 PT complementarity regions useful in treatment of inflammation



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13

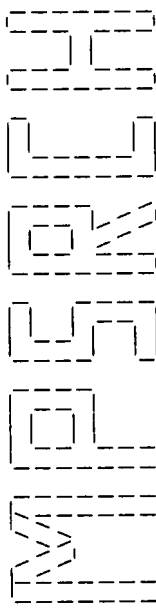
PI Leturcq DJ, Mathison JC, Moriarty AM, Tobias PS;  
PI Ulevitch RJ;  
DR WPI; 95-022719/03.  
DR P-PSDB; R64202.  
PT Hybridoma cell lines produce MAb which inhibit CD14-mediated cell  
PT activation - for detecting CD14 in a sample and to inhibit the  
PT binding of LPS to CD14.  
PS Disclosure; Fig 3; 91pp; English.  
CC Anti-human soluble CD14 receptor MAb 28C5 may be used to  
CC detect CD14 in cell samples, to inhibit binding of LPS to  
CC CD14 or a LPS/CD14 complex to a cell, to inhibit CD14-mediated  
CC activation of a cell expressing CD14 receptor, and for sepsis  
CC therapy.  
SQ Sequence 645 BP; 180 A; 170 C; 150 G; 145 T;

Query Match 77.8%; Score 21; DB 13; Length 645;  
Best Local Similarity 92.0%; Pred. No. 8.97e-03;  
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 268 caccaagtaatgagatccgacga 292  
Qy 1 CAGCAAGTAATCAGGATCCTCCGA 25  
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Job time : 14 secs.

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MPsrch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed Mar 19 08:32:59 1997; MaePar time 55.50 Seconds  
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Perfect Score: 27  
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Comp: GTGCTTTCATTACTCTAGGAGCTCC

Scoring table: TABLE default  
Gap 10

Nmatch STD : Dbase 0; Query 0

Searched: 279077 seqs, 411808665 bases x 2

Post-processing: Minimum Match 0\$  
Listing first 45 summaries

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10:PRO1 11:PRO2 12:ROD 13:SYN 14:UNC 15:VIR  
genbank94  
16:BCT1 17:BCT2 18:BCT3 19:BCT4 20:BCT5 21:BCT6 22:BCT7  
23:BCT8 24:BCT9 25:INV1 26:INV2 27:INV3 28:INV4 29:INV5  
30:INV6 31:INV7 32:MAM1 33:MAM2 34:MAM3 35:VRT1 36:VRT2  
37:VRT3 38:PAT1 39:PAT2 40:PAT3 41:PHG 42:PLN1 43:PLN2  
44:PLN3 45:PLN4 46:PLN5 47:PLN6 48:PLN7 49:PLN8 50:PRI1  
51:PRI2 52:PRI3 53:PRI4 54:PRI5 55:PRI6 56:PRI7 57:PRI8  
58:PRI9 59:PRI10 60:PRI11 61:PRI12 62:PRI13 63:ROD1  
64:ROD2 65:ROD3 66:ROD4 67:ROD5 68:ROD6 69:ROD7 70:ROD8  
71:STR 72:SYN 73:UNA 74:VRL1 75:VRL2 76:VRL3 77:VRL4  
78:VRL5 79:VRL6 80:VRL7 81:VRL8  
genbank-new5  
82:BCT 83:INV1 84:INV2 85:MAM 86:VRT 87:PAT 88:PHG  
89:PLN 90:PRI 91:ROD 92:STR 93:SYN 94:UNA 95:VRL  
u-embl46\_94  
96:part1

Statistics: Mean 7.264; Variance 2.639; scale 2.752

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	23	85.2	195	66	MUSIGKAAAC	Mouse Igk chain mRNA,	3.50e-05
2	23	85.2	228	65	MMU18577	Mus musculus immunogl	3.50e-05
3	23	85.2	273	67	MUSIGKCMK	Mouse Ig rearranged k	3.50e-05
4	23	85.2	307	64	MMIGGLA	Mus musculus (DBA/1)	3.50e-05
5	23	85.2	336	67	MUSIGKCMK	Mouse Ig rearranged k	3.50e-05
6	23	85.2	336	64	MMIGLC310	M.musculus mRNA for I	3.50e-05
7	23	85.2	336	64	MMIGLC404	M.musculus mRNA for I	3.50e-05
8	23	85.2	393	70	S50265	Ig VL-anti-CD4 mAb M-	3.50e-05
9	23	85.2	394	64	MMU01973	Mus musculus Balb/c a	3.50e-05
10	23	85.2	841	67	MUSIGKVR3	Mouse Ig germline kap	3.50e-05
11	21	77.8	312	66	MUSIGKARK	Mouse Ig kappa-chain	1.59e-03
12	21	77.8	318	65	MMVLZD4	M.musculus mRNA for i	1.59e-03
13	21	77.8	333	63	MDIGKVBV	M.domesticus Igk vari	1.59e-03
14	21	77.8	333	70	S54207	V kappa 2I=immunoglob	1.59e-03
15	21	77.8	360	67	MUSIGKAF	Mouse Ig active kappa	1.59e-03
16	21	77.8	363	67	MUSL341GKV	Mouse hybridoma Ig re	1.59e-03
17	21	77.8	363	67	MUSL931GKV	Mouse hybridoma Ig re	1.59e-03
18	21	77.8	396	70	SYN4C10L	Murine/Human chimeric	1.59e-03
19	21	77.8	671	67	MUSIGKVS	Mouse Ig germline kap	1.59e-03
20	21	77.8	841	67	MUSIGKVR2	Mouse Ig germline kap	1.59e-03
21	21	77.8	900	40	I08223	Sequence 1 from paten	1.59e-03
22	20	74.1	195	66	MUSIGKAAAB	Mouse Igk chain mRNA,	1.01e-02
23	20	74.1	245	64	MMIGKCVRH	M.musculus immunoglob	1.01e-02
24	20	74.1	255	64	MMIGKCVRD	M.musculus immunoglob	1.01e-02
25	20	74.1	264	64	MMIGKCVRI	M.musculus immunoglob	1.01e-02
26	20	74.1	266	64	MMIGKCVRC	M.musculus immunoglob	1.01e-02
27	20	74.1	270	64	MMIGKCVRG	M.musculus immunoglob	1.01e-02
28	20	74.1	270	64	MMIGKCVRB	M.musculus immunoglob	1.01e-02
29	20	74.1	270	64	MMIGKCVRF	M.musculus immunoglob	1.01e-02
30	20	74.1	279	66	MUSIGKAAA	Mouse Igk chain mRNA,	1.01e-02
31	20	74.1	292	65	MMU18599	Mus musculus immunogl	1.01e-02
32	20	74.1	297	65	MMU29629	Mus musculus anti-DNA	1.01e-02
33	20	74.1	302	67	MUSIGLAFJ	Mouse Ig kappa-chain	1.01e-02
34	20	74.1	321	64	MMIGLT82	Mouse immunoglobulin	1.01e-02
35	20	74.1	322	64	MMIGLT83	Mouse immunoglobulin	1.01e-02
36	20	74.1	323	70	S52318	Ig VJ=anti-carcinoemb	1.01e-02
37	20	74.1	333	67	MUSIGLVW21	Mus musculus (clone V	1.01e-02
38	20	74.1	333	65	MMVLIE10	Mouse mRNA for kappa-	1.01e-02
39	20	74.1	333	70	S42888	Ig V kappa =immunogl	1.01e-02
40	20	74.1	333	67	MUSIGL5B	Mouse IgL chain H2L2	1.01e-02
41	20	74.1	336	67	MUSIGKCMJ	Mouse Ig rearranged k	1.01e-02
42	20	74.1	336	67	MUSIGKCMJ	Mouse Ig rearranged k	1.01e-02
43	20	74.1	469	67	MUSIGKEK	Mouse Ig aberrantly r	1.01e-02
44	20	74.1	694	67	MUSIGKAM2	Mouse Ig kappa aberr	1.01e-02
45	20	74.1	833	64	MMIGK2	Part of the gene for	1.01e-02

ALIGNMENTS

RESULT 1  
LOCUS MUSIGKAAAC 195 bp mRNA  
DEFINITION Mouse Igk chain mRNA, VJ1 region.  
ACCESSION M57980  
NID g196406  
KEYWORDS J-region; V-region; anti-cytochrome c antibody;  
immunoglobulin kappa-chain; immunoglobulin light chain.  
SOURCE Mouse (BALB/c) secondary B cell hybridoma 2B5 mRNA, clone 2B5.F8.  
ORGANISM Mus musculus



Mar 19:08:32

US-08-612-929-27.rge

3

Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.

REFERENCE 1 (bases 1 to 195)  
AUTHORS Goshorn, S.C., Retzel, E. and Jemerson, R.  
TITLE Common structural features among monoclonal antibodies binding the same antigenic region of cytochrome c

J. Biol. Chem. 266 (4), 2134-2142 (1991)

JOURNAL 91115823

MEDLINE Location/Qualifiers

source  
1..195  
/organism="Mus musculus"  
/clone="2B5.F8"  
/strain="BALB/c"  
/sub\_species="domesticus"  
/cell\_line="2B5"  
/cell\_type="secondary B cell"  
/sequenced\_mol="cDNA to mRNA"  
/tissue\_type="hybridoma"

V\_region

1..156  
/partial  
/gene="IgM"  
/map="chromosome 6"

CDS

1..195  
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/map="chromosome 6"  
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/product="Ig kappa chain"  
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misc\_feature

19..39  
/gene="IgM"  
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/note="CDR2"

misc\_feature

136..162  
/gene="IgM"  
/map="chromosome 6"  
/note="CDR3"

J\_segment

156..195  
/gene="IgM"  
/map="chromosome 6"  
/note="J1"

BASE COUNT 52 a 50 c 51 g 42 t

ORIGIN Chromosome 6.

Query Match 85.2%; Score 23; DB 66; Length 195;

Best Local Similarity 96.0%; Pred. No. 3.50e-05;

Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 136 caccaagaatgagcgtctcgga 160

|||||

QY 1 CAGCAAGTAATGAGGATCTCCGA 25

RESULT 2

LOCUS MM018577 228 bp mRNA ROD 21-JUN-1995

DEFINITION Mus musculus immunoglobulin kappa light chain, variable region

mRNA, clone BALB/c-51, partial cds.

ACCESSION U18577

NTD g619707

KEYWORDS mouse.

SOURCE Mus musculus

ORGANISM Mus musculus

Mar 19:08:32

US-08-612-929-27.rge

4

Eukaryota; Eumycota group; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia; Sciurognathi; Myomorpha; Muridae; Mus. 1 (bases 1 to 228)

Roark, J.H., Kuntz, C.L., Nguyen, K.A., Caton, A.J. and Erikson, J.

Breakdown of B cell tolerance in a mouse model of systemic lupus

erythematosus

J. Exp. Med. 181 (3), 1157-1167 (1995)

JOURNAL 95173583

MEDLINE 2 (bases 1 to 228)

REFERENCE Roark, J.H.

AUTHORS Direct Submission

TITLE Submitted (14-DEC-1994) Jessica H. Roark, Wistar Institute, 3601

JOURNAL Spruce St., Philadelphia, PA 19104, USA

FEATURES

Location/Qualifiers  
1..228  
/strain="BALB/c"  
/organism="Mus musculus"  
/cell\_type="splenic B cell hybridoma"  
/tissue\_type="spleen"  
/dev\_stage="adult"  
1..>228  
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/product="immunoglobulin kappa light chain, variable region"

CDS

/db\_xref="PID:g619708"  
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FTLINHPVEEDAATYCCQSNEDPPTFGSGT"

BASE COUNT 61 a 57 c 57 g 53 t

ORIGIN

Query Match 85.2%; Score 23; DB 65; Length 228;

Best Local Similarity 100.0%; Pred. No. 3.50e-05;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 187 cagcaagaatgagcgtctctcc 209

|||||

QY 1 CAGCAAGTAATGAGGATCTCTCC 23

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Mar 19 08:32

US-08-612-929-27.rge

5

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CDS
<1..>273
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/db_xref="PID:q196988"
/translation="SCRAESVDYXGSLHHYQKQCPQPKLLISRASNLGSGIPAR
FSGVGRDTFTLTINPEADVATYYCQSNEDPPPTFGAGTKLEIKR"
BASE COUNT      69 a   72 c   66 g   65 t   1 others
ORIGIN
Chromosome 6.

Query Match      85.2%; Score 23; DB 67; Length 273;
Best Local Similarity 100.0%; Pred. No. 3.50e-05;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 214 caccaaaagtaatgagatcctcc 236
|||||
QY 1 CAGCAAGTAATGAGGATCCTCC 23

RESULT 4
LOCUS MMIGGL4 307 bp RNA ROD 05-AUG-1994
DEFINITION Mus musculus (DBA/1) mRNA for immunoglobulin gamma light chain
variable region.
ACCESSION Z26771
NID q436888
KEYWORDS immunoglobulin; immunoglobulin gamma; light chain joining region;
light chain variable region.
SOURCE house mouse.
ORGANISM
Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcoterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 307)
AUTHORS Mo,J.A., Scheynius,A., Nilsson,S. and Holmdahl,R.
TITLE Germline encoded IgG antibodies bind mouse cartilage in vivo
epitope and idiotype specific binding and inhibition
JOURNAL Scand. J. Immunol. (1993) In press
REFERENCE 2 (bases 1 to 307)
AUTHORS Mo,J.A.
TITLE Direct Submission
JOURNAL Submitted (30-SEP-1993) to the EMBL/GenBank/DBJ databases, John A
Mo, Department of Medical and Physiological, Department of, Medical
and Physiological Chemistry, Husargatan 3, Uppsala, 75123, Sweden
REFERENCE 3 (bases 1 to 307)
AUTHORS Mo,J.A., Scheynius,A., Nilsson,S. and Holmdahl,R.
TITLE Germline-encoded IgG antibodies bind mouse cartilage in vivo:
epitope- and idiotype-specific binding and inhibition
JOURNAL Scand. J. Immunol. 39 (2), 122-130 (1994)
MEDLINE 94126659
FEATURES
source
Location/Qualifiers
1..307
/organism="Mus musculus"
/strain="DBA/1"
/dev_stage="Adult"
/tissue_type="Lymph node"
/cell_type="B cell hybridoma"
/cell_line="CIIF4 hybridoma"
/chromosome="6"
1..272
/note="Light chain variable region"
V_segment 273..307
J_segment
/note="Joining region JK2"
BASE COUNT      81 a   77 c   77 g   72 t
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Mar 19 08:32

US-08-612-929-27.rge

6

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ORIGIN
Query Match      85.2%; Score 23; DB 64; Length 307;
Best Local Similarity 100.0%; Pred. No. 3.50e-05;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 250 caccaaaagtaatgagatcctcc 272
|||||
QY 1 CAGCAAGTAATGAGGATCCTCC 23

RESULT 5
LOCUS MUSIGKCMK 336 bp mRNA ROD 15-MAR-1989
DEFINITION Mouse Ig rearranged kappa-chain V-region mRNA from hybridoma
H37-77, partial cds.
ACCESSION M21524
NID q196985
KEYWORDS C-region; V-region; immunoglobulin light chain;
immunoglobulin-kappa; rearranged gene.
SOURCE Mouse (strain BALB/c) hybridoma H37-77, cDNA to mRNA.
ORGANISM
Mus musculus
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE 1 (bases 1 to 336)
AUTHORS Clarke,S.H., Huppi,K., Ruzinsky,D., Staudt,L., Gerhard,W. and
Weigert,M.
TITLE Inter- and intracolon diversity in the antibody response to
influenza hemagglutinin
JOURNAL J. Exp. Med. 161, 687-704 (1985)
MEDLINE 85159415
FEATURES
source
Location/Qualifiers
1..336
/organism="Mus musculus"
<1..>336
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/translation="DIETQSPASLVSLGQRATISCRASESVYSGKSFHHYQKRP
GQPKPLIYRASNLGSGIPARESGSRDTFTLTINPEADVATYYCQSNEDPPPTF
GAGTKLEIKR"
BASE COUNT      84 a   88 c   84 g   80 t
ORIGIN Chromosome 6.

Query Match      85.2%; Score 23; DB 67; Length 336;
Best Local Similarity 100.0%; Pred. No. 3.50e-05;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 277 caccaaaagtaatgagatcctcc 299
|||||
QY 1 CAGCAAGTAATGAGGATCCTCC 23

RESULT 6
LOCUS MMIGLC310 336 bp RNA ROD 07-MAY-1992
DEFINITION M.musculus mRNA for IG light chain VJ region (M-T310) .
ACCESSION X65091
NID g52288
KEYWORDS Ig light chain; VJ domain.
SOURCE house mouse.
ORGANISM
Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcoterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
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Mar 19 08:32

US-08-612-929-27.rge

7

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Sciuognathi; Myomorpha; Muridae; Murinae; Mus.
1 (bases 1 to 336)
AUTHORS      Weissenhorn, W.
TITLE        Direct Submission
JOURNAL      Submitted (10-MAR-1992) to the EMBL/GenBank/DBJ databases. W.
Weissenhorn, Institut fuer Immunologie, Goethestrasse 31, W-8000
Muenchen 2, FRG

2 (bases 1 to 336)
AUTHORS      Weissenhorn, W., Riethmueller, G., Weiss, E.M. and Rieber, E.P.
TITLE        Structural characterization of CD4 mAb
JOURNAL      Unpublished
FEATURES     Location/Qualifiers
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             region"
             /db_xref="PID:g52289"
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             GGGTKLEIKR"

BASE COUNT   89 a   90 c   81 g   76 t
ORIGIN
Query Match      85.2%; Score 23; DB 64; Length 336;
Best Local Similarity 96.0%; Pred. No. 3.50e-05;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 277 cagcaaaagttagtgagatcctccga 301
|||||
QY 1 CAGCAAGTAATCAGGATCCTCCGA 25

RESULT 7
LOCUS      MM1GLC404      336 bp      RNA      ROD      07-MAY-1992
DEFINITION M.musculus mRNA for IG light chain VJ region (M-T404).
ACCESSION   X65092
NID         g52292
KEYWORDS    Ig light chain; VJ domain.
SOURCE      house mouse.
ORGANISM    Mus musculus
            Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;
            Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
            Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
            Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
            Sciuognathi; Myomorpha; Muridae; Murinae; Mus.
1 (bases 1 to 336)
AUTHORS      Weissenhorn, W.
TITLE        Direct Submission
JOURNAL      Submitted (10-MAR-1992) to the EMBL/GenBank/DBJ databases. W.
Weissenhorn, Institut fuer Immunologie, Goethestrasse 31, W-8000
Muenchen 2, FRG

2 (bases 1 to 336)
AUTHORS      Weissenhorn, W., Riethmueller, G., Weiss, E.M. and Rieber, E.P.
TITLE        Structural characterization of CD4 mAb
JOURNAL      Unpublished
FEATURES     Location/Qualifiers
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             /strain="Balb/c"

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Mar 19 08:32

US-08-612-929-27.rge

8

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/cell_type="B-cell"
/cell_line="Hybridoma M-T404"
<1..>336
/codon_start=1
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region"
/db_xref="PID:g52293"
/translation="DIVLTQSPASIPMSLQQRATISCKASQSLDYGDSYMMNYQOKP
GQPKLLIYAASNLESIGIPARESGSGTDTFTLNHPVEEDAAATYYCQSSDDPTTF
GGGTKLEIKR"

BASE COUNT   89 a   90 c   81 g   76 t
ORIGIN
Query Match      85.2%; Score 23; DB 64; Length 336;
Best Local Similarity 96.0%; Pred. No. 3.50e-05;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 277 cagcaaaagttagtgagatcctccga 301
|||||
QY 1 CAGCAAGTAATCAGGATCCTCCGA 25

RESULT 8
LOCUS      S50265      393 bp      mRNA      ROD      02-APR-1993
DEFINITION Ig VJ-anti-CD4 mAb M-T310 variable region light chain [J], chimeric
antibody [mice, hybridoma cells, mRNA Partial, 393 nt].
ACCESSION   S50265
NID         g260765
KEYWORDS    mice hybridoma cells.
SOURCE      Mus sp.
ORGANISM    Unclassified.
REFERENCE    1 (bases 1 to 393)
AUTHORS      Weissenhorn, W., Scheuer, W., Kaluz, B., Schwirzke, M., Reiter, C.,
            Flieger, D., Lenz, H., Weiss, E.H., Rieber, E.P., Riethmueller, G. et.al.
            Combinatorial functions of two chimeric antibodies directed to
            human CD4 and one directed to the alpha-chain of the human
            interleukin-2 receptor
            Gene 121 (2), 271-278 (1992)
JOURNAL      93077041
MEDLINE
REMARK      GenBank staff at the National Library of Medicine created this
            entry [NCBI gibs9q 119503] from the original journal article.
            This sequence comes from Fig. 1c.
FEATURES     Location/Qualifiers
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             /partial
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             /note="Method: conceptual translation supplied by author.
             This sequence comes from Fig. 1c."
             /codon_start=1
             /product="anti-CD4 mAb M-T310 variable region light chain"
             /db_xref="PID:g260766"
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            ASQSLDYGDSYMMNYQOKPGQPKLLIYAASNLESIGIPARESGSGTDTFTLNHPV
            EEEDAAATYYCQSSDDPTTFGGGTKLEIK"

BASE COUNT   100 a  105 c   98 g   90 t
ORIGIN
Query Match      85.2%; Score 23; DB 70; Length 393;
Best Local Similarity 96.0%; Pred. No. 3.50e-05;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Mar 19 08:32

US-08-612-929-27.fge

9

Db 337 cagcaagaatgtaggagtcctcgga 361 mRNA ROD 24-SEP-1993  
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Qy 1 CAGCAAGTAATGAGGATCCTCCGA 25  
partial cds.  
RESULT 9 MMU01973 394 bp anti-CD18 Ig light chain variable region mRNA,  
LOCUS Mus musculus Balb/c partial cds.  
DEFINITION U01973  
ACCESSION g403071  
NID  
KEYWORDS  
SOURCE mouse.  
ORGANISM Mus musculus  
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;  
Eutheria; Rodentia; Myomorpha; Muridae; Mus.  
REFERENCE 1 (bases 1 to 394)  
AUTHORS Hsiao,K., Bajorath,J. and Harris,L.J.  
TITLE Humanization of 60.3, an anti-CD18 antibody  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 394)  
AUTHORS Harris,L.J.  
TITLE Direct Submission  
JOURNAL Submitted (21-SEP-1993) Linda J. Harris, Molecular Immunology,  
Bristol-Myers Squibb, Pharmaceutical Research Institute, 3005 First  
Avenue, Seattle, WA 98121 USA  
FEATURES  
source  
1..394  
/strain="Balb/c"  
/organism="Mus musculus"  
/cell\_line="60.3 hybridoma"  
/cell\_type="hybridoma (B-cell)"  
/tissue\_type="spleen"  
/dev\_stage="adult"  
sig\_peptide  
1..60  
/note="nucleotides 1-29 derived from PCR primer and may  
not reflect mRNA sequence"  
exon  
1..49  
/number=1  
/product="partial signal peptide"  
CDS  
1..394  
/partial  
/note="V gene is identical to Vk21c germline gene; uses  
Jk1"  
/codon\_start=1  
/product="Ig variable region, light chain"  
/db\_xref="PID:g403072"  
/translation="METDTLLLVLLWPGSTGDIVLTQSPASIVSLQQRATISCR  
ASEVSDYSGNSFMHWYQKPGQPKLLIYRASNLGSGIPARFSGSGSRDTFTINPV  
EADVDVATYYCQGSNEDPRTEGGTKLEIK"  
exon  
50..394  
/number=2  
/product="carboxyl end of signal peptide and mature heavy  
chain"  
misc\_feature  
61..135  
/standard\_name="FR1"  
mat\_peptide  
61..393  
/product="Ig variable region, light chain"  
misc\_feature  
136..168  
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misc\_feature  
169..219  
/standard\_name="FR2"  
misc\_feature  
220..228

Mar 19 08:32

US-08-612-929-27.fge

10

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misc\_feature 340..357 /standard\_name="FR3"  
misc\_feature 358..393 /standard\_name="CDR3"  
BASE COUNT 99 a 100 c 98 g 97 t  
ORIGIN  
Query Match 85.2%; Score 23; DB 64; Length 394;  
Best Local Similarity 96.0%; Pred. No. 3.50e-05;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Db 337 cagcaagaatgtaggagtcctcgga 361  
||||||| |||||||  
Qy 1 CAGCAAGTAATGAGGATCCTCCGA 25  
RESULT 10  
LOCUS MUSIGKVR3 841 bp DNA ROD 14-APR-1994  
DEFINITION Mouse Ig germline kappa V-region 9.5kb-V-kappa, V-kappa-21C.  
ACCESSION K02161  
NID g197492  
KEYWORDS C-region; V-region; germline; immunoglobulin light chain;  
immunoglobulin-kappa; immunoglobulin-kappa subgroup vk-21.  
SEGMENT 3 of 3  
SOURCE Mouse BALB/c embryo DNA, clones KM23 and KE5e.  
ORGANISM Mus musculus  
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;  
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.  
REFERENCE 1 (bases 1 to 841)  
AUTHORS Heinrich,G., Traunecker,A. and Tonegawa,S.  
TITLE Somatic mutation creates diversity in the major group of mouse  
immunoglobulin kappa-light chains  
JOURNAL J. Exp. Med. 159, 417-435 (1984)  
MEDLINE 84113346  
FEATURES  
source  
1..841  
/organism="Mus musculus"  
exon  
198..246  
/note="Ig kappa V-region 9.5kb-V-kappa"  
/number=1  
exon  
198..246  
/note="Ig kappa V-region 9.5kb-V-kappa signal peptide,  
exon 1; putative"  
CDS  
join(198..246,486..793)  
/partial  
/note="Ig kappa V-region 9.5kb-V-kappa"  
/codon\_start=1  
/db\_xref="PID:g197496"  
/translation="METDTLLLVLLWPGSTGDIVLTQSPASIVSLQQRATISCR  
ASEVSDYSGNSFMHWYQKPGQPKLLIYRASNLGSGIPARFSGSGSRDTFTINPV  
EADVDVATYYCQGSNEDP"  
sig\_peptide  
198..246  
/note="Ig kappa V-region 9.5kb-V-kappa signal peptide"  
/codon\_start=1  
exon  
198..246  
/note="Ig kappa V-region 9.5kb-V-kappa, exon 1; putative"  
sig\_peptide  
join(198..246,486..496)  
/note="Ig kappa V-region 9.5kb-V-kappa signal peptide"  
/codon\_start=1  
intron  
247..485  
/note="VK9.5 intron A"

Mar 19 08:32

US-08-612-929-27.rge

11

```

exon      486..793
           /note="Ig kappa V-region 9.5kb-V-kappa, exon 2; putative"
sig_peptide
           486..496
           /note="Ig kappa V-region 9.5kb-V-kappa signal peptide"
           /codon_start=1
exon      486..>794
           /note="Ig kappa V-region 9.5kb-V-kappa"
           /number=2
exon      486..496
           /note="Ig kappa V-region 9.5kb-V-kappa signal peptide,
           exon 2; putative"
           497..794
           /partial
mat_peptide
           /note="Ig kappa V-region 9.5kb-V-kappa mature peptide"
           /codon_start=1
idna      795..>841
           /note="V-J intervening DNA (5' end +/- 1 bp)"
misc_signal
           796..823
           /note="putative recombination recognition sequence;
           putative"
BASE COUNT 218 a 196 c 191 g 236 t
ORIGIN      About 39 kb after segment 2; chromosome 6.

Query Match      85.2%; Score 23; DB 67; Length 841;
Best Local Similarity 100.0%; Pred. No. 3.50e-05;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 773 cagcaaaagtaatgagatctcc 795
      |||||
Qy 1 CAGCAAGTAATGAGATCTCTCC 23

RESULT 11
LOCUS      MUSIGKABK 312 bp mRNA ROD 15-SEP-1990
DEFINITION Mouse Ig kappa-chain (anti-insulin Ab 127) mRNA V region, partial
            cds.
ACCESSION  M34529
NID         g196507
KEYWORDS    V-region; immunoglobulin heavy chain; immunoglobulin-kappa;
            processed gene.
SOURCE      Mouse (strain Balb/c), cDNA to mRNA.
ORGANISM    Mus musculus
            Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
            Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE   1 (bases 1 to 312)
AUTHORS     Ewulonu U.K., Nell, L.J. and Thomas, J.W.
TITLE       V-H and V-L gene usage by murine IgG antibodies that bind
            autologous insulin
JOURNAL     J. Immunol. 144, 3091-3098 (1990)
MEDLINE     90217518
FEATURES     Location/Qualifiers
            source
            1..312
            /organism="Mus musculus"
            <1..>312
            /note="Ig kappa-chain V-region"
            /codon_start=1
            /db_xref="PID:g196508"
            /translation="DIVLTQSPASIVSLQGRATISCRASESDYGNSEFMHWYQQK
            GPPKLLIYRASNLSESGIPARESGSGRTDTLTINPVEADVVASVYQQQSNEPPTF
            GG"
BASE COUNT  78 a 81 c 77 g 76 t
ORIGIN

Query Match      77.8%; Score 21; DB 66; Length 312;
```

Mar 19 08:32

US-08-612-929-27.rge

12

```

Best Local Similarity 95.7%; Pred. No. 1.59e-03;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 277 cagcaaaagtaatgaggaacctcc 299
      |||||
Qy 1 CAGCAAGTAATGAGGATCTCTCC 23

RESULT 12
LOCUS      MVL2D4 318 bp RNA ROD 16-MAY-1995
DEFINITION M.musculus mRNA for immunoglobulin light chain variable region
            (VL2D4).
ACCESSION  X86545
NID         g809058
KEYWORDS    immunoglobulin; immunoglobulin light chain; kappa chain;
            light chain; variable region.
SOURCE      house mouse.
ORGANISM    Mus musculus
            Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
            Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE   1 (bases 1 to 318)
AUTHORS     Cerato, E., Birkle, S., Portoukalian, J. and Aubry, J.
JOURNAL     Unpublished
REFERENCE   2 (bases 1 to 318)
AUTHORS     Cerato, E.M.
TITLE       Direct Submission
JOURNAL     Submitted (24-APR-1995) to the EMBL/GenBank/DBJ databases. E.M.
            Cerato, INSERM U211, Institut de Biologie, 9 quai Moncousu, 44035
            Nantes Cedex 01, FRANCE
FEATURES     Location/Qualifiers
            source
            1..318
            /organism="Mus musculus"
            /strain="BALB/c"
            /dev_stage="adult"
            /tissue_type="spleen"
            /cell_type="B cell hybridoma"
            /cell_line="2D4 hybridoma"
            /chromosome="12"
            /rearranged
            V_region
            16..318
            /note="anti-ganglioside asialo GM2 immunoglobulin"
            /product="immunoglobulin light chain variable region VL
            2D4"
BASE COUNT  75 a 84 c 80 g 79 t
ORIGIN

Query Match      77.8%; Score 21; DB 65; Length 318;
Best Local Similarity 92.0%; Pred. No. 1.59e-03;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 262 cagcaaaataatgagatcttcga 286
      |||||
Qy 1 CAGCAAGTAATGAGATCTCTCGA 25

RESULT 13
LOCUS      MDIGKVB 333 bp RNA ROD 05-NOV-1994
DEFINITION M.domesticus IgK variable region.
ACCESSION  Z22133
NID         g297695
KEYWORDS    anti-DNA antibody; IgK gene; IgK variable region; immunoglobulin.
SOURCE      western European house mouse.
ORGANISM    Mus musculus domesticus
            Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;
```

Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria; Euthera; Glires; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Mus.

1 (bases 1 to 333)

Tillman,D.M., Jou,N.T., Hill,R.J. and Marion,T.N.

Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cell stimulation in (NZB x NZW)F1 mice

J. Exp. Med. 176 (3), 761-779 (1992)

92381444

2 (bases 1 to 333)

Direct Submission

Marion,T.N.

Submitted (23-MAR-1993) to the EMBL/GenBank/DBJ databases. Tony N. Marion, Microbiology and Immunology, University of, Tennessee, Memphis, 858 Madison Avenue, Memphis, TN, 38163, USA

Location/Qualifiers

1..333

/organism="Mus domesticus"

/strain="(NZB x NZW)F1"

/dev stage="somatic variant"

/tissue\_type="spleen"

/cell\_type="hybridoma"

/cell\_line="202p.38"

/isolates="mouse #202"

/chromosome="6"

/sex="Female"

<1..>333

/gene="Igk"

/codon start=1

/function="kappa light chain variable region for anti-DNA antibody; VK21 family"

/product="immunoglobulin variable region"

/db xref="PID:g297696"

/translation="DIVLTQSPASIVSLGQRATISCRASESDNYG1SPMWFOOKP

QPPKLLIYAASNGSGVPARESGSGTDFSLIHMEEDTAMFCQSQSEVPTTF

GGGTKLEIK"

BASE COUNT 84 a 86 c 84 g 78 t 1 others

ORIGIN

Query Match 77.8%; Score 21; DB 63; Length 333;

Best Local Similarity 92.0%; Pred. No. 1.59e-03;

Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 277 cagcaagtaagagaggttcctccga 301

|||||

QY 1 CAGCAAAAGTAATGAGGATCCTCCGA 25

RESULT 14

LOCUS S54207 333 bp mRNA ROD 26-MAR-1993

DEFINITION V kappa 21-immunoglobulin light chain variable region [mice, HIV-1 BRU immunized BALB/c, mRNA Partial, 333 nt].

ACCESSION S54207

NID g264866

KEYWORDS

SOURCE mice HIV-1 BRU immunized BALB/c.

ORGANISM Mus sp.

Unclassified.

REFERENCE 1 (bases 1 to 333)

AUTHORS Pirofski,L.A., Thomas,E.K. and Scharff,M.D.

TITLE Variable region gene utilization and mutation in a group of neutralizing murine anti-human immunodeficiency virus type 1 principal neutralizing determinant antibodies

JOURNAL AIDS Res. Hum. Retroviruses 9 (1), 41-49 (1993)

MEDLINE 93152285

REMARK GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 124489] from the original journal article.

This sequence comes from Fig. 2.

FEATURES

source

Location/Qualifiers

1..333

/organism="Mus sp."

/note="mice"

1..333

/partial

/gene="V<kappa>21"

/notes="mismatch(62[I->M]); Description: immunoglobulin light chain variable region, anti-HIV-1 monoclonal antibody 110.3; Method: conceptual translation supplied by author. This sequence comes from Fig. 2. Author-given protein sequence is in conflict with the conceptual translation. anti-HIV-1 monoclonal antibody 110.3"

/codon start=1

/product="immunoglobulin light chain variable region"

/db xref="PID:g264867"

/translation="DVVLTPQSPASIVSLGQRATISCKASQSDYDGDSTMYWYQOKP

QPPKLLIHAASNLVSCIPARESGSGTDFTLIHHPVEEDAAITYCQSQSEDPPTF

GGGTKLEIK"

BASE COUNT 87 a 85 c 85 g 76 t

ORIGIN

Query Match 77.8%; Score 21; DB 70; Length 333;

Best Local Similarity 95.7%; Pred. No. 1.59e-03;

Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 277 cagcaagtaattgaggtctctcc 299

|||||

QY 1 CAGCAAAAGTAATGAGGATCCTCC 23

RESULT 15

LOCUS MUSIGKAF 360 bp mRNA ROD 30-AUG-1991

DEFINITION Mouse Ig active kappa chain mRNA V-region (V-D-J).

ACCESSION M61046

NID g196679

KEYWORDS anti-CD4; immunoglobulin light chain; monoclonal antibody.

SOURCE Mouse, cDNA to mRNA.

ORGANISM Mus musculus

Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria; Euthera; Rodentia; Myomorpha; Muridae; Murinae.

REFERENCE 1 (bases 1 to 360)

AUTHORS Attanasio,R., Dilley,D., Buck,D.W., Maino,V.C., Lohman,K.L., Kanda,P. and Kennedy,R.C.

Structural characterization of a cross-reactive idiotype shared by monoclonal antibodies specific for the human CD4 molecule

J. Biol. Chem. 266, 14611-14619 (1991)

91317827

FEATURES

source

Location/Qualifiers

1..360

/organism="Mus musculus"

/strain="BALB/c"

/sub species="domesticus"

/cell\_line="SP20/spleen fusion hybridoma"

/sequenced\_mol="cDNA to mRNA"

70..114

/note="CDR1"

/product="anti-human CD4 antibody"

160..180

misc\_feature

misc\_feature



\*\*\*\*\*

WATERMAN

(TM)

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Release 2.1D John F. Collins, Biocomputing Research Unit.  
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MParch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed Mar 19 08:38:19 1997; MasPar time 67.22 Seconds  
Tabular output not generated. 295.243 Million cell updates/sec

Title: >US-08-612-929-53

Description: (1-45) from US08612929.seq

Perfect Score: 45

N.A. Sequence: 1 AAGCGCTCCCAAGCTGTCAATATGATGCTGATGATATATACAC 45

Comp: TTCGGGAGGGTTTCACAACTAATACCACTATCAATATACCTTG

Scoring table: TABLE default

Gap 10

Nmatch STD : Dbase 0; Query 0

Searched: 630489 seqs, 220513910 bases x 2

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

EST-STS  
1:EST1 2:EST2 3:EST3 4:EST4 5:EST5 6:EST6 7:EST7 8:EST8  
9:EST9 10:EST10 11:EST11 12:EST12 13:EST13 14:EST14  
15:EST15 16:EST16 17:EST17 18:EST18 19:EST19 20:EST20  
21:EST21 22:EST22 23:EST23 24:EST24 25:EST25 26:EST26  
27:EST27 28:EST28 29:EST29 30:EST30 31:EST31 32:EST32  
33:EST33 34:EST34 35:EST35 36:EST36 37:EST37 38:EST38  
39:EST39 40:EST40 41:EST41 42:EST42 43:EST43 44:EST44  
45:EST45 46:EST46 47:EST47 48:EST48 49:EST49 50:EST50  
51:EST51 52:EST52 53:EST53 54:EST54 55:EST55 56:EST56  
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69:EST69 70:EST70 71:EST71 72:EST72 73:EST73 74:EST74  
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81:EST81 82:EST82 83:EST83 84:EST84 85:EST85 86:EST86  
87:EST87 88:EST88 89:EST89 90:EST90 91:EST91 92:EST92  
93:EST93 94:EST94 95:EST95 96:EST96 97:EST97 98:EST98  
99:EST99

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EST-STS-TWO  
100:EST100 101:EST101 102:EST102 103:EST103 104:EST104  
105:EST105 106:EST106 107:EST107 108:EST108 109:EST109  
110:EST110 111:EST111 112:EST112 113:EST113 114:EST114  
115:EST115 116:EST116 117:EST117 118:EST118 119:EST119  
120:EST120 121:EST121 122:EST122 123:EST123 124:EST124  
125:EST125 126:EST126 127:EST127 128:EST128 129:EST129

130:STS2 131:STS3 132:STS4 133:STS5 134:STS6 135:STS7  
136:STS8 137:STS9 138:STS10 139:STS11 140:STS12  
141:STS13 142:STS14 143:STS15 144:STS16 145:STS17  
146:STS18 147:STS19 148:STS20 149:STS21 150:STS22  
151:STS23 152:STS24 153:STS25 154:STS26 155:STS27  
156:STS28 157:STS29 158:STS30 159:STS31 160:STS32  
161:STS33 162:STS34 163:STS35 164:STS36 165:STS37  
166:STS38 167:STS39 168:STS40 169:STS41 170:STS42  
171:STS43 172:STS44 173:STS45 174:STS46

Statistics: Mean 7.747; Variance 2.176; scale 3.560

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	22	48.9	313	1	ATTS2998	A. thaliana transcrib 1.47e-05
2	19	42.2	292	131	G06364	human STS WI-7035. 1.41e-02
c 3	19	42.2	353	33	H88129	ys75d12.sl Homo sapie 1.41e-02
c 4	19	42.2	362	174	HS690296	human STS SHGC-6155 c 1.41e-02
c 5	19	42.2	362	134	GI7690	human STS SHGC-6155 c 1.41e-02
c 6	19	42.2	389	166	H5899314	yz84g03.rl Homo sapie 1.41e-02
c 7	19	42.2	389	142	N79899	yz84g03.rl Homo sapie 1.41e-02
c 8	19	42.2	389	71	N79899	yz84g03.rl Homo sapie 1.41e-02
c 9	19	42.2	463	57	N36147	yz29c03.sl Homo sapie 1.41e-02
c 10	18	40.0	182	108	T25334	EST060 Homo sapiens c 1.22e-01
c 11	18	40.0	259	35	H96107	yt97c12.sl Homo sapie 1.22e-01
c 12	18	40.0	269	51	M78099	EST01689 Homo sapiens 1.22e-01
c 13	18	40.0	299	22	H52906	SW3ICA458SK Brugia ma 1.22e-01
c 14	18	40.0	300	116	T54600	yb41a05.sl Homo sapie 1.22e-01
c 15	18	40.0	309	112	T41640	10221 Arabidopsis tha 1.22e-01
c 16	18	40.0	322	80	R30940	yh60c03.sl Homo sapie 1.22e-01
c 17	18	40.0	324	104	T07002	EST04891 Homo sapiens 1.22e-01
c 18	18	40.0	330	21	H48510	yt33f08.sl Homo sapie 1.22e-01
c 19	18	40.0	334	48	HUM224A03B	Human aorta cDNA 5'-e 1.22e-01
c 20	18	40.0	335	87	R55511	yj79h09.sl Homo sapie 1.22e-01
c 21	18	40.0	338	74	R10829	yf37b10.sl Homo sapie 1.22e-01
c 22	18	40.0	376	98	R91466	yq08a11.sl Homo sapie 1.22e-01
c 23	18	40.0	385	107	T19193	d08013t Homo sapiens 1.22e-01
c 24	18	40.0	387	128	T98507	ye60g02.sl Homo sapie 1.22e-01
c 25	18	40.0	396	96	R84415	yp89h09.sl Homo sapie 1.22e-01
c 26	18	40.0	406	93	R76483	yf61c11.rl Homo sapie 1.22e-01
c 27	18	40.0	409	61	N49078	yy79c04.sl Homo sapie 1.22e-01
c 28	18	40.0	411	164	HS666293	za14h10.sl Homo sapie 1.22e-01
c 29	18	40.0	416	100	R96162	yt84c11.sl Homo sapie 1.22e-01
c 30	18	40.0	423	57	N34383	yy12h06.sl Homo sapie 1.22e-01
c 31	18	40.0	427	66	N63295	yz88h06.sl Homo sapie 1.22e-01
c 32	18	40.0	438	27	H67932	yy53c04.rl Homo sapie 1.22e-01
c 33	18	40.0	441	17	H38046	yp58c10.rl Homo sapie 1.22e-01
c 34	18	40.0	445	97	R88605	ym93e02.rl Homo sapie 1.22e-01
c 35	18	40.0	454	133	G13723	human STS SHGC-1250 c 1.22e-01
c 36	18	40.0	459	87	R55337	yg88c08.sl Homo sapie 1.22e-01
c 37	18	40.0	470	163	HS591325	yz93d03.rl Homo sapie 1.22e-01
c 38	18	40.0	473	71	N80390	za14h10.rl Homo sapie 1.22e-01
c 39	18	40.0	492	28	H72500	ys07e04.rl Homo sapie 1.22e-01
c 40	18	40.0	517	117	T59660	yb66f11.sl Homo sapie 1.22e-01
c 41	18	40.0	535	89	R60158	yh12d10.sl Homo sapie 1.22e-01
c 42	18	40.0	565	63	N53488	yy42f11.sl Homo sapie 1.22e-01



Mar 19 08:38

US-08-612-929-53.rst

3

43 18 40.0 581 56 N32030 yw96e02.sl Homo sapie 1.22e-01  
44 18 40.0 587 54 N25532 yw76c05.sl Homo sapie 1.22e-01  
45 18 40.0 601 8 H05802 y177d08.sl Homo sapie 1.22e-01

ALIGNMENTS

RESULT 1  
LOCUS ATTS2998 313 bp RNA EST 31-MAY-1994  
DEFINITION A. thaliana transcribed sequence; clone FA1102; 5' end.  
ACCESSION Z33940  
NID 9496427  
KEYWORDS expressed sequence tag; partial cDNA sequence.  
SOURCE thale cress.  
ORGANISM Arabidopsis thaliana  
Eukaryotae; mitochondrial eukaryotes; Chlorophyta/Embryophyta  
group; Charophyta/Embryophyta group; Embryophyta; Magnoliophyta;  
Magnoliopsida; Dilleniidae; Capparales; Brassicaceae; Arabidopsis.  
1 (bases 1 to 313)  
Philipps,G. and Gigot,C.  
Direct Submission  
Submitted (30-MAY-1994) to the EMBL/GenBank/DBJ databases. CNRS,  
GDR-1003 ACS, INRA, Laboratoire de Biologie Moleculaire, BP 27,  
31326 Castanet-Tolosan cedex, France.  
E-mail:gdt-svptoulouse.inra.fr. On behalf of: Laboratoire de  
Biologie Moleculaire des Plantes - CNRS, Gigot Claude / I512, 12  
Rue du General Zimmer, 67084 Strasbourg Cedex, France.  
E-mail:philippes@scilla.u-strasbg.fr  
2 (bases 1 to 313)  
CNRS.

THE Arabidopsis thaliana transcribed genome: the GDR cDNA program  
Unpublished  
Cloning vector: Lambda ZAPII;  
Physiological condition: leaves strips incubated 2/3/4 days  
in liquid culture medium. full automatic.

FEATURES  
source  
1..313  
/organism="Arabidopsis thaliana"  
/clone="FA1102"  
/tissue type="sliced leaves of A.thaliana ecotype  
columbia"  
/clone.lib="Strasbourg-A"  
BASE COUNT 74 a 76 c 60 g 99 t 4 others  
ORIGIN

Query Match 48.9%; Score 22; DB 1; Length 313;  
Best Local Similarity 86.7%; Pred. No. 1.47e-05;  
Matches 26; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
Db 242 cctccacaagtggtattatgaagtgata 271  
||||| | ||||| | ||||| | |||||  
Qy 5 CCTCCCAAGTGTGATTATGATGATGATA 34

RESULT 2  
LOCUS G06364 292 bp DNA STS 19-OCT-1995  
DEFINITION human STS WI-7035.  
ACCESSION G06364  
NID g859609  
KEYWORDS STS sequence; primer; sequence tagged site.  
SOURCE human STSs derived from sequences in dbEST and the Unigene  
collection.  
ORGANISM Homo sapiens  
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;

Mar 19 08:38

US-08-612-929-53.rst

4

Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;  
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;  
Catarrhini; Hominiidae; Homo.  
1 (bases 1 to 292)

REFERENCE  
AUTHORS Hudson,T.  
TITLE Whitehead Institute/MIT Center for Genome Research; Physically  
Mapped ESTs  
JOURNAL Unpublished (1995)  
COMMENT

Contact: Thomas Hudson  
Whitehead Institute/MIT Center for Genome Research  
Whitehead Institute for Biomedical Research  
9 Cambridge Center, Cambridge MA 02142 USA  
Tel: 617 252 1900  
Fax: 617 252 1902  
Email: thudson@genome.wi.mit.edu

Primer A: TAATTAAGTGTCTCCCACTTAAAC  
Primer B: ATTTGGGATTAATAAGTGAAACCA  
STS size: 200  
PCR Profile:

Presoak:  
Denaturation:  
Annealing: 56 degrees C  
Polymerization:  
PCR Cycles: 35  
Thermal Cycler:  
Protocol:  
Template: 10 ng  
Primer: each 5 pM  
dNTPs: each 4 nM  
Taq Polymerase: 0.025 units/ul  
Total Vol: 20 ul

Buffer:  
MgCl2: 1.5 mM  
KCl: 50 mM  
Tris-HCL: 10 mM  
pH: 9.3

Prepared with primer pairs derived from V00564 --- Unigene.

FEATURES  
source  
1..292  
Location/Qualifiers  
/organism="Homo sapiens"  
/note="human"  
1..200  
/map="738\_B\_6; 812\_E\_2; 815\_D\_4; 884\_F\_7; 907\_A\_8;  
924\_A\_1; 929\_A\_6; 940\_B\_4; 945\_B\_5; 945\_D\_1; 946\_D\_1;  
841\_A\_10; 846\_E\_11; 825\_C\_(2,11)"  
primer\_bind 1..25  
/map="738\_B\_6; 812\_E\_2; 815\_D\_4; 884\_F\_7; 907\_A\_8;  
924\_A\_1; 929\_A\_6; 940\_B\_4; 945\_B\_5; 945\_D\_1; 946\_D\_1;  
841\_A\_10; 846\_E\_11; 825\_C\_(2,11)"  
primer\_bind complement(176..200)  
/map="738\_B\_6; 812\_E\_2; 815\_D\_4; 884\_F\_7; 907\_A\_8;  
924\_A\_1; 929\_A\_6; 940\_B\_4; 945\_B\_5; 945\_D\_1; 946\_D\_1;  
841\_A\_10; 846\_E\_11; 825\_C\_(2,11)"  
BASE COUNT 92 a 32 c 32 g 124 t 12 others  
ORIGIN

Query Match 42.2%; Score 19; DB 131; Length 292;  
Best Local Similarity 77.1%; Pred. No. 1.41e-02;  
Matches 27; Conservative 0; Mismatches 8; Indels 0; Gaps 0;



Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.

## REFERENCE

AUTHORS

JOURNAL

COMMENT

1 (bases 1 to 362)

Myers, R.M.

Unpublished (1996)

Contact: Richard M. Myers

Stanford Human Genome Center (SHGC)

Stanford University School of Medicine

Department of Genetics, M-344, Stanford, CA 94305, USA

Tel: 415/7259687

Fax: 415/7259689

Email: myers@shgc.stanford.edu

Primer A: TTGTGCTATTTTCAGAGAA

Primer B: GCTCATCGCTTATCATCTG

STS size: 268

PCR Profile:

Initial incubation: 94 degrees C for 90 seconds

Denaturation: 94 degrees C for 15 seconds

Annealing: 62 degrees C for 23 seconds

Polymerization: 72 degrees C for 30 seconds

PCR Cycles: 30

Thermal Cycler: Perkin Elmer 9600

Protocol:

Template: 25 ng

Primer: each 1 uM

dNTPs: each 200 uM

Taq Polymerase: 0.05 units/ul

Total Vol: 10 ul

Buffer:

MgCl2: 2.5 mM

KCl: 50 mM

Tris-HCl: 20 mM

pH: 8.3

Chromosome 13.

Location/Qualifiers

1..362

/organism="Homo sapiens"

/note="human"

52..319

/map="13"

52..71

/map="13"

complement(300..319)

/map="13"

BASE COUNT 104 a 75 c 54 g 113 t 16 others

ORIGIN

Query Match

Best Local Similarity 42.2%; Score 19; DB 134; Length 362;

Matches 26; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Db 21 tcanatcatcatcatcatcatcatcatcttg 54

||||| ||| ||||| ||||| ||||| |||||

Cp 43 TCATATAACTATCATCACCATCATATCAACTTTC 10

RESULT

6

ID HS899314 standard; RNA; EST; 389 BP.

AC N79899;

DT 04-APR-1996 (Rel. 47, Created)

DT 13-APR-1996 (Rel. 47, Last updated, Version 3)

DE yz84g03.r1 Homo sapiens cDNA clone 289780 5' similar to contains

DE Alu repetitive element;.

RW EST.

OS Homo sapiens (human)

OC Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;

OC Theria; Eutheria; Primates; Haplorhini; Catarrhini; Homnidae.

RN [1]

RP 1-389

RA Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M.,

RA Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M.,

RA Parsons J., Rifkin L., Rohlfing T., Soares M., Tan F.,

RA Trevasaki E., Waterston R., Williamson A., Wohlmann P., Wilson R.;

RT "The WashU-Merck EST Project";

RL Unpublished.

CC Contact: Wilson RK WashU-Merck EST Project Washington University

CC School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,

CC MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email:

CC est@watson.wustl.edu High quality sequence stops: 380 Source: IMAGE

CC Consortium, LNL This clone is available royalty-free through LNL

CC ; contact the IMAGE Consortium (info@image.llnl.gov) for further

CC information. NCBI gi: 1242600

FH Key

FH Location/Qualifiers

FT source

FT 1..389

FT /organism="Homo sapiens"

FT /clone="289780"

FT /note="human"

FT &lt;1..&gt;389

FT mRNA

SQ Sequence 389 BP; 92 A; 87 C; 108 G; 101 T; 1 other;

Query Match

Best Local Similarity 42.2%; Score 19; DB 166; Length 389;

Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 224 ccacatcatccagcactttggaggcc 250

||||| | || ||||| |||||

Cp 29 CCATCATATCAACACTTTCGGAGGCC 3

RESULT

7

LOCUS N79899 389 bp mRNA EST 02-APR-1996

DEFINITION yz84g03.r1 Homo sapiens cDNA clone 289780 5' similar to contains

Alu repetitive element;.

ACCESSION N79899

NID g1242600

KEYWORDS EST.

SOURCE

human clone=289780 primer=reverse ET library=Soares multiple

sclerosis 2NBHSP vector=pT7T3D (Pharmacia) with a modified

polylinker V TYPE: phagemid:host=DH10B (ampicillin resistant)

Rsitel=Not I Rsite2=Eco RI 46 year old male. 1st strand cDNA was

primed with a Not I - oligo(dT) primer

[5'-TCTTACCAATCTGAAGTGGGAGCGCGCATTTTTTTTTTTTTTTT-3'],

double-stranded cDNA was size selected, ligated to Eco RI adapters

(Pharmacia), digested with Not I and cloned into the Not I and Eco

RI sites of a modified pT7 vector (Pharmacia). Library went

through one round of normalization to a Cot = 5. Library

constructed by Bento Soares and M.Fatima Bonaldo. RNA from 4

multiple sclerosis lesions from one patient was kindly provided by

Dr. Kevin G. Becker (NINDS/NIH).

ORGANISM

Homo sapiens



REFERENCE  
AUTHORS Sarcopharygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;  
1 (bases 1 to 463) Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,  
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,  
Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P. and  
Wilson, R.

TITLE The WashU-Merck EST Project  
JOURNAL Unpublished (1995)  
COMMENT

Contact: Wilson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800  
Fax: 314 286 1810

Email: est@watson.wustl.edu  
High quality sequence stops: 362

Source: IMAGE Consortium, LINL  
This clone is available royalty-free through LINL ; contact the  
IMAGE Consortium (info@image.linl.gov) for further information.

FEATURES  
source Location/Qualifiers

1..463  
/organism="Homo sapiens"  
/clone="272644"  
/note="human"  
mRNA <1..>463

BASE COUNT 115 a 123 c 86 g 139 t  
ORIGIN

Query Match 42.2%; Score 19; DB 57; Length 463;  
Best Local Similarity 88.0%; Pred. No. 1.41e-02;  
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 284 ggcctcccaagtgttttagat 308

|||||

Qy 3 GGCCTCCCAAGTGTGATTATCAT 27

RESULT 10

LOCUS T25334 182 bp mRNA EST 21-AUG-1995  
DEFINITION EST060 Homo sapiens cDNA clone BL29-60.  
ACCESSION T25334  
NID 9559978

KEYWORDS EST.

SOURCE human clone=BL29-60 library=BL29 Burkitt's lymphoma, Pascalis  
Sideras vector=lambda ZAP 2 primer=47 Rsite=EcoRI Rsite2=EcoRI  
oligo dT-primed cDNA prepared from polyA RNA from BL29 cell line.  
Size fractionated from 300bp to 3000bp. cDNA cloned into lambda Zap  
using EcoRI linkers in random orientation.

ORGANISM Homo sapiens

Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;  
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;  
Sarcopharygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;  
Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 182)

REFERENCE  
AUTHORS Sanders, R., Larsson, C., Wallin, E., Islam, K.B. and Smith, C.I.E.

TITLE Partial sequencing and chromosome mapping of clones from a human

Burkitt's lymphoma cDNA library

Unpublished (1994)

Other ESTs: EST060R

Map: Chromosome 3

Contact: Sanders R

Pharmacia Biotech  
Bjorkrgatan 30, S-751 82 Uppsala, Sweden  
Tel: 18-165194, 18-166019  
Fax: 18-166396  
Email: RS026918@supbdt.pharmacia.se.

FEATURES  
source Location/Qualifiers

1..182  
/organism="Homo sapiens"  
/clone="BL29-60"  
/note="human"  
mRNA <1..>182  
/gene="D3S2969E"  
/map="3"

BASE COUNT 78 a 31 c 16 g 57 t  
ORIGIN

Query Match 40.0%; Score 18; DB 108; Length 182;

Best Local Similarity 76.5%; Pred. No. 1.22e-01;  
Matches 26; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Db 44 ttaacattaccatcatctctcatcacacatt 77

|||||

Cp 44 TTATATAACTATCACCATCAATCAACACTTT 11

RESULT 11

LOCUS H96107 259 bp mRNA EST 07-DEC-1995  
DEFINITION yt97cl2.sl Homo sapiens cDNA clone 232246 3' similar to contains  
Alu repetitive element?.

ACCESSION H96107

NID g1109249

KEYWORDS EST.

SOURCE clone=232246 primer=Promega -21ml3 library=Soares pineal gland  
N3HPG vector=pt7T3D (Pharmacia) with a modified polylinker  
host=DHI08 (ampicillin resistant) Rsite=Not I Rsite2=Eco RI 1st  
strand cDNA was primed with a Not I - oligo(dT) primer [5'  
TGTTACCAATCTGAAGTGGAGGGCGCGCTTTTTTTTTTTT 3',  
double-stranded cDNA was size selected, ligated to Eco RI adapters  
(Pharmacia), digested with Not I and cloned into the Not I and Eco  
RI sites of a modified pT73 vector (Pharmacia). Library  
constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM Homo sapiens

Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;  
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;  
Sarcopharygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;  
Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 259)

REFERENCE

AUTHORS

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,  
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,  
Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P. and  
Wilson, R.

TITLE The WashU-Merck EST Project

JOURNAL Unpublished (1995)

COMMENT

Contact: Wilson RK

WashU-Merck EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence stops: 249

Source: IMAGE Consortium, LINL

Mar 19 08:38

US-08-612-929-53.rst

13

This clone is available royalty-free through LML; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

# FEATURES

source

Location/Qualifiers  
1..259  
/organism="Homo sapiens"  
/clone="232246"

## BASE COUNT

ORIGIN

51 a 79 c 67 g 60 t 2 others  
40.0%; Score 18; DB 35; Length 259;  
Best Local Similarity 100.0%; Pred. No. 1.22e-01;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match

Matches

Db 210 ggcctcccaagtgttga 227

|||||

Qy 3 GGCCTCCCAAGTGTGA 20

RESULT 12

## LOCUS

DEFINITION EST01689 Homo sapiens cDNA clone HHCPC14 similar to Alu repetitive element.

## ACCESSION

NID 9273836

KEYWORDS EST.

## SOURCE

human clone=HHCPC14 library-Subtracted Hippocampus, Strataene hippocampus library (#4 above) was subtracted with a fibroblast cell line cDNA library (Strataene cat. #936209; #138 lung fibroblast cell line; oligo-dT + random primed cDNA synthesis; LambdaZAP-II vector, 1.0kb average insert size.) by the method of Sive & St. John (Nucl. Acids Res. 16:10937, 1988).

## ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 269)

AUTHORS Adams,M.D., Dubnick,M., Kerlavage,A.R., Moreno,R., Kelley,J.M., Utterback,T.R., Nagle,J.W., Fields,C. and Venter,J.C.

TITLE Sequence identification of 2,375 human brain genes

JOURNAL Nature 355 (6361), 632-634 (1992)

MEDLINE 92168112

## COMMENT

Contact: Kerlavage AR  
The Institute for Genomic Research  
932 Clopper Road, Gaithersburg, MD 20878  
Tel: 3018699056  
Fax: 3018699423  
Email: arkerlav@tigr.org.

## FEATURES

source

Location/Qualifiers  
1..269  
/organism="Homo sapiens"  
/clone="HHCPC14"  
/note="human"

## mRNA

<1..>269  
/gene="D051098F"

## BASE COUNT

ORIGIN

76 a 52 c 51 g 87 t 3 others  
40.0%; Score 18; DB 51; Length 269;  
Best Local Similarity 100.0%; Pred. No. 1.22e-01;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match

Best Local Similarity

Matches

14  
T54600  
yb41a05.s1 Homo sapiens cDNA clone 73712 3' contains Alu repetitive element.

Mar 19 08:38

US-08-612-929-53.rst

14

Db 79 ggcctcccaagtgttga 96

|||||

Qy 3 GGCCTCCCAAGTGTGA 20

RESULT 13

## LOCUS

DEFINITION H52906 299 bp mRNA EST 31-JAN-1996

ACCESSION SW31CA458K Brugia malayi cDNA clone SW31CA458 5'.

NID H52906

KEYWORDS g992906

SOURCE EST.

clone=SW31CA458 primer=pBluescript SK library=Brugia malayi infective larva cDNA (SAM94WL-Bml3) strain=TRS Labs vector=lamba UniZap XR host=XLI-Blue MRF' RsiteI=EcoR I Rsite2=Xho I Lymphatic filarial nematode parasite of humans. mRNA was prepared from third stage infective larvae of Brugia malayi isolated from mosquitoes 10 days after infection and converted to double stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNapol I. The library had 1.6 x 10E6 independent recombinants and average insert size was 900 base pairs. The library was constructed by Wenhong Lu. The library is available from Dr. S.A. Williams, email swilliams@smith.smith.edu.

## ORGANISM

Brugia malayi  
Eukaryota; mitochondrial eukaryotes; Metazoa/Eumycota group; Metazoa; Eumetazoa; Bilateria; Pseudocoelomata; Nematoda; Secernentea; Spirurida; Spirurida; Spirurina; Filarioidea; Onchocercidae; Onchocercinae; Brugia.

1 (bases 1 to 299)

## REFERENCE

AUTHORS

Blaxter,M.L., Raghavan,N., Ghosh,I., Guiliano,D., Lu,W., Williams,S.A., Slatko,B. and Scott,A.L.

## TITLE

Genes expressed in Brugia malayi infective third stage larvae

JOURNAL

Mol. Biochem. Parasitol. (1996) In press

## COMMENT

Contact: Steven A. Williams  
Molecular Parasitology  
Smith College Department of Biological Sciences  
Department of Biological Sciences, Clark Science Center, Smith College, Northampton, MA, 01063, USA  
Tel: 4135853826  
Fax: 4135853786  
Email: swilliams@smith.smith.edu.

## FEATURES

source

Location/Qualifiers  
1..299  
/organism="Brugia malayi"  
/clone="SW31CA458"  
/strain="TRS Labs"

## mRNA

<1..>299  
BASE COUNT 129 a 31 c 61 g 73 t 5 others

## ORIGIN

Query Match 40.0%; Score 18; DB 22; Length 299;  
Best Local Similarity 82.1%; Pred. No. 1.22e-01;  
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Db 102 ttgataatgctgatgataagaa 129

|||||

Qy 17 TTGATTATGATGCTGATATATCAA 44

RESULT 14

## LOCUS

DEFINITION T54600 300 bp mRNA EST 08-FEB-1995

yb41a05.s1 Homo sapiens cDNA clone 73712 3' contains Alu repetitive element.

Mar 19 08:38

US-08-612-929-53.fst

15

ACCESSION T54600  
 NID 9656461  
 KEYWORDS EST.  
 SOURCE human clone=73712 library=Stratagene fetal spleen (#937205)

vector=pBluescript SK- host=SOIR cells (kanamycin resistant)  
 primer=21ml3 RseI=EcORI RseI=2=Hoi Pooled fetal spleens. Cloned  
 unidirectionally. Primer: Oligo dT. Average insert size: 1.0 kb;  
 Uni-ZAP XR Vector; 5' adaptor sequence: 5'-CAATTCGCCAGC-3'; 3'  
 adaptor sequence: 5'-CTCGAGTTTTTTTTTTTTTTTT-3'.

# ORGANISM

Homo sapiens  
 Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;  
 Eutheria; Primates; Catarrhini; Hominidae; Homo.

# REFERENCE

1 (bases 1 to 300)

# AUTHORS

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,  
 Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,S., Marra,M.,  
 Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevaskis,E.,  
 Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.

# TITLE

WashU-Merck EST Project

# JOURNAL

Unpublished (1995)

# COMMENT

Contact: Wilson RK  
 WashU-Merck EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence stops: 238

Source: IMAGE Consortium, LLNL

This clone is available royalty-free through LLNL; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.

Possible reversed clone: polyT not found.

# FEATURES

source

1..300

/organism="Homo sapiens"

/clone="73712"

/note="human"

BASE COUNT 92 a 68 c 88 g 42 t 10 others

# ORIGIN

Query Match 40.0%; Score 18; DB 116; Length 300;

Best Local Similarity 83.3%; Pred. No. 1.22e-01;

Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 252 atcgnaagcaacantttggaggc 275

|||| || ||||| ||||| |||||

Cp 27 ATCATATCAACACTTTCGGAGGC 4

# RESULT

15

LOCUS T41640 309 bp mRNA EST 07-AUG-1995

DEFINITION 10221 Arabidopsis thaliana cDNA clone 62E2TM.

# ACCESSION

T41640

NID 9931282

# KEYWORDS

EST.

SOURCE thale cress clone=62E2TM library=Lambda-PRL2 strain=var columbia  
 vector=lambda Zip-Lox RseI=Sal RseI=2=Not Lambda PRL2 is a cDNA  
 library derived from equal quantities of 4 pools of mRNA. The mRNA  
 sources were 1) 7 day germinated etiolated seedlings; 2) tissue  
 culture grown roots; 3) staged plants half with 24 hour light  
 cycle, half on 16 hr light, 8 hour dark- rosettes; 4) same plants  
 as 3 but aerial tissue (stems, flowers and siliques. The vector is  
 BRU's lambda Zip-Lox. The cDNA inserts were directionally cloned  
 with Sal-Not arms using oligo dT primed cDNA.

Mar 19 08:38

US-08-612-929-53.fst

16

# ORGANISM

Arabidopsis thaliana  
 Eucaryotae; Embryophyta; Magnoliophyta; Magnoliopsida; Capparales;  
 Brassicaceae; Arabidopsis.

# REFERENCE

1 (bases 1 to 309)

# AUTHORS

Newman,T., de Bruijn,F.J., Green,P., Keegstra,K., Kende,H.,  
 McIntosh,L., Ohlrogge,J., Raikhel,N., Somerville,S., Thomasow,M.,  
 Retzel,E. and Somerville,C.

# TITLE

Genes galore: a summary of methods for accessing results from  
 large-scale partial sequencing of anonymous Arabidopsis cDNA clones  
 Plant Physiol. 106, 1241-1255 (1994)

# JOURNAL

# COMMENT

Contact: Thomas Newman

MSU-DOE Plant Research Laboratory

Michigan State University

MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E.

Lansing, MI

Tel: 517-353-0854

Fax: 517-353-9168

Email: 22313tcn81bm.cl.msu.edu.

# FEATURES

source

1..309

/organism="Arabidopsis thaliana"

/clone="62E2TM"

/strain="var columbia"

/note="thale cress"

BASE COUNT 93 a 53 c 71 g 77 t 15 others

# ORIGIN

Query Match 40.0%; Score 18; DB 112; Length 309;

Best Local Similarity 80.0%; Pred. No. 1.22e-01;

Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Db 210 ttttgantatgatngtggngcat 234

||||| ||||| ||||| ||||| ||

Qy 15 TGTTCATTATGATGCGTAGATTAT 39

Search completed: Wed Mar 19 08:39:35 1997

Job time : 76 secs.

Result	No.	Score	Query		DB	ID	Description	Pred. No.
			Match	Length				
c	1	45	100.0	393	14	Q83520	Humanized antibody 3B	7 56e-14
	2	44	97.8	63	14	Q83508	IL-4 CDR1 gene fragment	2.71e-13
	3	44	97.8	67	14	Q83507	IL-4 CDR1 gene fragment	2.71e-13
	4	41	91.1	333	11	Q65554	Mouse anti-HIV mu5.5	1.23e-11
	5	41	91.1	333	12	Q70372	Anti HIV antibody lig	1.23e-11
	6	41	91.1	333	12	Q70376	Chimeric anti HIV ant	1.23e-11
	7	41	91.1	333	11	Q65558	Mouse-human chimeric	1.23e-11
	8	41	91.1	334	1	N90492	Gene fragment of immu	1.23e-11

PT from high affinity mAbs - useful in treatment of IL-4-mediated



PT and IgE-mediated allergic conditions  
 PS Disclosure; Page 71-72; 97pp; English.  
 CC A humanized antibody light chain variable region and signal  
 CC sequence is given in R75355. The signal sequence is also  
 CC provided in R70194. The sequences of the 3 CDRs  
 CC are identical to mouse anti-human IL-4 Mab 3B9 light chain  
 CC CDRs (given in R70195-97).  
 SQ Sequence 393 BP; 97 A; 98 G; 105 G; 93 T;

Query Match 100.0%; Score 45; DB 14; Length 393;  
 Best Local Similarity 100.0%; Pred. No. 7.56e-14;  
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 127 aaggctcccaagtgtgattatggtgatggtatgattatgaac 171  
 ||||||||||||||||||||||||||||||||||||||||||||  
 Qy 1 AAGGCTCCCAAGTGTGATTATGATGCTGATGATTATATGAAC 45

## RESULT 2

ID Q83508 standard; DNA; 63 BP.  
 AC Q83508;  
 DT 20-SEP-1995 (first entry)  
 DE IL-4 CDR1 gene fragment.  
 KW Humanized antibody; antibody engineering; monoclonal antibody;  
 KW Mab; interleukin-4; IL-4; allergy; heavy chain; CDR;  
 KW complementarity determining region; ss.  
 OS Synthetic.  
 PN W09507301-A.  
 PD 16-MAR-1995.  
 PF 07-SEP-1994; U10308.  
 PR 07-SEP-1993; US-117366.  
 PR 14-OCT-1993; US-136783.  
 PA (SMIK ) SMITHKLINE BEECHAM CORP.  
 PA (SMIK ) SMITHKLINE BEECHAM PLC.  
 PI Gross MS, Holmes SD, Sylvester DR;  
 DR WPI; 95-123387/16.  
 PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived  
 PT from high affinity mAbs - useful in treatment of IL-4-mediated  
 PT and IgE-mediated allergic conditions  
 PS Example 3; Page 28; 97pp; English.  
 CC A humanized antibody was designed to contain mouse CDRs (from  
 CC anti-IL-4 Mab 3B9 Mab) within a human antibody framework. A  
 CC synthetic heavy chain was made using the oligonucleotides given  
 CC in Q83498-502 and amplified by PCR using the primers given in  
 CC Q83503-04. The construct was ligated into vector pCD, along  
 CC with a signal sequence (Q83494) and an IgG1 human constant  
 CC region. The CDR gene regions of a pre-existing light chain  
 CC framework were replaced with synthetic IL-4 CDR genes constructed  
 CC from oligonucleotides given in Q83505-08 (CDR1), Q83509-10 (CDR2),  
 CC and Q83511-12 (CDR3). The synthetic VL (Q73986) was ligated into  
 CC the vector. The anti-IL4 engineered antibody was expressed in  
 CC COS and CHO cells.  
 SQ Sequence 63 BP; 17 A; 16 C; 11 G; 19 T;

Query Match 97.8%; Score 44; DB 14; Length 63;  
 Best Local Similarity 100.0%; Pred. No. 2.71e-13;  
 Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 19 gttcataactatcacatcataatacaactttggaggcct 62  
 ||||||||||||||||||||||||||||||||||||||||||||  
 Cp 45 GTTCATATAACTATCACCATATAATCAACACTTTGGGAGGCCT 2

## RESULT 3

Query Match 97.8%; Score 44; DB 14; Length 63;  
 Best Local Similarity 100.0%; Pred. No. 2.71e-13;  
 Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 19 gttcataactatcacatcataatacaactttggaggcct 62  
 ||||||||||||||||||||||||||||||||||||||||||||  
 Cp 45 GTTCATATAACTATCACCATATAATCAACACTTTGGGAGGCCT 2

ID Q83507 standard; DNA; 67 BP.

AC Q83507;  
 DT 20-SEP-1995 (first entry)  
 DE IL-4 CDR1 gene fragment.  
 KW Humanized antibody; antibody engineering; monoclonal antibody;  
 KW Mab; interleukin-4; IL-4; allergy; heavy chain; CDR;  
 KW complementarity determining region; ss.

OS Synthetic.  
 PN W09507301-A.  
 PD 16-MAR-1995.  
 PF 07-SEP-1994; U10308.  
 PR 07-SEP-1993; US-117366.  
 PR 14-OCT-1993; US-136783.

PA (SMIK ) SMITHKLINE BEECHAM CORP.  
 PA (SMIK ) SMITHKLINE BEECHAM PLC.  
 PI Gross MS, Holmes SD, Sylvester DR;  
 DR WPI; 95-123387/16.  
 PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived  
 PT from high affinity mAbs - useful in treatment of IL-4-mediated  
 PT and IgE-mediated allergic conditions  
 PS Example 3; Page 28; 97pp; English.

CC A humanized antibody was designed to contain mouse CDRs (from  
 CC anti-IL-4 Mab 3B9 Mab) within a human antibody framework. A  
 CC synthetic heavy chain was made using the oligonucleotides given  
 CC in Q83498-502 and amplified by PCR using the primers given in  
 CC Q83503-04. The construct was ligated into vector pCD, along  
 CC with a signal sequence (Q83494) and an IgG1 human constant  
 CC region. The CDR gene regions of a pre-existing light chain  
 CC framework were replaced with synthetic IL-4 CDR genes constructed  
 CC from oligonucleotides given in Q83505-08 (CDR1), Q83509-10 (CDR2),  
 CC and Q83511-12 (CDR3). The synthetic VL (Q73986) was ligated into  
 CC the vector. The anti-IL4 engineered antibody was expressed in  
 CC COS and CHO cells.  
 SQ Sequence 67 BP; 20 A; 12 C; 17 G; 18 T;

Query Match 97.8%; Score 44; DB 14; Length 67;  
 Best Local Similarity 100.0%; Pred. No. 2.71e-13;  
 Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 6 aggcctcccaagtgtgattatggtgatggtatgattatgaac 49  
 ||||||||||||||||||||||||||||||||||||||||||||  
 Qy 2 AGGCTCCCAAGTGTGATTATGATGCTGATGATTATATGAAC 45

## RESULT 4

ID Q65554 standard; cDNA; 333 BP.  
 AC Q65554;  
 DT 27-JAN-1995 (first entry)  
 DE Mouse anti-HIV mu5.5 light chain variable region cDNA.  
 KW Immunoglobulin; light chain; anti-HIV antibody; neutralisation;  
 KW human immunodeficiency virus; variable region; VL chain; murine; ds.  
 OS Mus musculus.

FH Key Location/Qualifiers  
 FT misc.feature 70..114  
 FT /tag= a  
 FT /note= "encodes CDR1"  
 FT misc.feature 160..180  
 FT /tag= b  
 FT /note= "encodes CDR2"  
 FT misc.feature 277..303  
 FT /tag= c  
 FT /note= "encodes CDR3"  
 PN J06125783-A.  
 PD 10-MAY-1994.

```

PF 28-DEC-1991; 359808.
PR 28-DEC-1991; JP-359808.
PA (KAGA-) ZH KAGAKU KESSEI-RYOHO KENKYUSHO.
DR WPI; 94-187942/23.
P-PSDB; R55123.
PT Mouse-human chimeric anti-HIV antibody heavy and light chains -
PT and recombinant antibody consisting of the H- and L-chains,
PT useful in AIDS therapy
PS Example 3; Fig 4; 22pp; Japanese.
CC Murine monoclonal antibodies mu 39.1 and mu 5.5 both neutralise HIV.
CC The heavy and light chain variable regions from these antibodies
CC were sequenced (Q65551-Q65554). The murine anti-HIV CD8s were
CC introduced into human framework regions to construct chimeric
CC antibodies (Q65555-Q65558).
SQ Sequence 333 BP; 88 A; 83 C; 86 G; 76 T;

Query Match 91.1%; Score 41; DB 11; Length 333;
Best Local Similarity 95.6%; Pred. No. 1.23e-11;
Matches 43; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 70 aagccagccaaagtgtgattatgatgtgatgttatatgaac 114
||||| ||||||| ||||||| ||||||| ||||||| |||||||
Qy 1 AAGCCCTCCCAAGCTGTCATTATGATGCTGATAGTATTATGAAC 45

RESULT 5
ID Q70372 standard; cDNA to mRNA; 333 BP.
AC Q70372;
DT 09-MAR-1995 (first entry)
DE Anti HIV antibody light chain variable region.
KW Antibody; heavy chain; light chain; human immunodeficiency virus;
KW HIV; acquired immune deficiency syndrome; AIDS: treatment;
KW prophylaxis; Mus musculus; Homo sapiens; ss.
OS Mus musculus.
FH Key Location/Qualifiers
FT CDS 1..333
FT /*tag= a
FT /product= Antibody light chain variable region.
PN W09415969-A.
PD 21-JUL-1994.
PF 14-JAN-1993; J00039.
PR 14-JAN-1993; AU-032671.
PR 14-JAN-1993; WO-J00039.
PA (KAGA ) CHEMO SERO THERAPEUTIC RES INST.
PI Eda Y, Kimachi K, Maeda H, Osatomi K, Shiozaki K;
PI Tokiyoshi S;
PD WPI; 94-249145/30.
P-PSDB; R60302.
DR Recombinant chimeric anti HIV antibody - useful for the treatment
PT and prevention of HIV
PS Claim 15; Figure 4; 51pp; Japanese.
CC The recombinant antibody light chain has neutralising activity
CC against HIV. Chimeric antibodies comprising both mouse and human
CC sequences are useful in the treatment/prevention of AIDS caused by
CC HIV. This sequence is obtained from the mu5.5 anti HIV monoclonal
CC antibody producing cell.
SQ Sequence 333 BP; 88 A; 83 C; 86 G; 76 T;

Query Match 91.1%; Score 41; DB 12; Length 333;
Best Local Similarity 95.6%; Pred. No. 1.23e-11;
Matches 43; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 70 aagccagccaaagtgtgattatgatgtgatgttatatgaac 114
||||| ||||||| ||||||| ||||||| ||||||| |||||||

```

Qy 1 AAGGCTCCCAAGCTGTTGATTATGATGCTGATAGTATTATGAAC 45

RESULT 6

ID Q70376 standard; cDNA to mRNA; 333 BP.

AC Q70376;

DT 13-MAR-1995 (first entry)

DE Chimeric anti HIV antibody light chain variable region.

KW Anticbody; heavy chain; light chain; human immunodeficiency virus;

KW HIV; acquired immune deficiency syndrome; AIDS: treatment;

OS prophylaxis; Mus musculus; Homo sapiens; ss.

OS Chimeric Homo sapiens

OS Chimeric Mus musculus.

FH Key Location/Qualifiers

FT CDS 1..333

FT /\*tag= a

FT /product= Antibody light chain variable region.

FN W09415969-A.

PD 21-JUL-1994.

PF 14-JAN-1993; J00039.

PR 14-JAN-1993; AU-032671.

PR 14-JAN-1993; WO-J00039.

PA (KAGA ) CHEMA SERO THERAPEUTIC RES INST.

PI Eda Y, Kimachi K, Maeda H, Osatomi K, Shiosaki K;

PI Tokiyoshi S;

PI WPI; 94-249145/30.

DR P-FSDB; R60306.

PT Recombinant chimeric anti HIV antibody - useful for the treatment

PT and prevention of HIV

PS Claim 14; Figure 12; 51pp; Japanese.

CC The recombinant antibody light chain has neutralising activity

CC against HIV. Chimeric antibodies comprising both mouse and human

CC sequences are useful in the treatment/prevention of AIDS caused by

CC HIV. This sequence is derived from the mu5.5 anti HIV monoclonal

CC antibody producing cell.

CC Sequence 333 BP; 95 A; 90 C; 88 G; 60 T;

Qy 70 aagccagcagaagtgtgattatgattggtgatggtatgataac 114

Qy 1 AAGGCTCCCAAGCTGTTGATTATGATGCTGATAGTATTATGAAC 45

Query Match 91.1%; Score 41; DB 12; Length 333;

Best Local Similarity 95.6%; Pred. No. 1.23e-11;

Matches 43; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 70 aagccagcagaagtgtgattatgattggtgatggtatgataac 114

Qy 1 AAGGCTCCCAAGCTGTTGATTATGATGCTGATAGTATTATGAAC 45

RESULT 7

ID Q65558 standard; cDNA; 333 BP.

AC Q65558;

DT 30-JAN-1995 (first entry)

DE Mouse-human chimeric anti-HIV mu5.5-derived light chain V region.

KW Immunoglobulin; heavy chain; anti-HIV antibody; neutralisation;

KW human immunodeficiency virus; variable region; VL chain; murine;

KW chimeric; humanised; ds.

OS Chimeric Mus musculus.

OS Chimeric Homo sapiens.

FH Key Location/Qualifiers

FT misc feature 70..114

FT /\*tag= a

FT /note= "encodes murine CDR1"

FT misc feature 160..180

FT /\*tag= b

FT /note= "encodes murine CDR2"

FT misc feature 277..303

```
FT /*tag= c
FT /note= *encodes murine CDR3*
PN J06125783-A.
PD 10-MAY-1994.
PF 28-DEC-1991; 359808.
PR 28-DEC-1991; JP-359808.
PA (KAGA-) 2H KAGAKU KESSEI-RYOHO KENKYUSHO.
DR WPI; 94-187942/23.
DR P-PSDB; R55127.
PT Mouse-human chimeric anti-HIV antibody heavy and light chains -
PT and recombinant antibody consisting of the H- and L-chains,
PT useful in AIDS therapy
PS Claim 5; Fig 12; 22pp; Japanese.
CC Murine monoclonal antibodies mu 39.1 and mu 5.5 both neutralise HIV.
CC The heavy and light chain variable regions from these antibodies
CC were sequenced (Q65551-Q65554). The murine anti-HIV CDRs were
CC introduced into human framework regions to construct chimeric
CC antibodies (Q65555-Q65558).
SQ Sequence 333 BP; 95 A; 90 C; 88 G; 60 T;

Query Match 91.1%; Score 41; DB 11; Length 333;
Best Local Similarity 95.6%; Pred. No. 1.23e-11;
Matches 43; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 70 aaggccagcaaaagtgattgatgatggtgatgattatgaac 114
||||| ||||||| ||||||| ||||||| ||||||| |||||||
Qy 1 AAGGCTCCCAAAAGTGTGATTATGATGCTGATAGTTATATGAC 45
```

```
RESULT 8
ID N90492 standard; DNA; 334 BP.
AC N90492;
DT 20-OCT-1989 (first entry)
DE Gene fragment of immunoglobulin L chain variable region.
KW Gene fragment; immunoglobulin; L chain variable region; HIV.
OS Mus muscularis
FH Key Location/Qualifiers
FT CDS 1..333
FT /*tag= a
FT EP-327000-A.
PN 09-AUG-1989.
PF 30-JAN-1989; 101583.
PR 30-JAN-1988; JP-20255.
PR 08-JUL-1988; JP-171385.
PA (KAGA) The Chemo-Sero-Therapeutic Research Institute.
PI Maeda H, Eda Y, Kimachi K, Tokiyoshi S, Matsushita S, Hattori T,
PI Takatsuki K;
DR WPI; 89-229050/32.
PT Chimeric anti-human immune virus antibodies - contg. mouse variable
PT regions and human constant regions for diagnosis, treatment and
PT prevention of AIDS
PS Claim 6; page 15; 33pp; English.
CC The gene fragment encodes an L chain variable region from an
CC immunoglobulin with anti-HIV neutralising activity. It is used, with an
CC H chain variable region gene fragment (see N90491), to produce a chimeric
CC anti-HIV antibody with mouse variable regions and human constant regions.
CC The antibody retains its original specificity, but have much lower
CC antigenicity to humans. See also P90541, N90493 and N90495.
SQ Sequence 334 BP; 91 A; 83 C; 81 G; 79 T;

Query Match 91.1%; Score 41; DB 1; Length 334;
Best Local Similarity 95.6%; Pred. No. 1.23e-11;
Matches 43; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Db 70 aaggccagcaaaagtgattgatgatggtgatgattatgaac 114
||||| ||||||| ||||||| ||||||| ||||||| |||||||
Qy 1 AAGGCTCCCAAAAGTGTGATTATGATGCTGATAGTTATATGAC 45

RESULT 9
ID Q73986 standard; cDNA; 393 BP.
AC Q73986;
DT 20-SEP-1995 (first entry)
DE Humanized antibody 3B9 light chain.
KW Humanized antibody; antibody engineering; monoclonal antibody;
KW MAb; interleukin-4; IL-4; allergy; ds.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 1..393
FT /*tag= a
FT sig_peptide 1..60
FT /*tag= b
FT mat_peptide 61..393
FT /*tag= c
PN W09507301-A.
PD 16-MAR-1995.
PF 07-SEP-1994; U01308.
PR 07-SEP-1993; US-117366.
PR 14-OCT-1993; US-136783.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PI Gross MS, Holmes SD, Sylvester DR;
DR WPI; 95-123387/16.
DR P-PSDB; R75355.
PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived
PT from high affinity mAbs - useful in treatment of IL-4-mediated
PT and IgE-mediated allergic conditions
PS Disclosure; Fig.5; 97pp; English.
CC A humanized antibody light chain variable region and signal
CC sequence is given in R75355. The signal sequence is also
CC provided in R70194. The sequences of the first 2 CDRs
CC are identical to mouse anti-human IL-4 MAb 3B9 light chain
CC CDRs (given in R70195-96), but the third (R70201) differs
CC by a single amino acid from the native mouse CDR (R70197).
SQ Sequence 393 BP; 97 A; 96 C; 108 G; 92 T;
```

```
Query Match 91.1%; Score 41; DB 14; Length 393;
Best Local Similarity 95.6%; Pred. No. 1.23e-11;
Matches 43; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 127 aaggccagcaaaagtgattgatgatggtgatgattatgaac 171
||||| ||||||| ||||||| ||||||| ||||||| |||||||
Qy 1 AAGGCTCCCAAAAGTGTGATTATGATGCTGATAGTTATATGAC 45

RESULT 10
ID Q83490 standard; cDNA; 396 BP.
AC Q83490;
DT 20-SEP-1995 (first entry)
DE Mouse MAb 3B9 light chain.
KW Chimeric antibody; humanized antibody; antibody engineering;
KW monoclonal antibody; MAb; interleukin-4; IL-4; allergy; ds.
OS Mus sp.
FH Key Location/Qualifiers
FT CDS 1..396
FT /*tag= a
FT sig_peptide 1..60
FT /*tag= b
```



Mar 19 08:36

US-08-612-929-53.mg

11

PF 11-OCT-1989; 010415.  
PR 17-OCT-1988; US-260558.  
PA (BECT) Becton Dickinson Co.  
PI Hinton R, Oi VT;  
DR WPI; 90-126329/17.  
DR P-PSDB; R04132.  
PT New chimeric variants of murine antibody anti-leucine -  
PT contg. human antibody regions, and DNA encoding sequences.  
PS Claim 1; Fig 2; 12pp; English.  
CC Variants of murine monoclonal anti-CD4 antibody, anti-leu3A can be  
CC used to form chimeric mouse-variable, human-constant region Abs  
CC suggested as being useful as a vaccine to HIV. 246 T;  
SQ Sequence 900 BP; 261 A; 206 C; 187 G; 246 T;

Query Match 91.1%; Score 41; DB 1; Length 900;  
Best Local Similarity 95.6%; Pred. No. 1.23e-11;  
Matches 43; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 618 aaggccagccaagtgtgattatgattgattgattatgattatgaac 662  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
QY 1 AAGGCTCCCAAGTGTGATTATGATGCTGCTAGCTATATGAAC 45

RESULT 14

ID Q36609 standard; DNA; 393 BP.  
AC Q36609;  
DT 02-JUN-1993 (first entry)  
DE Anti-CD4 antibody MT 3.10 light chain variable region.  
KW immunosuppression; tissue transplantation; graft; L chain; V region;  
KW T-helper cell inhibition; transplant rejection; MAb;  
KW interleukin-2 receptor; ss.  
FH Key Location/Qualifiers  
FT sig\_peptide 1..60  
FT /\*tag= a  
FT mat\_peptide 61..393  
FT /\*tag= b  
FT /note= "J1 region begins at position 361"  
PN DE143214-A.  
PD 28-JAN-1993.  
PF 30-DEC-1991; 143214.  
PR 25-JUL-1991; DE-124759.  
PR 30-DEC-1991; DE-143214.  
PA (BOEF ) BOEHRINGER MANNHEIM GMBH.  
PI Kaluza B, Riethmuller G, Scheuer W, Weidle U;  
DR WPI; 93-037582/05.  
DR P-PSDB; R32123.  
PT Synergistic antibody compsn. for use as immunosuppressant -  
PT comprises monoclonal anti-CD4 antibodies and monoclonal anti-IL2R  
PT alpha- or anti-IL2R beta antibodies  
PS Claim 5; Page 11; 18pp; German.  
CC This sequence encodes the light chain variable region of a preferred  
CC anti-CD4 monoclonal antibody for use in the claimed synergistic  
CC composition. Mab MT 3.10 is deposited as clone 3.101/sB10 (ECACC  
CC 90090702). The anti-CD4 antibody is used with at least one anti-IL2R  
CC alpha or beta antibody. Individually the antibodies are strongly  
CC inhibiting and when used together their immunosuppressive properties  
CC are improved; they synergistically inhibit T-helper cell  
CC proliferation to effectively inhibit transplant rejection at low  
CC doses without significantly reducing the general immune response.  
CC See Q36607-Q36616.  
SQ Sequence 393 BP; 100 A; 105 C; 98 G; 90 T;

Query Match 86.7%; Score 39; DB 6; Length 393;  
Best Local Similarity 93.3%; Pred. No. 1.52e-10;

Mar 19 08:36

US-08-612-929-53.mg

12

Matches 42; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 130 aaggccagccaagtgtgattatgattgattgattatgattatgaac 174  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
QY 1 AAGGCTCCCAAGTGTGATTATGATGCTGCTAGCTATATGAAC 45

RESULT 15

ID T04019 standard; cDNA; 717 BP.  
AC T04019;  
DT 02-JUL-1996 (first entry)  
DE Anti-EGFR single chain antibody (Clone 4 B 2).  
KW Single chain antibody; antibody; epidermal growth factor receptor;  
KW EGFR; tumour; cancer; glioma; melanoma; carcinoma; diagnosis;  
KW assessment; phage antibody library; ss.  
OS Mus musculus.  
FH Key Location/Qualifiers  
FT CDS 1..717  
FT /\*tag= a  
FT /product= Single chain antibody.  
PN M09525167-A1.  
PD 21-SEP-1995.  
PF 16-MAR-1995; E00978.  
PR 17-MAR-1994; EP-104160.  
PR 02-DEC-1994; EP-118970.  
PA (MERE ) MERCK PATENT GMBH.  
PI Adan J, Ansell KH, Bendig MM, Blasco F, Guesow D;  
PI Kettleborough AC, Mitjans F, Pluats J, Rosell E;  
DR WPI; 95-336972/43.  
DR P-PSDB; R79866.  
PT Anti-EGFR antibodies and single chain Fv antibody fragments -  
PT obtained from phage-antibody libraries, useful for diagnosis and  
PT therapy of tumours  
PS Claim 4; Page 57; 93pp; English.  
CC Anti-epidermal growth factor receptor (EGFR) single chain antibodies  
CC and antibodies constructed from anti-EGFR antibody fragments can be  
CC used for diagnosis of tumours and assessment of tumour growth in  
CC vitro and in vivo. They may also be used in a pharmaceutical  
CC composition for the therapy of e.g. melanomas, gliomas and carcinomas.  
CC The antibodies and fragments are derived from mice but are humanised  
CC so as to cause minimum reaction against them. They are produced  
CC using the phage antibody library. (See T04011-T04026 and  
CC R79858-R79873)  
SQ Sequence 717 BP; 165 A; 169 C; 213 G; 170 T;

Query Match 86.7%; Score 39; DB 18; Length 717;  
Best Local Similarity 93.3%; Pred. No. 1.52e-10;  
Matches 42; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 472 aaggccagccaagtgtgattatgattgattgattatgattatgaac 516  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
QY 1 AAGGCTCCCAAGTGTGATTATGATGCTGCTAGCTATATGAAC 45

Search completed: Wed Mar 19 08:37:58 1997  
Job time : 15 secs.

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WATERMAN

(TM)

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HPsrch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed Mar 19 08:36:16 1997; MspPar time 63.91 Seconds  
Tabular output not generated. 579,960 Million cell updates/sec

Title: >US-08-612-929-53

Description: (1-45) from US08612929.seq

Perfect Score: 45

N.A. Sequence: 1 AAGGCTCCCAAGTCTGATTATGATGTCATATGATATGATGAC 45

Comp: TTCGGAGGGTTTCAACACTACTACACTATCAATATCTTG

Scoring table: TABLE default

Gap 10

Nmatch STD : Dbase 0; Query 0

Searched: 279077 seqs, 411808665 bases x 2

Post-processing: Minimum Match 0%

Listing first 45 summaries

Databases: 1:BCT 2:FON 3:INV1 4:INV2 5:ORG 6:MAM 7:VRT 8:PIN 9:PRI

10:PRO1 11:PRO2 12:ROD 13:SYN 14:UNC 15:VIR

genbank94

16:BCT1 17:BCT2 18:BCT3 19:BCT4 20:BCT5 21:BCT6 22:BCT7

23:BCT8 24:BCT9 25:INV1 26:INV2 27:INV3 28:INV4 29:INV5

30:INV6 31:INV7 32:MAM1 33:MAM2 34:MAM3 35:VRT1 36:VRT2

37:VRT3 38:PAT1 39:PAT2 40:PAT3 41:PHG 42:PIN1 43:PIN2

44:PIN3 45:PIN4 46:PIN5 47:PIN6 48:PIN7 49:PIN8 50:PRI1

51:PRI2 52:PRI3 53:PRI4 54:PRI5 55:PRI6 56:PRI7 57:PRI8

58:PRI9 59:PRI10 60:PRI11 61:PRI12 62:PRI13 63:ROD1

64:ROD2 65:ROD3 66:ROD4 67:ROD5 68:ROD6 69:ROD7 70:ROD8

71:STR 72:SYN 73:UNA 74:VRL1 75:VRL2 76:VRL3 77:VRL4

78:VRL5 79:VRL6 80:VRL7 81:VRL8

genbank-new5

82:BCT 83:INV1 84:INV2 85:MAM 86:VRT 87:PAT 88:PHG

89:PIN 90:PRI 91:ROD 92:STR 93:SYN 94:UNA 95:VRL

u-embl46.94

96:part1

Statistics: Mean 8.084; Variance 4.056; scale 1.993

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	41	91.1	245	64	MMIGKVRH	M.musculus immunoglob	9.84e-14
2	41	91.1	255	64	MMIGKVRD	M.musculus immunoglob	9.84e-14
3	41	91.1	262	64	MMIGKVRG	M.musculus immunoglob	9.84e-14
4	41	91.1	264	64	MMIGKVR1	M.musculus immunoglob	9.84e-14
5	41	91.1	266	64	MMIGKVR2	M.musculus immunoglob	9.84e-14
6	41	91.1	270	64	MMIGKVR3	M.musculus immunoglob	9.84e-14
7	41	91.1	270	64	MMIGKVR4	M.musculus immunoglob	9.84e-14
8	41	91.1	270	64	MMIGKVR5	M.musculus immunoglob	9.84e-14
9	41	91.1	279	66	MUSIGKAAAA	Mouse Igk chain mRNA	9.84e-14
10	41	91.1	286	65	MMU29628	Mus musculus anti-DNA	9.84e-14
11	41	91.1	297	65	MMU29629	Mus musculus anti-DNA	9.84e-14
12	41	91.1	333	67	MMU07207	Mus musculus clone 31	9.84e-14
13	41	91.1	333	67	MUSIGL5B	Mouse IgL chain H2L2	9.84e-14
14	41	91.1	333	70	S42888	Ig V kappa =immunoglob	9.84e-14
15	41	91.1	333	70	S54207	V kappa 21=immunoglob	9.84e-14
16	41	91.1	336	66	MUSIGKAAW	Mouse Ig rearranged k	9.84e-14
17	41	91.1	350	66	MUSIGKABBC	Mouse Ig kappa chain	9.84e-14
18	41	91.1	354	67	MUSL711GKV	Mouse hybridoma Ig re	9.84e-14
19	41	91.1	360	67	MUSIGKAF	Mouse Ig active kappa	9.84e-14
20	41	91.1	363	67	MUSL341GKV	Mouse hybridoma Ig re	9.84e-14
21	41	91.1	363	67	MUSL931GKV	Mouse hybridoma Ig re	9.84e-14
22	41	91.1	363	67	MUSL2021GK	Mouse hybridoma Ig re	9.84e-14
23	41	91.1	900	40	I08223	Sequence 1 from paten	9.84e-14
24	40	88.9	318	66	MUSIGGVKB	Mouse immunoglobulin	5.00e-13
25	39	86.7	292	65	MMU18599	Mus musculus immunogl	2.52e-12
26	39	86.7	333	65	MMVLE10	Mouse mRNA for kappa-	2.52e-12
27	39	86.7	336	64	MMIGLC404	M.musculus mRNA for I	2.52e-12
28	39	86.7	336	64	MMIGLC310	M.musculus mRNA for I	2.52e-12
29	39	86.7	342	62	S78338	Ig V=anti-CD19 antib	2.52e-12
30	39	86.7	393	70	S50265	Ig V=anti-CD4 mAb M-	2.52e-12
31	37	82.2	351	66	MUSIGKABBH	Mouse Ig kappa chain	6.20e-11
32	37	82.2	388	64	MMU07814	Mus musculus BALB/c a	6.20e-11
33	37	82.2	397	40	I08225	Sequence 5 from paten	3.03e-10
34	36	80.0	317	67	MUSIGVACR	Mus musculus Ig rearr	3.03e-10
35	36	80.0	353	66	MUSIGKABBD	Mouse Ig kappa chain	3.03e-10
36	35	77.8	351	66	MUSIGKABBF	Mouse Ig kappa chain	1.46e-09
37	35	77.8	353	66	MUSIGKABBG	Mouse Ig kappa chain	1.46e-09
38	34	75.6	313	70	S74550	Ig V kappa =rheumatoi	6.98e-09
39	34	75.6	336	67	MUSIGVACP	Mus musculus Ig rearr	6.98e-09
40	33	73.3	353	66	MUSIGKABBE	Mouse Ig kappa chain	3.29e-08
41	31	68.9	238	65	MMU18563	Mus musculus immunogl	7.01e-07
42	29	64.4	336	64	MMIGLC413	M.musculus mRNA for I	1.41e-05
43	25	55.6	271	65	MMU29627	Mus musculus anti-DNA	4.58e-03
44	25	55.6	333	12	MM51468	Mus musculus clone 4F	4.58e-03
45	25	55.6	333	91	MMU51468	Mus musculus clone 4F	4.58e-03

## ALIGNMENTS

RESULT 1  
LOCUS MMIGKVRH 245 bp RNA ROD 13-OCT-1993  
DEFINITION M.musculus immunoglobulin kappa light chain (DBA/1) gene, v region.  
ACCESSION Z25456  
NID 9407846  
KEYWORDS Igk gene; immunoglobulin; light chain; variable region.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;

Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 245)  
AUTHORS Mo, J.A., Bona, C.A. and Holmdahl, R.  
TITLE Variable region gene selection of immunoglobulin G expressing B cells with specificity for a defined epitope on type II collagen  
JOURNAL Eur. J. Immunol. (1993) In press  
REFERENCE 2 (bases 1 to 245)  
AUTHORS Mo, J.A.  
TITLE Direct Submission  
JOURNAL Submitted (02-AUG-1993) to the EMBL/GenBank/DBJ databases. John A Mo, Department of Medical and Physiological, Department of, Medical and Physiological Chemistry, Husargatan 3, Uppsala, 75123, Sweden

REFERENCE 3 (bases 1 to 245)  
AUTHORS Mo, J.A., Bona, C.A. and Holmdahl, R.  
TITLE Variable region gene selection of immunoglobulin G-expressing B cells with specificity for a defined epitope on type II collagen  
JOURNAL Eur. J. Immunol. 23 (10), 2503-2510 (1993)  
MEDLINE 94009207

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ORIGIN

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Qy 1 AAGGCTCCCAAGTGTGATTATGATGCTGATGCTATATGAAC 45

RESULT 2  
LOCUS MMIGKCVRD 255 bp RNA ROD 13-OCT-1993  
DEFINITION M.musculus immunoglobulin kappa light chain (DBA/1) gene, v region.  
ACCESSION Z25448  
NID 9407836

KEYWORDS Igk gene; immunoglobulin; light chain; variable region.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 255)  
AUTHORS Mo, J.A., Bona, C.A. and Holmdahl, R.  
TITLE Variable region gene selection of immunoglobulin G expressing B cells with specificity for a defined epitope on type II collagen  
JOURNAL Eur. J. Immunol. (1993) In press  
REFERENCE 2 (bases 1 to 255)  
AUTHORS Mo, J.A.  
TITLE Direct Submission  
JOURNAL Submitted (02-AUG-1993) to the EMBL/GenBank/DBJ databases. John A Mo, Department of Medical and Physiological, Department of, Medical and Physiological Chemistry, Husargatan 3, Uppsala, 75123, Sweden

REFERENCE 3 (bases 1 to 255)  
AUTHORS Mo, J.A., Bona, C.A. and Holmdahl, R.  
TITLE Variable region gene selection of immunoglobulin G-expressing B cells with specificity for a defined epitope on type II collagen  
JOURNAL Eur. J. Immunol. 23 (10), 2503-2510 (1993)  
MEDLINE 94009207

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Location/Qualifiers  
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BASE COUNT 71 a 65 c 64 g 55 t  
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Query Match 91.1%; Score 41; DB 64; Length 255;  
Best Local Similarity 95.6%; Pred. No. 9.84e-14;  
Matches 43; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 28 aagccagcacaagtgtgattatgatgtgtagtattatgaac 72  
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Qy 1 AAGGCTCCCAAGTGTGATTATGATGCTGATGCTATATGAAC 45

RESULT 3  
LOCUS MMIGKCVRE 262 bp RNA ROD 13-OCT-1993  
DEFINITION M.musculus immunoglobulin kappa light chain (DBA/1) gene, v region.  
ACCESSION Z25450  
NID 9407838

KEYWORDS Igk gene; immunoglobulin; light chain; variable region.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 262)  
AUTHORS Mo, J.A., Bona, C.A. and Holmdahl, R.  
TITLE Variable region gene selection of immunoglobulin G expressing B cells with specificity for a defined epitope on type II collagen

JOURNAL	Submitted (02-AUG-1993) to the EMBL/GenBank/DBJ databases. John A. Mo, Department of Medical and Physiological, Department of, Medical and Physiological Chemistry, Husargatan 3, Uppsala, 75123, Sweden
REFERENCE	3 (bases 1 to 264)
AUTHORS	Mo, J. A., Bona, C. A. and Holmdahl, R.
TITLE	Variable region gene selection of immunoglobulin G-expressing B cells with specificity for a defined epitope on type II collagen
JOURNAL	Eur. J. Immunol. 23 (10), 2503-2510 (1993)
MEDLINE	94009207
FEATURES	Location/Qualifiers
source	1..264 /organism="Mus musculus" /strain="DBA/1"

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CDS	/dev_stage="adult" /tissue_type="lymph node" /cell_type="B cell hybridoma" /cell_line="CIICB391 hybridoma" /chromosome="6"			

Best Local Similarity 95.6%; Pred. No. 9.84e-14;  
Matches 43; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 37 aagccagccaagtgttattatgatggtgatagtatatgaac 81  
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Qy 1 AAGCCCTCCCAAGTGTTCATTATGATGGTGATGATTATGAAC 45

RESULT LOCUS	5	MMIGKVCRC	266 bp	RNA	ROD	13-OCT-1993

**NID** g407834  
**KEYWORDS** IgK gene; immunoglobulin; light chain; variable region.  
**SOURCE** house mouse.  
**ORGANISM** *Mus musculus*  
Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;  
Eukaryotae; Metazoa; Bilateria; Coelomata; Deuterostomia; Chordata;  
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;  
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;  
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.  
1 (bases 1 to 266)  
**REFERENCE** Mo, J.A., Bona, C.A. and Holmdahl, R.  
**AUTHORS**  
**TITLE** Variable region gene selection of immunoglobulin G expressing B  
cells with specificity for a defined epitope on type II collagen

JOURNAL	
REFERENCE	Eur. J. Immunol. (1993) In press
AUTHORS	2 (bases 1 to 266)
TITLE	Mo,J.A.
JOURNAL	Direct Submission
REFERENCE	Submitted (02-AUG-1993) to the EMBL/GenBank/DBJ databases. John A Mo, Department of Medical and Physiological, Department of Medical and Physiological Chemistry, Husargatan 3, Uppsala, 75123, Sweden
	3 (bases 1 to 266)





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V_region      /strain="DBA/1"
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BASE COUNT    71 a 68 c 68 g 63 t
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Query Match   91.1%; Score 41; DB 64; Length 270;
Best Local Similarity 95.6%; Pred. No. 9.84e-14;
Matches 43; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 43 aagggcagccaagtgttgattgatggtgatgatttatgaac 87
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Qy 1  AAGGCTCCCAAGTGTGATTATGATGCTGATGATTATATGAAC 45
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BASE COUNT    71 a 68 c 68 g 63 t
ORIGIN
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Query Match   91.1%; Score 41; DB 64; Length 270;
Best Local Similarity 95.6%; Pred. No. 9.84e-14;
Matches 43; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 43 aagggcagccaagtgttgattgatggtgatgatttatgaac 87
      ||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Qy 1  AAGGCTCCCAAGTGTGATTATGATGCTGATGATTATATGAAC 45
      AASNLESGIPARFSGSGGTDTLNIHPVEEDAATYYCQSNEDP"

BASE COUNT    71 a 68 c 68 g 63 t
ORIGIN
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RESULT 8
LOCUS      MMICKVRG 270 bp RNA ROD 13-OCT-1993
DEFINITION M.musculus immunoglobulin kappa light chain (DBA/1) gene, v region.
ACCESSION  Z25454
NID        g407842
KEYWORDS   Igk gene; immunoglobulin; light chain; variable region.
SOURCE     house mouse.
ORGANISM   Mus musculus
            Eukaryota; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
            Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
            Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata;
            Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
            Sciurognathi; Myomorpha; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 270)
            Mo,J.A., Bona,C.A. and Holmdahl,R.
            Variable region gene selection of immunoglobulin G expressing B
            cells with specificity for a defined epitope on type II collagen
            Eur. J. Immunol. (1993) In press
REFERENCE  2 (bases 1 to 270)
            Mo,J.A.
            Direct Submission
            Submitted (02-AUG-1993) to the EMBL/GenBank/DBJ databases. John A
            Mo, Department of Medical and Physiological, Department of, Medical
            and Physiological Chemistry, Husargatan 3, Uppsala, 75123, Sweden
            3 (bases 1 to 270)
            Mo,J.A., Bona,C.A. and Holmdahl,R.
            Variable region gene selection of immunoglobulin G-expressing B
            cells with specificity for a defined epitope on type II collagen
            Eur. J. Immunol. 23 (10), 2503-2510 (1993)
JOURNAL     94009207
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V_region      /cell_line="CIICB340 hybridoma"
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BASE COUNT    71 a 68 c 68 g 63 t
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Query Match   91.1%; Score 41; DB 64; Length 270;
Best Local Similarity 95.6%; Pred. No. 9.84e-14;
Matches 43; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 43 aagggcagccaagtgttgattgatggtgatgatttatgaac 87
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Qy 1  AAGGCTCCCAAGTGTGATTATGATGCTGATGATTATATGAAC 45
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BASE COUNT    71 a 68 c 68 g 63 t
ORIGIN
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Query Match   91.1%; Score 41; DB 64; Length 270;
Best Local Similarity 95.6%; Pred. No. 9.84e-14;
Matches 43; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy 1  AAGGCTCCCAAGTGTGATTATGATGCTGATGATTATATGAAC 45
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BASE COUNT    71 a 68 c 68 g 63 t
ORIGIN
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```

RESULT 9
LOCUS      MUSICKAAAA 279 bp mRNA ROD 07-MAR-1995
DEFINITION Mouse Igk chain mRNA, VJ5 region.
ACCESSION  M57978
NID        g196402
KEYWORDS   J-region; V-region; anti-cytochrome c antibody;
            immunoglobulin kappa-chain; immunoglobulin light chain.
SOURCE     Mouse (BALB/c) secondary B cell hybridoma 1G3 mRNA, clone 1G3.E3.
ORGANISM   Mus musculus
            Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
            Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE  1 (bases 1 to 279)
            Goshorn,S.C., Retzel,E. and Jemmerson,R.
            Common structural features among monoclonal antibodies binding the
            same antigenic region of cytochrome c
            J. Biol. Chem. 266 (4), 2134-2142 (1991)
JOURNAL     91115823
MEDLINE
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            /tissue_type="hybridoma"
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Best Local Similarity 95.6%; Pred. No. 9.84e-14;
Matches 43; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 13 aagcgccagcaagtggtgattatgatgtgatgtatgatgaac 57
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QY 1 AAGGCTCCCAAGTGTGATTATGATGCTGATGATTATATGAAC 45

RESULT 10
LOCUS MMU29628 286 bp mRNA ROD 08-DEC-1995
DEFINITION Mus musculus anti-DNA antibody Ig kappa chain mRNA, V-J region,
hybridoma 52.60, partial cds.
ACCESSION U29628
NID g996124
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
Murinae; Mus.
REFERENCE 1 (bases 1 to 286)
AUTHORS Ibrahim,S.M., Weigert,M., Basu,C., Erikson,J. and Radic,M.Z.
TITLE Light chain contribution to specificity in anti-DNA antibodies
JOURNAL J. Immunol. 155 (6), 3223-3233 (1995)
MEDLINE 95403997
REFERENCE 2 (bases 1 to 286)
AUTHORS Ibrahim,S.M., Weigert,M., Basu,C., Erikson,J. and Radic,M.Z.
TITLE Direct Submission
JOURNAL Submitted (21-JUN-1995) Saleh M. Ibrahim, Molecular Biology,
Princeton University, Princeton, NJ 08544, USA
FEATURES
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CDS
74 a 75 c 69 g 68 t

BASE COUNT
ORIGIN
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Best Local Similarity 95.6%; Pred. No. 9.84e-14;
Matches 43; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 70 aagcgccagcaagtggtgattatgatgtgatgtatgatgaac 114
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QY 1 AAGGCTCCCAAGTGTGATTATGATGCTGATGATTATATGAAC 45

RESULT 11
LOCUS MMU29629 297 bp mRNA ROD 08-DEC-1995
DEFINITION Mus musculus anti-DNA antibody Ig kappa chain mRNA, V-J region,
hybridoma 52.46B, partial cds.
ACCESSION U29629
NID g996126
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
Murinae; Mus.
REFERENCE 1 (bases 1 to 297)
AUTHORS Ibrahim,S.M., Weigert,M., Basu,C., Erikson,J. and Radic,M.Z.
TITLE Light chain contribution to specificity in anti-DNA antibodies
JOURNAL J. Immunol. 155 (6), 3223-3233 (1995)
MEDLINE 95403997
REFERENCE 2 (bases 1 to 297)
AUTHORS Ibrahim,S.M., Weigert,M., Basu,C., Erikson,J. and Radic,M.Z.
TITLE Direct Submission
JOURNAL Submitted (21-JUN-1995) Saleh M. Ibrahim, Molecular Biology,
Princeton University, Princeton, NJ 08544, USA
FEATURES
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/isolate="Hybridoma 52.46B"
/chromosome="6"
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ORIGIN

Query Match      91.1%; Score 41; DB 65; Length 297;
Best Local Similarity 95.6%; Pred. No. 9.84e-14;
Matches 43; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 70 aagcgccagcaagtggtgattatgatgtgatgtatgatgaac 114
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QY 1 AAGGCTCCCAAGTGTGATTATGATGCTGATGATTATATGAAC 45

RESULT 12
LOCUS MMU07207 333 bp mRNA ROD 08-OCT-1994
DEFINITION Mus musculus clone 31 anti-C5a Ig light chain V region mRNA,
partial cds.
ACCESSION U07207
NID g459212
KEYWORDS
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JOURNAL	AIDS Res. Hum. Retroviruses 8 (6), 1107-1115. (1992)
MEDLINE	92368728
REMARK	GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 111983] from the original journal article. This sequence comes from Fig. 2.

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FEATURES
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Location/Qualifiers
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antibody C beta 1; This sequence comes from Fig. 2.
antibody C beta 1"
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/db_xref="PID:g254223"
/translation="DIVLTQSPASVLAVSGQRATISKASQSDYDGDSSVMNWVQKRP
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GSGTKLTK"

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BASE COUNT	91 a	82 c	81 g	79 t
ORIGIN				
Query Match		91.1%	Score 41;	DB 70; Length 333;
Best Local Similarity		95.6%	Pred. No. 9,84e-14;	
Matches 43; Conservative			0; Mismatches 2;	Indels 0; Gaps 0;

**Db** 70 aagcccgagcaaatgttgattatgatggtagtatatgaac 114  
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
**Ov** 1 AGGCGCTCCAAAGTCTTGATTATGATGGTAGTTATGAAC 45

LOCUS	554207	333 bp	mRNA	ROD	26-MAR-1993
DEFINITION	V kappa 21-immunoglobulin light chain variable region [mice, HIV-1 BRO immunized BALB/c. mRNA Partial, 333 nt].				

ACCESSION S54207  
NID 9264866  
KEYWORDS  
SOURCE mice HIV-1 BRU immunized BALB/c.  
ORGANISM Mus sp.  
Unclassified.

REFERENCE	1 (bases 1 to 333)
AUTHORS	Pirofski, L.A., Thomas, E.K. and Scharff, M.D.
TITLE	Variable region gene utilization and mutation in a group of neutralizing murine anti-human immunodeficiency virus type 1 principal neutralizing determinant antibodies
JOURNAL	AIDS Res. Hum. Retroviruses 9 (1), 41-49 (1993)

MEDLINE 93152285  
 REMARK GenBank staff at the National Library of Medicine created this  
 entry (NCBI gibsseq 124489) from the original journal article.  
 This sequence comes from Fig. 2.

FEATURES	Location/Qualifiers
source	1..333 /organism="Mus sp." /note="mice"
CDS	1..333 /partial /gene="V $\kappa$ 21" /note="mismatch (62 [I->M]); Description: immunoglobulin light chain variable region, anti-HIV-1 monoclonal antibody 110.3; Method: conceptual translation supplied by author. This sequence comes from Fig. 2. Author-given

```

protein sequence is in conflict with the conceptual
translation. anti-HIV-1 monoclonal antibody 110.3"
/codon_start=1
/product="immunoglobulin light chain variable region"
/db_xref="PMID:g264867"
/translations="DWVLTSPGASLAVSLGORATISCKASQVDYQZSYNNYQQR
COPPKL1LHAASNLVSGIPAFSCGSQGTDLINIPVEEDSAYTCOOSIEDPPTF

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BASE COUNT		87 a		85 c		85 g		76 t	
ORIGIN									
Query Match		91.1%		Score 41;		DB 70;		Length 333;	
Best Local Similarity		95.6%		Pred. No. 9,84e-14;					
Matches		43.		Conservative		0.		Mismatches 2;	
								Index 0;	
								Gaps 0;	

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Db      70  aagccagccaagtgttgattatgatggtgatgttatatgaac 114
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Qy      1  AAGCCTCCCAAGCTTGATTATGATGGTGATAGTTATATGAAC 45

```

Search completed: Wed Mar 19 08:37:24 1997  
Job time : 68 secs.



43 13 61.9 569 171 MW9332 ma03d10.r1 Soares mou 1.17e+00  
 44 13 61.9 958 169 MW1677 ma93q09.r1 Soares mou 1.17e+00  
 c 45 13 61.9 4626 174 HSW5842 human chromosome 7 ST 1.17e+00

## ALIGNMENTS

RESULT 1  
 LOCUS R21117 451 bp mRNA EST 18-APR-1995  
 DEFINITION YG52e11.r1 Homo sapiens cDNA clone 36023 5' similar to SP:S20969  
 S20969 NA/CA,K ANTIFORTER - ;  
 ACCESSION R21117  
 NID g77598  
 KEYWORDS EST.  
 SOURCE human clone-36023 library=Soares infant brain LNB vector=Lafmid BA host=DH10B (ampicillin resistant) primer=M13RP1 Rsite1-Not I  
 Reite2-Hind III Whole brain from a 73 days post natal female. 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' AACTGGAGAATTCCGGCCGAGCAATTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Hind III adaptors (Pharmacia), digested with Not I and directionally cloned into the Not I and Hind III sites of the Lafmid BA vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM Homo sapiens  
 Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 451)  
 AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevasakis,E., Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.

TITLE The WashU-Merck EST Project  
 JOURNAL Unpublished (1995)

COMMENT GDB: G00-408-524  
 Contact: Wilson RK  
 WashU-Merck EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810

Email: est@watson.wustl.edu  
 High quality sequence stops: 303  
 Source: IMAGE Consortium, LNL  
 This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES Location/Qualifiers  
 source 1..451

/organism="Homo sapiens"  
 /clone="36023"  
 /note="human"

BASE COUNT 72 a 119 c 138 g 119 t 3 others  
 ORIGIN

Query Match 76.2%; Score 16; DB 77; Length 451;  
 Best Local Similarity 94.4%; Pred. No. 1.02e-04;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 324 cctctgtatgggtgttt 341  
 ||||| |||||  
 Qy 2 CCTCGGTATGGGTGTT 19

RESULT 2  
 LOCUS T02032 311 bp mRNA EST 10-NOV-1992  
 DEFINITION WST02753 Caenorhabditis elegans cDNA clone CEESY50.  
 ACCESSION T02032  
 NID g278513  
 KEYWORDS EST.

SOURCE Nematodes clone=CEESY50 library=Early embryo, Stratagene (cat. #937007) primer=M13 Forward.  
 ORGANISM Caenorhabditis elegans  
 Eukaryota; Animalia; Eumetazoa; Nematoda; Secernentea; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae.

REFERENCE 1 (bases 1 to 311)  
 AUTHORS McCombie,W.R., Kelley,J.M., Aubin,L., Goscoechea,M., FitzGerald,M.G., Wu,A., Adams,M.D., Dubnick,M., Kerlavage,A.R., Venter,J.C. and Fields,C.A.

JOURNAL Unpublished (1993) Contact: Kerlavage AR-The Institute for Genomic Research-932 Clopper Road,Gaithersburg,MD 20878-Tel: (301) 869 9056-Fax: (301) 869 9423 Email: arkerlav@tigr.org

## COMMENT

Contact: Kerlavage AR  
 The Institute for Genomic Research  
 932 Clopper Road, Gaithersburg, MD 20878  
 Tel: 3018699056  
 Fax: 3018699423  
 Email: arkerlav@tigr.org.

FEATURES Location/Qualifiers

source 1..311  
 /organism="Caenorhabditis elegans"  
 /clone="CEESY50"  
 /note="Nematodes"

BASE COUNT 138 a 23 c 71 g 67 t 12 others  
 ORIGIN

Query Match 71.4%; Score 15; DB 103; Length 311;  
 Best Local Similarity 100.0%; Pred. No. 2.67e-03;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 140 accataccggaggt 154

|||||  
 Cp 15 ACCCATACGGAGGT 1

RESULT 3  
 LOCUS CEK129A9R 313 bp mRNA EST 12-DEC-1995  
 DEFINITION C.elegans cDNA clone yk129a9 : 3' end, single read.  
 ACCESSION D64977

NID g1117417  
 KEYWORDS EST (expressed sequence tag).  
 SOURCE Caenorhabditis elegans (strain CB1489 him-8(e1489), ) (library: Yuji kohara unpublished cDNA) Hermaphrodite, male varied whole animal cDNA to mRNA.

ORGANISM Caenorhabditis elegans  
 Eukaryotae; mitochondrial eukaryotes; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditoidea; Rhabditidae; Caenorhabditis.

REFERENCE 1 (bases 1 to 313)  
 AUTHORS Kohara,Y., Motohashi,T., Tabara,H., Sugimoto,A., Watanabe,H. and Nishigaki,A.

TITLE Toward an expression map of the C.elegans genome  
 JOURNAL Unpublished (1995)  
 COMMENT Submitted (23-Aug-1995) to DDBJ by: Yuji Kohara  
 Gene Library Lab.





Mar 19 08:41

US-08-612-929-54.rst

7

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RESULT 6
LOCUS RICS14394A 460 bp mRNA EST 27-JUL-1995
DEFINITION Rice cDNA, partial sequence (S14394_1A).
ACCESSION D48269
NID g701978
KEYWORDS EST (expressed sequence tag).
SOURCE Oryza sativa (strain Nipponbare, ) Green shoot (8 days old) cDNA to
ORNA.

ORGANISM Oryza sativa
Eukaryotae; mitochondrial eukaryotes; Viridiplantae;
Charophyta/Embryophyta group; Embryophyta; Magnoliophyta;
Liliopsida; Poales; Poaceae; Oryza.
REFERENCE 1 (bases 1 to 460)
AUTHORS Sasaki, T., Miyao, A. and Yamamoto, K.
TITLE Rice cDNA from shoot
JOURNAL Unpublished (1995)
COMMENT PROJECT = 'RGP'
Submitted (14-Feb-1995) to DDBJ by:
Takui Sasaki
Rice Genome Research Program
National Institute of Agrobiological Resources
2-1-2 Kanondai
Tsukuba Ibaraki
Japan 305
Phone: 0298-38-7441
Fax : 0298-38-7468.

```

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FEATURES
source
1..460
/organism="Oryza sativa"
/strain="Nipponbare"
/dev_stage="Green shoot (8 days old)"
/sequenced_mol="cDNA to mRNA"
BASE COUNT 111 a 116 c 109 g 120 t 4 others
ORIGIN
Query Match 71.4%; Score 15; DB 102; Length 460;
Best Local Similarity 94.1%; Pred. No. 2.67e-03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 104 cctccggtatgggggtt 120
|||||
Qy 2 CCTCCGGTATGGGTGTT 18

RESULT 7
LOCUS CELK101B2R 241 bp mRNA EST 12-DEC-1995
DEFINITION C.elegans cDNA clone yk101b2 : 3' end, single read.
ACCESSION D66478
NID g1116862
KEYWORDS EST (expressed sequence tag).
SOURCE Caenorhabditis elegans (strain CB1489 him-8(e1489), ) (library:
Yuji kohara unpublished cDNA) Hermaphrodite, male varied whole
animal cDNA to mRNA.

ORGANISM Caenorhabditis elegans
Eukaryotae; mitochondrial eukaryotes; Metazoa; Nematoda;
Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea;
Rhabditidae; Caenorhabditis.
REFERENCE 1 (bases 1 to 241)
AUTHORS Kohara, Y., Motohashi, T., Tabara, H., Sugimoto, A., Watanabe, H. and
Nishigaki, A.
TITLE Toward an expression map of the C.elegans genome
JOURNAL Unpublished (1995)
COMMENT Submitted (23-Aug-1995) to DDBJ by:
Yuji Kohara

```

Mar 19 08:41

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8

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Gene Library Lab.
National Institute of Genetics
Yata 1111, Mishima Shizuoka
411 Japan
Phone: 0559-81-6854
Fax : 0559-81-6855
Email:ykohara@dbj.nig.ac.jp.

FEATURES
source
1..241
/organism="Caenorhabditis elegans"
/strain="CB1489 him-8(e1489)"
/dev_stage="varied"
/sequenced_mol="cDNA to mRNA"
/sex="Hermaphrodite, male"
/tissue_type="whole animal"
/clone_lib="Yuji kohara unpublished cDNA"
BASE COUNT 101 a 31 c 55 g 53 t 1 others
ORIGIN
Query Match 66.7%; Score 14; DB 5; Length 241;
Best Local Similarity 100.0%; Pred. No. 6.06e-02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

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Db 191 gtatgggtgtttcc 204
|||||
Qy 8 GTATGGGTGTTTCC 21

RESULT 8
LOCUS SSO3B07 312 bp RNA EST 30-AUG-1995
DEFINITION S.scrofa mRNA; expressed sequence tag (5'; clone o3b07).
ACCESSION F14577
NID g972417
KEYWORDS cofilin; EST; expressed sequence tag.
SOURCE pig.
ORGANISM Sus scrofa
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Sarcotrygii; Mammalia; Eutheria; Artiodactyla;
Suiformes; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 312)
AUTHORS Wintroe, A.K., Fredholm, M. and Davies, W.
TITLE Evaluation and characterization of a porcine small intestine cDNA
library
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 312)
AUTHORS Wintroe, A.K.
TITLE Direct Submission
JOURNAL Submitted (26-JUL-1995) to the EMBL/GenBank/DBJ databases.
Wintroe A.K., The Royal Veterinary and Agricultural University,
Department of Animal Science and Animal Health, Division of Animal
Genetics, Bulowsvej 13, 1870 Frederiksberg C, DENMARK

```

```

FEATURES
source
1..312
/organism="Sus scrofa"
/tissue_type="small intestine"
/clone_lib="directionally cloned cDNA in X11-blue MRF"
/clone="o3b07"
1..>312
/note="expressed sequence tag; pid:e196635"
/codon_start=1
/product="cofilin"
/db_xref="PID:g972418"
/translation="MAGCAVAVSGYIKVFNDAKVRKSTPEVKKRYAVLFCIXEDK
KNITILEEGKEIILVGDVGQXVDDPYATFATPKMLPKDCRYLIDATYETKSKKXLUFI

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US-08-612-929-54.rst

9

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BASE COUNT      72 a      73 c      96 g      60 t      11 others
ORIGIN
FW*
Query Match      66.7%; Score 14; DB 103; Length 312;
Best Local Similarity 84.2%; Pred. No. 6.06e-02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 5 cctccgggtggtgctntc 23
    ||||| ||| ||| ||
Qy 2 CCTCCGGTATGGGTGTTTC 20

RESULT 9
LOCUS CELK072C1R 333 bp mRNA EST 11-DEC-1995
DEFINITION C.elegans cDNA clone yk72c1 : 3' end, single read.
ACCESSION D66007
NID g1116169
KEYWORDS EST(expressed sequence tag).
SOURCE Caenorhabditis elegans (strain CB1489 him-8(e1489), ) (library:
Yuji kohara unpublished cDNA) Hermaphrodite, male varied whole
animal cDNA to mRNA.
ORGANISM
Caenorhabditis elegans
Eukaryotae; mitochondrial eukaryotes; Metazoa; Nematoda;
Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea;
Rhabditidae; Caenorhabditis.
REFERENCE 1 (bases 1 to 333)
AUTHORS Kohara,Y., Motohashi,T., Tabara,H., Sugimoto,A., Watanabe,H. and
Nishigaki,A.
TITLE Toward an expression map of the C.elegans genome
JOURNAL Unpublished (1995)
COMMENT Submitted (23-Aug-1995) to DDBJ by:
Yuji Kohara
Gene Library Lab.
National Institute of Genetics
Yata 1111, Mishima Shizuoka
411 Japan
Phone: 0559-81-6854
Fax : 0559-81-6855
Email:ykohara@dbj.nig.ac.jp.
FEATURES
Location/Qualifiers
source
1..333
/organism="Caenorhabditis elegans"
/strain="CB1489 him-8(e1489)"
/dev stage="varied"
/sequenced_mol="cDNA to mRNA"
/sex="Hermaphrodite, male"
/tissue type="whole animal"
/clone lib="Yuji kohara unpublished cDNA"
BASE COUNT 150 a 27 c 80 g 70 t 6 others
ORIGIN

Query Match 66.7%; Score 14; DB 4; Length 333;
Best Local Similarity 93.3%; Pred. No. 6.06e-02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 123 accatnccggaggt 137
    ||||| ||||| ||
Cp 15 ACCCATCCGGAGGT 1

RESULT 10
LOCUS CELK130F5R 339 bp mRNA EST 12-DEC-1995
DEFINITION C.elegans cDNA clone yk130f5 : 3' end, single read.

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US-08-612-929-54.rst

10

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ACCESSION D65087
NID g1117514
KEYWORDS EST(expressed sequence tag).
SOURCE Caenorhabditis elegans (strain CB1489 him-8(e1489), ) (library:
Yuji kohara unpublished cDNA) Hermaphrodite, male varied whole
animal cDNA to mRNA.
ORGANISM
Caenorhabditis elegans
Eukaryotae; mitochondrial eukaryotes; Metazoa; Nematoda;
Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea;
Rhabditidae; Caenorhabditis.
REFERENCE 1 (bases 1 to 339)
AUTHORS Kohara,Y., Motohashi,T., Tabara,H., Sugimoto,A., Watanabe,H. and
Nishigaki,A.
TITLE Toward an expression map of the C.elegans genome
JOURNAL Unpublished (1995)
COMMENT Submitted (23-Aug-1995) to DDBJ by:
Yuji Kohara
Gene Library Lab.
National Institute of Genetics
Yata 1111, Mishima Shizuoka
411 Japan
Phone: 0559-81-6854
Fax : 0559-81-6855
Email:ykohara@dbj.nig.ac.jp.
FEATURES
Location/Qualifiers
source
1..339
/organism="Caenorhabditis elegans"
/strain="CB1489 him-8(e1489)"
/dev stage="varied"
/sequenced_mol="cDNA to mRNA"
/sex="Hermaphrodite, male"
/tissue type="whole animal"
/clone lib="Yuji kohara unpublished cDNA"
BASE COUNT 132 a 37 c 76 g 91 t 3 others
ORIGIN

Query Match 66.7%; Score 14; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 6.06e-02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 194 gtatgggtgtttcc 207
    ||||| ||||| |||||
Qy 8 GTATGGGTGTTTCC 21

RESULT 11
LOCUS H39637 343 bp mRNA EST 16-AUG-1995
DEFINITION y056h08.r1 Homo sapiens cDNA clone 181983 5'.
ACCESSION H39637
NID g915689
KEYWORDS EST.
SOURCE human clone=181983 library=Soares breast 3NBH8et vector=pf7T3D
(Pharmacia) with a modified polylinker host=DH10B (ampicillin
resistant) primer=M13R1 Rsite1=Not I Rsite2=Eco RI Adult human.
1st strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAGTGGAGCGCGCCCTTTTCTTTTCTTTT 3',
double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia),
digested with Not I and cloned into the Not I and Eco RI sites of a
modified pf7T3 vector (Pharmacia). library went through one round
of normalization to a Cot = 20. library constructed by Benito Soares
and M.Fatima Bonaldo.
ORGANISM
Homo sapiens
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;

```

REFERENCE  
AUTHORS

Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;  
Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 343)  
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,  
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,  
Trevaaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and  
Wilson, R.

TITLE  
JOURNAL  
COMMENT

The WashU-Merck EST Project  
Unpublished (1995)

Contact: Wilson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810

Email: est@watson.wustl.edu  
High quality sequence stops: 297  
Source: IMAGE Consortium, LNL  
This clone is available royalty-free through LNL ; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES  
source

1..343  
/organism="Homo sapiens"  
/clone="181983"  
/note="human"

BASE COUNT 82 a 92 c 89 g 75 t 5 others

Query Match 66.7%; Score 14; DB 18; Length 343;  
Best Local Similarity 85.0%; Pred. No. 6.06e-02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 155 ggaacacaccacacagctgg 174  
||||||| ||| |||  
Cp 21 GGAACACCCATACCGGAGG 2

RESULT 12  
LOCUS R35538 432 bp mRNA EST 02-MAY-1995  
DEFINITION y964g04.r1 Homo sapiens cDNA clone 37508 5' .  
ACCESSION R35538  
NID g792439

KEYWORDS  
SOURCE

EST.  
human clone=37508 library=Soares infant brain IN18 vector=Lafmid BA  
host=DH10B (ampicillin resistant) primer=M13Rpl Rsite1=Not I  
Rsite2=Hind III Whole brain from a 73 days post natal female. 1st  
strand cDNA was primed with a Not I - oligo(dT) primer [5'  
AAGTGGACAAATTCGGCGCCGACGAAATTTTTTTTTTTT 3']; double-stranded  
cDNA was ligated to Hind III adaptors (Pharmacia), digested with  
Not I and directionally cloned into the Not I and Hind III sites of  
the Lafmid BA vector. Library went through one round of  
normalization. Library constructed by Bento Soares and M.Fatima  
Bonaldo.

ORGANISM Homo sapiens  
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;  
Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS

1 (bases 1 to 432)  
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,  
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,  
Trevaaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and  
Wilson, R.

TITLE  
JOURNAL  
COMMENT

The WashU-Merck EST Project  
Unpublished (1995)

GDB: G00-410-049  
Contact: Wilson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810

Email: est@watson.wustl.edu  
High quality sequence stops: 302  
Source: IMAGE Consortium, LNL  
This clone is available royalty-free through LNL ; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES  
source

1..432  
/organism="Homo sapiens"  
/clone="37508"  
/note="human"

BASE COUNT 92 a 120 c 119 g 94 t 7 others

Query Match 66.7%; Score 14; DB 81; Length 432;  
Best Local Similarity 80.0%; Pred. No. 6.06e-02;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 407 acntcggtctgtgttc 426  
||| ||| ||||| |||||  
Qy 1 ACCTCGGTATCGGTGTTTC 20

RESULT 13  
LOCUS N52367 483 bp mRNA EST 15-FEB-1996  
DEFINITION y22906.s1 Homo sapiens cDNA clone 284507 3' .  
ACCESSION N52367  
NID g1193533

KEYWORDS  
SOURCE

EST.  
human clone=284507 primer=m13 -40 forward library=Soares multiple  
sclerosis 2NBHSP vector=pT73D (Pharmacia) with a modified  
polylinker V TYPE: phagemid host=DH10B (ampicillin resistant)  
Rsite1=Not I Rsite2=Eco RI 46 year old male. 1st strand cDNA was  
primed with a Not I - oligo(dT) primer  
[5'-TGTTCACCAATCTGAAGTGGAGCGCGCATTTTTTTTTTTTTTTT-3'],  
double-stranded cDNA was size selected, ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not I and Eco  
RI sites of a modified pT7 vector (Pharmacia). Library went  
through one round of normalization to a Cot = 5. Library  
constructed by Bento Soares and M.Fatima Bonaldo. RNA from 4  
multiple sclerosis lesions from one patient was kindly provided by  
Dr. Kevin G. Becker (NINDS/NIH).

ORGANISM Homo sapiens  
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;  
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;  
Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;  
Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS

1 (bases 1 to 483)  
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,  
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,  
Trevaaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and  
Wilson, R.

TITLE  
JOURNAL

The WashU-Merck EST Project  
Unpublished (1995)



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US-08-612-929-54.rst

15

Source: IMAGE Consortium, L1NL  
This clone is available royalty-free through L1NL ; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Trace considered overall poor quality.

FEATURES

source  
1..190  
/organism="Homo sapiens"  
/clone="Z31830"  
<1..>190  
3 a 44 c 64 g 54 t 25 others  
BASE COUNT  
ORIGIN  
Query Match 61.9%; Score 13; DB 34; Length 190;  
Best Local Similarity 84.2%; Pred.No. 1.17e+00;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 2 cctccgggtggtgtctc 20  
||||||| ||| ||| ||  
Qy 2 CCTCCGGTATGGGTGTTTC 20

Search completed: Wed Mar 19 08:42:58 1997  
Job time : 66 secs.

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MParch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed Mar 19 08:41:17 1997; MasPar time 10.34 Seconds  
177.156 Million cell updates/sec

Tabular output not generated.

Title: &gt;US-08-612-929-54

Description: (1-21) from US08612929.seq

Perfect Score: 21

N.A. Sequence: 1 ACCTCGGGTATGGCTGTTC 21

Comp: TGGAGGCCATACCCACARAGG

Scoring table: TABLE default

Gap 10

Nmatch STD : Dbase 0; Query 0

Searched: 113505 seqs, 43611913 bases x 2

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: n-geneseq25

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13  
14:part14 15:part15 16:part16 17:part17 18:part18  
19:part19 20:part20 21:part21 22:part22

Statistics: Mean 5.199; Variance 2.769; scale 1.878

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query Match	Length	ID	Description	Pred. No.
1	21	100.0	117 14	Q83498 Heavy chain variable	9.79e-04
2	21	100.0	423 14	Q83493 Humanized antibody 3B	9.79e-04
c 3	20	95.2	91 9	Q51746 Oligonucleotide probe	4.23e-03
4	15	71.4	91 9	Q51746 Oligonucleotide probe	4.48e+00
c 5	14	66.7	10897 20	T09187 MuTV putative oncogen	1.65e+01
6	13	61.9	32 17	T06048 Primer for subcloning	5.81e+01
7	13	61.9	85 7	Q44071 HUH-G14.	5.81e+01
8	13	61.9	85 7	Q44055 HUH-G4.	5.81e+01

c 9	13	61.9	330 18	T19543	Human gene signature	5.81e+01
c 10	13	61.9	354 7	Q42266	Encodes gamma chain V	5.81e+01
c 11	13	61.9	354 13	Q75544	Humanized antibody he	5.81e+01
c 12	13	61.9	354 7	Q42267	Encodes gamma chain V	5.81e+01
c 13	13	61.9	357 12	Q70373	Chimeric anti HIV ant	5.81e+01
c 14	13	61.9	357 11	Q65555	Mouse-human chimeric	5.81e+01
c 15	13	61.9	357 12	Q70369	Anti HIV antibody hea	5.81e+01
c 16	13	61.9	357 11	Q65551	Mouse anti-HIV mu39.1	5.81e+01
c 17	13	61.9	360 19	T09300	Marine anti-Protein C	5.81e+01
c 18	13	61.9	414 6	Q34573	Plasmod pXOM1.	5.81e+01
c 19	13	61.9	417 19	T09299	Murine anti-Protein C	5.81e+01
c 20	13	61.9	417 18	T19077	Human gene signature	5.81e+01
c 21	13	61.9	423 14	Q83492	Chimeric antibody 3B9	5.81e+01
c 22	13	61.9	425 7	Q44060	H65 heavy chain varia	5.81e+01
c 23	13	61.9	483 14	Q83491	Mouse MAb 3B9 heavy c	5.81e+01
c 24	13	61.9	723 7	Q42284	V-J(kappa)/(Gly)4Ser	5.81e+01
c 25	13	61.9	723 7	Q42285	V-J(gamma)/(Gly)4Ser	5.81e+01
c 26	13	61.9	738 12	Q70612	IL-6 binding inhibito	5.81e+01
c 27	13	61.9	769 6	Q37624	Vdelta1 (genomic).	5.81e+01
c 28	13	61.9	1065 17	T02472	Cowpox virus T2-equiv	5.81e+01
c 29	13	61.9	1107 11	Q68716	GDI D4 cDNA.	5.81e+01
c 30	13	61.9	1159 7	Q40592	JSC1 precursor DNA.	5.81e+01
c 31	13	61.9	1405 13	Q79667	Escherichia coli glyA	5.81e+01
c 32	13	61.9	1406 13	Q75378	DNA encoding the E. c	5.81e+01
c 33	13	61.9	2054 2	Q11648	D-aminopeptidase gene	5.81e+01
c 34	13	61.9	2559 2	Q13850	PhibacIn PSBX fragmen	5.81e+01
c 35	13	61.9	2896 4	Q24135	Vector comprising alp	5.81e+01
c 36	13	61.9	3273 13	Q78178	Ammonia monooxygenase	5.81e+01
c 37	13	61.9	8808 22	T32227	Plasmod pBE146.	5.81e+01
c 38	13	61.9	9643 1	N80859	Sequence of entire HI	5.81e+01
c 39	13	61.9	9672 3	Q20616	ROD HIV-2 isolate com	5.81e+01
c 40	13	61.9	11141 20	T15820	TBE virus strain Neud	5.81e+01
c 41	13	61.9	12364 2	Q13607	ACV synthetase gene,	5.81e+01
c 42	13	61.9	12364 2	Q13547	ACVS gene pcbAB.	5.81e+01
c 43	12	57.1	84 22	T15288	cDNA encoding rat pre	1.96e+02
c 44	12	57.1	4234 15	Q87819	Agmenellum quadruplic	1.96e+02
c 45	12	57.1	6513 22	T18986	Drosophila para volta	1.96e+02

## ALIGNMENTS

RESULT	1
ID	Q83498 standard; DNA; 117 BP.
AC	Q83498;
DT	20-SEP-1995 (first entry)
DE	Heavy chain variable region fragment.
KW	Humanized antibody; antibody engineering; monoclonal antibody;
KW	MAb; interleukin-4; IL-4; allergy; heavy chain; ss.
OS	Synthetic.
PN	W09507301-A.
PD	16-MAR-1995.
PF	07-SEP-1994; U10308.
PR	07-SEP-1993; US-117366.
PR	14-OCT-1993; US-136783.
PA	(SMIK ) SMITHKLINE BEECHAM CORP.
PA	(SMIK ) SMITHKLINE BEECHAM PLC.
PI	Gross MS, Holmes SD, Sylvester DR;
DR	WPI; 95-123387/16.
PT	Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived
PT	from high affinity mAbs - useful in treatment of IL-4-mediated
PT	and IgE-mediated allergic conditions
PS	Example 3; Page 61; 9/pp; English.
CC	A humanized antibody was designed to contain mouse CDRs (from
CC	anti-IL-4 MAb 3B9 MAb) within a human antibody framework. A

Mar 19 08:39

US-08-612-929-54.rmg

3

CC synthetic heavy chain was made using the oligonucleotides given  
CC in Q83498-502 and amplified by PCR using the primers given in  
CC Q83503-04. The construct was ligated into vector pCD, along  
CC with a signal sequence (Q83494) and an IgG1 human constant  
CC region. The CDR gene regions of a pre-existing light chain  
CC framework were replaced with synthetic IL-4 CDR genes constructed  
CC from oligonucleotides given in Q83505-08 (CDR1), Q83509-10 (CDR2),  
CC and Q83511-12 (CDR3). The synthetic VL (Q73986) was ligated into  
CC the vector. The anti-IL4 engineered antibody was expressed in  
CC COS and CHO cells.

SQ Sequence 117 BP; 18 A; 40 C; 28 G; 31 T;

Query Match 100.0%; Score 21; DB 14; Length 117;  
Best Local Similarity 100.0%; Pred. No. 9.79e-04;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 89 acctccggtatgggtgttcc 109  
|||||  
Qy 1 ACCTCCGGTATGGGTGTTC 21

RESULT 2

ID Q83493 standard; cDNA; 423 BP.  
AC Q83493;  
DE 20-SEP-1995 (first entry)  
DT Humanized antibody 3B9 heavy chain.  
KW Humanized antibody; antibody engineering; monoclonal antibody;  
KW MAb; interleukin-4; IL-4; allergy; ds.  
OS Homo sapiens.

FH Key Location/Qualifiers  
FT CDS 1..423  
FT /\*tag= a  
FT sig\_peptide 1..57  
FT /\*tag= b  
FT mat\_peptide 58..423  
FT /\*tag= c  
PN W09507301-A.  
PD 16-MAR-1995.

PF 07-SEP-1994; U10308.  
PR 07-SEP-1993; US-117366.  
PR 14-OCT-1993; US-136783.  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
PA (SMIK ) SMITHKLINE BEECHAM PLC.  
PI Gross MS, Holmes SD, Sylvester DR;  
DR WPI; 95-123387/16.  
DR P-PSDB; R70192.  
PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived  
PT from high affinity mAbs - useful in treatment of IL-4-mediated  
PT and IgE-mediated allergic conditions  
PS Disclosure; Fig.4; 97pp; English.  
CC A humanized antibody heavy chain variable region and signal  
CC sequence is given in R70192. The signal sequence is also  
CC provided in R70193. The CDR sequences of the construct are  
CC identical to the native CDRs of mouse anti-human IL-4 MAb  
CC 3B9 (R70198-200).  
SQ Sequence 423 BP; 84 A; 131 C; 102 G; 106 T;

Query Match 100.0%; Score 21; DB 14; Length 423;  
Best Local Similarity 100.0%; Pred. No. 9.79e-04;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 151 acctccggtatgggtgttcc 171  
|||||  
Qy 1 ACCTCCGGTATGGGTGTTC 21

Mar 19 08:39

US-08-612-929-54.rmg

4

RESULT 3  
ID Q51746 standard; cDNA; 91 BP.

AC Q51746;  
DT 31-MAY-1994 (first entry)  
DE Oligonucleotide probe MK14-A  
KW Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;  
KW ss.

OS Synthetic.  
PN EP-571911-A.  
PD 01-DEC-1993.  
PF 24-MAY-1992; US-889651.  
PR 26-MAY-1992; US-889651.  
PA (BECT ) BECTON DICKINSON CO.  
PI Shank DD, Spears PA;  
DR WPI; 93-378844/48.  
PT New oligo:nucleotide probes specific for Mycobacteria - used for  
PT detection and amplification of Mycobacteria nucleic acid in  
PT samples

PS Claim 3; Page 14; 23pp; English.  
CC Oligonucleotide probe MK14-A consists of nucleotides 5-95 of MK14  
CC (Q51735). It hybridized to all spp. of mycobacteria tested, but  
CC cross reacted to a few non-mycobacterial spp. The probe may  
CC be useful as an initial screen for mycobacterial infection.  
CC See also Q51735-45 and Q51747-59.  
SQ Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;

Query Match 95.2%; Score 20; DB 9; Length 91;  
Best Local Similarity 0.0%; Pred. No. 4.23e-03;  
Matches 0; Conservative 20; Mismatches 0; Indels 0; Gaps 0;

Db 22 vhhhsvhvhhvhhvsvvv 41  
|||||  
Cp 21 GGAAACACCCATACCGGAGG 2

RESULT 4

ID Q51746 standard; cDNA; 91 BP.  
AC Q51746;  
DT 31-MAY-1994 (first entry)  
DE Oligonucleotide probe MK14-A  
KW Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;  
KW ss.  
OS Synthetic.  
PN EP-571911-A.  
PD 01-DEC-1993.  
PF 24-MAY-1992; US-889651.  
PR 26-MAY-1992; US-889651.  
PA (BECT ) BECTON DICKINSON CO.  
PI Shank DD, Spears PA;  
DR WPI; 93-378844/48.

PT New oligonucleotide probes specific for Mycobacteria - used for  
PT detection and amplification of Mycobacteria nucleic acid in  
PT samples

PS Claim 3; Page 14; 23pp; English.  
CC Oligonucleotide probe MK14-A consists of nucleotides 5-95 of MK14  
CC (Q51735). It hybridized to all spp. of mycobacteria tested, but  
CC cross reacted to a few non-mycobacterial spp. The probe may  
CC be useful as an initial screen for mycobacterial infection.  
CC See also Q51735-45 and Q51747-59.  
SQ Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;

Query Match 71.4%; Score 15; DB 9; Length 91;

Best Local Similarity 0.0%; Pred. No. 4.48e+00;  
Matches 0; Conservative 18; Mismatches 3; Indels 0; Gaps 0;

Db 26 havhvhvhhvhhvhhvhhv 46

Oy 1 ACCTCGGTATGGGTGTTCC 21

## RESULT 5

ID T09187 standard; DNA; 10897 BP.  
AC T09187;  
DE MuTu putative oncogene MN genomic DNA.  
KW MuTu; endogenous; cellular component; MN; HeLa cell; diagnosis;  
KW lymphocytic choriomeningitis virus; LCMV; putative oncogene;  
KW treatment; neoplastic; pre-neoplastic; disease; antisense therapy;  
KW antibody; vaccine; vertebrate; immunisation; ss.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT misc\_feature 1973  
FT /tag= a  
FT /note= "given as "?" in specification"  
FT exon 3536..3950  
FT /tag= b  
FT /number= 1  
FT exon 5125..5154  
FT /tag= c  
FT /number= 2  
FT exon 5350..5518  
FT /tag= d  
FT /number= 3  
FT exon 5650..5792  
FT /tag= e  
FT /number= 4  
FT exon 5882..5974  
FT /tag= f  
FT /number= 5  
FT exon 7375..7441  
FT /tag= g  
FT /number= 6  
FT exon 8776..8933  
FT /tag= h  
FT /number= 7  
FT exon 9446..9590  
FT /tag= i  
FT /number= 8  
FT exon 9705..9731  
FT /tag= j  
FT /number= 9  
FT exon 10349..10430  
FT /tag= k  
FT /number= 10  
FT exon 10561..10751  
FT /tag= l  
FT /number= 11  
PN W09534650-A2.  
PD 21-DEC-1995.  
PR 15-JUN-1994; US-260190.  
PR 07-JUN-1995; US-447504.  
PR 07-JUN-1995; US-487077.  
PR 07-JUN-1995; US-481658.  
PR 07-JUN-1995; US-486756.  
PR 07-JUN-1995; US-485049.

PR 07-JUN-1995; US-485862.  
PR 07-JUN-1995; US-485863.  
PA (CIBA ) CIBA CORNING DIAGNOSTICS CORP.  
PA (VIRO-) INST VIROLOGY.  
PI Pastorek J, Pastorekova S, Zavada J;  
DR WPI; 96-049679/05.  
PT MN gene, protein and nucleic acid fragments - used as primers and  
PT probes in the detection of MN antigens and antibodies, and in the  
PT treatment of (pre)neoplastic disease  
PS Claim 1; Fig 3; 102pp; English.  
CC The present sequence is the complete MuTu endogenous cellular  
CC component, MN, genomic DNA, which was isolated from lymphocytic  
CC choriomeningitis virus (LCMV) infected HeLa cells. Persistent LCMV,  
CC the exogenous MuTu transmissible agent (MX), infection increases  
CC the expression level of the MN gene. MN is a putative oncogene,  
CC and can therefore be used in the development of prods. for the  
CC diagnosis and treatment of neoplastic (NP), or pre-NP diseases.  
CC NP diseases can be treated using DNA antisense to MN transcribed  
CC mRNA, anti-MN protein antibodies can be used for the diagnosis NP  
CC or pre-NP diseases and a vaccine contg. immunogenic amounts of the  
CC MN protein can be used to immunise a vertebrate against a NP  
CC disease associated with MN antigen expression.  
SQ Sequence 10897 BP; 2634 A; 2738 C; 2647 G; 2857 T;

Query Match 66.7%; Score 14; DB 20; Length 10897;  
Best Local Similarity 85.0%; Pred. No. 1.65e+01;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 1541 gaaactccctactctgaggt 1560

||||| ||| |||| |||||  
Cp 20 GAACACCCATACCGAGGT 1

## RESULT 6

ID T06048 standard; cDNA; 32 BP.  
AC T06048;  
DT 18-MAR-1996 (first entry)  
DE Primer for subcloning PM95 antigen sequence.  
KW Blowfly larvae; blowfly strike; antigen; PM95; vaccine;  
KW prophylaxis; treatment; Lucilla cuprina; antibody; ss.  
OS Synthetic.  
PN AU9517609-A.  
PD 02-NOV-1995.  
PF 21-APR-1995; 017609.  
PR 22-APR-1994; AU-005235.  
PA (CSIR ) COMMONWEALTH SCI & IND RES ORG.  
PI Casu RE, Eisenmann CH, Tellam RL;  
DR WPI; 96-000017/01.  
PT DNA encoding the blowfly larvae PM95 antigen - used to produce  
PT antigenic compans. for use in vaccines for the prophylaxis or  
PT treatment of blowfly strike in sheep  
PS Example 7; Page 34; 63pp; English.  
CC Host cells transformed with the PM95 antigen coding sequence can be  
CC used for the production of the antigen for its use in a vaccine.  
CC The vaccine is used for the prophylaxis or treatment of blowfly  
CC strike in sheep. The antigen can also be used to produce antibodies  
CC which can be used to provide passive immunisation against blowfly  
CC strike. Two primers (T06048, T06049) were used to subclone the PM95  
CC antigen gene into a baculovirus transfer vector.  
SQ Sequence 32 BP; 6 A; 8 C; 10 G; 8 T;

Query Match 61.9%; Score 13; DB 17; Length 32;  
Best Local Similarity 88.2%; Pred. No. 5.81e+01;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;



Mar 19 08:39

US-08-612-929-S4.rmg

7

Db 8 tcgcgaatgggtgtttc 24  
 |||| |||||  
 Qy 4 TCCTGATGCGGTTC 20

# RESULT 7

ID Q44071 standard; DNA; 85 BP.  
 AC Q44071;  
 DT 28-OCT-1993 (first entry)  
 DE HUH-G14.  
 KW Antibody; variable domain; light; L; heavy; H; PCR;  
 KW polymerase chain reaction; H65; monoclonal antibody; MAB; ss.  
 OS Synthetic.  
 PN W09311794-A.  
 PD 24-JUN-1993.  
 PF 14-DEC-1992; U10906.  
 PR 13-DEC-1991; US-808464.  
 PA (XOMA ) XOMA CORP.  
 PI Fishwild DM, Kohn FR, Little RG, Studnicka GM;  
 DR WPI; 93-213827/26.  
 PT Antibodies prepn. used for treatment of auto-immune diseases - by  
 PT replacement of critical residues to reduce immunogenicity but  
 PT retain binding affinity, etc.  
 PS Example 6; Fig 7b; 160pp; English.  
 CC Example 6 describes the construction of the gene encoding the  
 CC humanised H65 heavy chain contg. the moderate risk residues.  
 CC The humanised heavy chain was assembled from the oligonucleotides  
 CC given in Q44070-75.  
 SQ Sequence 85 BP; 25 A; 21 C; 18 G; 21 T;

Query Match 61.9%; Score 13; DB 7; Length 85;  
 Best Local Similarity 88.2%; Pred. No. 5.81e+01;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 47 ctccagtggtgtgttt 63  
 |||| |||||  
 Qy 3 CTCCGATGCGGTGTTT 19

# RESULT 8

ID Q44055 standard; DNA; 85 BP.  
 AC Q44055;  
 DT 28-OCT-1993 (first entry)  
 DE HUH-G4.  
 KW Antibody; variable domain; light; L; heavy; H; PCR;  
 KW polymerase chain reaction; H65; monoclonal antibody; MAB; ss.  
 OS Synthetic.  
 PN W09311794-A.  
 PD 24-JUN-1993.  
 PF 14-DEC-1992; U10906.  
 PR 13-DEC-1991; US-808464.  
 PA (XOMA ) XOMA CORP.  
 PI Fishwild DM, Kohn FR, Little RG, Studnicka GM;  
 DR WPI; 93-213827/26.  
 PT Antibodies prepn. used for treatment of auto-immune diseases - by  
 PT replacement of critical residues to reduce immunogenicity but  
 PT retain binding affinity, etc.  
 PS Example 2b; Fig 7a; 160pp; English.  
 CC Example 2b describes the construction of the gene encoding the  
 CC humanised H65 heavy chain variable region. The humanised V- and  
 CC J-segments of the heavy chain were assembled from six oligonucleotides  
 CC (Q44052-57). The oligonucleotides were amplified with PCR primers  
 CC (Q44058-59). The DNA sequence of the assembled V/J-region is given

Mar 19 08:39

US-08-612-929-S4.rmg

8

CC in Q44060.  
 SQ Sequence 85 BP; 23 A; 22 C; 18 G; 22 T;  
 Query Match 61.9%; Score 13; DB 7; Length 85;  
 Best Local Similarity 88.2%; Pred. No. 5.81e+01;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 47 ctccagtggtgtgttt 63  
 |||| |||||  
 Qy 3 CTCCGATGCGGTGTTT 19

# RESULT 9

ID T19543 standard; cDNA to mRNA; 330 BP.  
 AC T19543;  
 DT 28-JUN-1996 (first entry)  
 DE Human gene signature HUMGS00607.  
 KW Gene signature; messenger RNA; mRNA; relative abundance; frequency;  
 KW human; cloning; mapping; non-biased library; diagnosis; detection;  
 KW cell typing; abnormal cell function; ss.  
 OS Homo sapiens.  
 PN W09514772-A1.  
 PD 01-JUN-1995.  
 PF 11-NOV-1994; J01916.  
 PR 12-NOV-1993; JP-355504.  
 PA (MATS/) MATSUBARA K.  
 PA (OKUB/) OKUBO K.  
 PI Matsubara K, Okubo K;  
 DR WPI; 95-206931/27.  
 PT Identifying gene signatures in 3'-directed human cDNA library - e.g.  
 PT for diagnosis of abnormal cell function, by preparing cDNA that  
 PT reflects relative abundance of corresp. mRNA in specific human  
 PT tissues

PS Claim 1; Page 413; 2245pp; Japanese.  
 CC A single-stranded DNA (or its complementary strand or the corresp.  
 CC double-stranded DNA) which comprises one of the 7837 "GS" sequences  
 CC given in T19001-T26837 and which is able to hybridise to part of  
 CC human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)  
 CC sequences were obtained from 3'-directed cDNA libraries prepared  
 CC from various human tissues; synthesis of cDNA was initiated from the  
 CC 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-  
 CC untranslated sequence is unique to a particular mRNA species, almost  
 CC all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library  
 CC is constructed so as to reflect accurately the relative abundance of  
 CC different mRNAs in the particular tissue from which it was derived.  
 CC The appearance frequency of a given GS in a cDNA library can be  
 CC determined (esp. using primers and probes derived from the GS  
 CC sequences) as a means of diagnosing abnormal cell function or for  
 CC recognising different cell types.  
 SQ Sequence 330 BP; 61 A; 80 C; 84 G; 89 T;

Query Match 61.9%; Score 13; DB 18; Length 330;  
 Best Local Similarity 84.2%; Pred. No. 5.81e+01;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 85 gaaccaccagcgagg 103  
 |||| |||||  
 Cp 20 GAACACCCATACCGAGG 2

# RESULT 10

ID Q42266 standard; cDNA; 354 BP.  
 AC Q42266;  
 DT 13-SEP-1993 (first entry)

DE Encodes gamma chain V-region of hel H65 antibody fragment.  
 KW Type I ribosome-inactivating protein; ricin; momordin;  
 KW immunoconjugate; autoimmune disease; cell killing; toxin;  
 KW human engineered antibody; variable region; heavy chain;  
 KW cell targeting; chimeric antibody; ss.  
 OS Synthetic.  
 PN W09309130-A.  
 PD 13-MAY-1993.  
 PF 04-NOV-1992; U09487.  
 PR 04-NOV-1991; US-787567.  
 PR 19-JUN-1992; US-901707.  
 PA (XOMA ) XOMA CORP.  
 PI Berhard SL, Better MD, Carroll SF, Lane JA, Lei SP.  
 DR WPI; 93-167617/20.  
 PT Analogues of type I ribosome inactivating protein - useful as  
 PT cytotoxic agents, immuno toxins for treating autoimmune diseases,  
 PT cancer, graft versus host disease and selective cell killing in-vivo  
 PS Example 5; Page 117; 163pp; English.  
 CC The invention covers analogues of the plant type I RIP gelonin  
 CC which have a non-naturally occurring Cys residue in a position  
 CC which enables the analogue to be conjugated via a disulphide  
 CC linkage to a molecule which specifically binds to a target cell.  
 CC Pref. target-cell binding molecules are antibodies or their  
 CC fragments. Human engineered H65 antibody fragments (i.e. selected  
 CC murine-encoded amino acids are replaced to make the H65 antibody  
 CC less immunogenic to humans) were conjugated to various gelonin  
 CC analogues. The resulting immunoconjugates can be used as cytotoxic  
 CC therapeutic agents.  
 SQ Sequence 354 BP; 88 A; 89 C; 98 G; 79 T;

Query Match 61.9%; Score 13; DB 7; Length 354;  
 Best Local Similarity 88.2%; Pred. No. 5.81e+01;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 153 aaacaccacacactggag 169  
 ||||| |||||  
 Cp 19 AAACACCCATACCGGAG 3

RESULT 11  
 ID Q75544 standard; DNA; 354 BP.  
 AC Q75544;  
 DT 27-JUL-1995 (first entry)  
 DE Humanised antibody hel gamma chain.  
 KW Type I ribosome-inactivating proteins; RIPs; humanised antibodies;  
 KW hel gamma chain; cytotoxic therapeutic agents; autoimmune disease;  
 KW cancer; graft-versus-host disease; ss.  
 OS Synthetic.  
 PN W09426910-A.  
 PD 24-NOV-1994.  
 PF 12-MAY-1994; U05348.  
 PR 12-MAY-1993; US-064691.  
 PA (XOMA ) XOMA CORP.  
 PI Better MD, Carroll SS, Studnicka GM, Carroll SF;  
 DR WPI; 95-006804/01.  
 PT Polynucleotide(s) encoding type I ribosome-inactivating proteins  
 PT - which are suitable for use as components of cytotoxic  
 PT therapeutic agents.  
 PS Example 7; Page 171; 221pp; English.  
 CC Q75544 encodes the humanised antibody hel gamma chain, which was  
 CC conjugated to gelonin type I ribosome-activating proteins (RIPs),  
 CC to produce immunoconjugate cytotoxic therapeutic agents  
 CC (CTAs). CTAs can be used in the treatment of diseases where  
 CC the elimination of a particular cell type is desired, such as

CC autoimmune disease, cancer and graft-versus-host disease.  
 SQ Sequence 354 BP; 88 A; 89 C; 98 G; 79 T;

Query Match 61.9%; Score 13; DB 13; Length 354;  
 Best Local Similarity 88.2%; Pred. No. 5.81e+01;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 153 aaacaccacacactggag 169  
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 Cp 19 AAACACCCATACCGGAG 3

RESULT 12  
 ID Q42267 standard; cDNA; 354 BP.  
 AC Q42267;  
 DT 13-SEP-1993 (first entry)  
 DE Encodes gamma chain V-region of he2 and he3 H65 antibody fragment.  
 KW Type I ribosome-inactivating protein; ricin; momordin;  
 KW immunoconjugate; autoimmune disease; cell killing; toxin;  
 KW human engineered antibody; variable region; heavy chain;  
 KW cell targeting; chimeric antibody; ss.  
 OS Synthetic.  
 PN W09309130-A.  
 PD 13-MAY-1993.  
 PF 04-NOV-1992; U09487.  
 PR 04-NOV-1991; US-787567.  
 PR 19-JUN-1992; US-901707.  
 PA (XOMA ) XOMA CORP.  
 PI Berhard SL, Better MD, Carroll SF, Lane JA, Lei SP.  
 DR WPI; 93-167617/20.  
 PT Analogues of type I ribosome inactivating protein - useful as  
 PT cytotoxic agents, immuno toxins for treating autoimmune diseases,  
 PT cancer, graft versus host disease and selective cell killing in-vivo  
 PS Example 5; Page 118; 163pp; English.  
 CC The invention covers analogues of the plant type I RIP gelonin  
 CC which have a non-naturally occurring Cys residue in a position  
 CC which enables the analogue to be conjugated via a disulphide  
 CC linkage to a molecule which specifically binds to a target cell.  
 CC Pref. target-cell binding molecules are antibodies or their  
 CC fragments. Human engineered H65 antibody fragments (i.e. selected  
 CC murine-encoded amino acids are replaced to make the H65 antibody  
 CC less immunogenic to humans) were conjugated to various gelonin  
 CC analogues. The resulting immunoconjugates can be used as cytotoxic  
 CC therapeutic agents.  
 SQ Sequence 354 BP; 83 A; 86 C; 102 G; 83 T;

Query Match 61.9%; Score 13; DB 7; Length 354;  
 Best Local Similarity 88.2%; Pred. No. 5.81e+01;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 153 aaacaccacacactggag 169  
 ||||| |||||  
 Cp 19 AAACACCCATACCGGAG 3

RESULT 13  
 ID Q70373 standard; cDNA to mRNA; 357 BP.  
 AC Q70373;  
 DT 13-MAR-1995 (first entry)  
 DE Chimeric anti HIV antibody heavy chain variable region.  
 KW Antibody; heavy chain; light chain; human immunodeficiency virus;  
 KW HIV; acquired immune deficiency syndrome; AIDS; treatment;  
 KW prophylaxis; Mus musculus; Homo sapiens; ss.  
 OS Chimeric Homo sapiens.

Mar 19 08:39

US-08-612-929-54.rng

11

```
OS Chimeric Mus musculus.
FH Key Location/Qualifiers
FT CDS 1..357
FT /tag= a
FT /product= Antibody heavy chain variable region.
PN W09415969-A.
PD 21-JUL-1994.
PF 14-JAN-1993; J00039.
PR 14-JAN-1993; AU-032671.
PR 14-JAN-1993; WO-J00039.
PA (KAGA ) CHERO SERO THERAPEUTIC RES INST.
PI Eda Y, Kimachi K, Maeda H, Osatomi K, Shiosaki K;
PI Tokiyoshi S;
DR WPI; 94-249145/30.
DR P-PSDB; R60303.
PT Recombinant chimeric anti HIV antibody - useful for the treatment
PT and prevention of HIV
PS Claim 3; Figure 9; 51pp; Japanese.
CC The recombinant antibody heavy chain has neutralising activity
CC against HIV. Chimeric antibodies comprising both mouse and human
CC sequences are useful in the treatment/prevention of AIDS caused by
CC HIV. This sequence is derived from the mu39.1 anti HIV monoclonal
CC antibody producing cell.
SQ Sequence 357 BP; 95 A; 88 C; 100 G; 74 T;

Query Match 61.9%; Score 13; DB 12; Length 357;
Best Local Similarity 88.2%; Pred. No. 5.81e+01;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 153 aaacaccaatactggag 169
||||| |||| ||||
Cp 19 AACACCCATACCGGAG 3

RESULT 14
ID Q65555 standard; cDNA; 357 BP.
AC Q65555;
DT 30-JAN-1995 (first entry)
DE Mouse-human chimeric anti-HIV mu39.1-derived heavy chain V region.
KW Immunoglobulin; heavy chain; anti-HIV antibody; neutralisation;
KW human immunodeficiency virus; variable region; VH chain; murine;
KW chimeric; humanised; ds.
OS Chimeric Mus musculus.
FH Key Location/Qualifiers
FT misc_feature 91..105
FT /tag= a
FT /note= "encodes murine CDR1"
FT misc_feature 148..198
FT /tag= b
FT /note= "encodes murine CDR2"
FT misc_feature 295..324
FT /tag= c
FT /note= "encodes murine CDR3"
PN J06125783-A.
PD 10-MAY-1994.
PF 28-DEC-1991; 359808.
PR 28-DEC-1991; JP-359808.
PA (KAGA-) 2H KAGAKU KESSEI-RYOHO KENKYUSHO.
DR WPI; 94-187942/23.
DR P-PSDB; R55124.
PT Mouse-human chimeric anti-HIV antibody heavy and light chains -
PT and recombinant antibody consisting of the H- and L-chains,
PT useful in AIDS therapy
```

Mar 19 08:39

US-08-612-929-54.rng

12

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PS Claim 1; Fig 9; 22pp; Japanese.
CC Murine monoclonal antibodies mu 39.1 and mu 5.5 both neutralise HIV.
CC The heavy and light chain variable regions from these antibodies
CC were sequenced (Q65551-Q65554). The murine anti-HIV CDRs were
CC introduced into human framework regions to construct chimeric
CC antibodies (Q65555-Q65558).
SQ Sequence 357 BP; 95 A; 88 C; 100 G; 74 T;

Query Match 61.9%; Score 13; DB 11; Length 357;
Best Local Similarity 88.2%; Pred. No. 5.81e+01;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 153 aaacaccaatactggag 169
||||| |||| ||||
Cp 19 AACACCCATACCGGAG 3

RESULT 15
ID Q70369 standard; cDNA to mRNA; 357 BP.
AC Q70369;
DT 09-MAR-1995 (first entry)
DE Anti HIV antibody heavy chain variable region.
KW Antibody; heavy chain; light chain; human immunodeficiency virus;
KW HIV; acquired immune deficiency syndrome; AIDS; treatment;
KW prophylaxis; Mus musculus; Homo sapiens; ss.
OS Mus musculus.
FH Key Location/Qualifiers
FT CDS 1..357
FT /tag= a
FT /product= Antibody heavy chain variable region.
PN W09415969-A.
PD 21-JUL-1994.
PF 14-JAN-1993; J00039.
PR 14-JAN-1993; AU-032671.
PR 14-JAN-1993; WO-J00039.
PA (KAGA ) CHERO SERO THERAPEUTIC RES INST.
PI Eda Y, Kimachi K, Maeda H, Osatomi K, Shiosaki K;
PI Tokiyoshi S;
DR WPI; 94-249145/30.
DR P-PSDB; R60299.
PT Recombinant chimeric anti HIV antibody - useful for the treatment
PT and prevention of HIV
PS Claim 4; Figure 1; 51pp; Japanese.
CC The recombinant antibody heavy chain has neutralising activity
CC against HIV. Chimeric antibodies comprising both mouse and human
CC sequences are useful in the treatment/prevention of AIDS caused by
CC HIV. This sequence is obtained from the mu39.1 anti HIV monoclonal
CC antibody producing cell.
SQ Sequence 357 BP; 104 A; 74 C; 94 G; 85 T;

Query Match 61.9%; Score 13; DB 12; Length 357;
Best Local Similarity 88.2%; Pred. No. 5.81e+01;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 153 aaacaccaatactggag 169
||||| |||| ||||
Cp 19 AACACCCATACCGGAG 3

Search completed: Wed Mar 19 08:41:32 1997
Job time : 15 secs.
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WATERMAN

(TM)

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MPerch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed Mar 19 08:39:54 1997; MasPar time 52.80 Seconds  
Tabular output not generated. 327.560 Million cell updates/sec

Title: >US-08-612-929-54  
Description: (1-21) from US08612929.seq  
Perfect Score: 21  
N.A. Sequence: 1 ACCTCGGATGCGGTTCCT 21  
Comp: TGGAGGCCATACCCACAAAGG

Scoring table: TABLE default  
Gap 10

Nmatch STD : Dbase 0; Query 0

Searched: 279077 seqs, 411808665 bases x 2

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Databases: emb1-new5  
1:BCT 2:FUN 3:INV1 4:INV2 5:ORG 6:MAM 7:VRT 8:PLN 9:PRI  
10:PRO1 11:PRO2 12:ROD 13:SYN 14:UNC 15:VIR

Database: genbank94

16:BCT1 17:BCT2 18:BCT3 19:BCT4 20:BCT5 21:BCT6 22:BCT7  
23:BCT8 24:BCT9 25:INV1 26:INV2 27:INV3 28:INV4 29:INV5  
30:INV6 31:INV7 32:MAM1 33:MAM2 34:MAM3 35:VRT1 36:VRT2  
37:VRT3 38:VRT4 39:VRT5 40:VRT6 41:VRT7 42:VRT8 43:VRT9  
44:PLN1 45:PLN2 46:PLN3 47:PLN4 48:PLN5 49:PLN6 50:PLN7  
51:PRI1 52:PRI2 53:PRI3 54:PRI4 55:PRI5 56:PRI6 57:PRI7  
58:PRI8 59:PRI9 60:PRI10 61:PRI11 62:PRI12 63:PRI13  
64:ROD1 65:ROD2 66:ROD3 67:ROD4 68:ROD5 69:ROD6 70:ROD7  
71:STR 72:SYN 73:UNA 74:VRL1 75:VRL2 76:VRL3 77:VRL4  
78:VRL5 79:VRL6 80:VRL7 81:VRL8

Database: genbank-new5

82:BCT 83:INV1 84:INV2 85:MAM 86:VRT 87:PAT 88:PHG

89:PLN 90:PRI 91:ROD 92:STR 93:SYN 94:UNA 95:VRL

Database: u-emb146 94

96:part1

Statistics: Mean 6.699; Variance 2.391; scale 2.802

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	16	76.2	3312	18	ECPPSGENE	E.coli pps gene for p	2.09e+00
2	16	76.2	3662	18	ECOPPEPSYN	E.coli phosphoenolpyr	2.09e+00
3	15	71.4	438	70	S75897	Ig VH-IgG heavy chain	1.14e+01
4	15	71.4	1661	70	S77714S2	Ifi56-interferon-alpha	1.14e+01
5	15	71.4	1953	56	HSU45983	Human G protein-coupl	1.14e+01
6	15	71.4	1953	9	HS459831	Human G protein-coupl	1.14e+01
7	15	71.4	3233	79	HTVENVSP	Human T-cell leukemia	1.14e+01
8	15	71.4	4657	22	PFINAW	Pseudomonas fluoresce	1.14e+01
9	15	71.4	4824	26	CEU02289	Caenorhabditis elegans	1.14e+01
10	15	71.4	8204	96	MYHP10RF	Bacteriophage HP1 (mu	1.14e+01
11	15	71.4	11215	29	DROUBXX2	Drosophila melanogast	1.14e+01
12	15	71.4	11216	27	DMCTCTGEN	D.melanogaster Cctg g	1.14e+01
13	15	71.4	29989	26	CEUK03C7	Caenorhabditis elegans	1.14e+01
14	15	71.4	32355	41	BHU24159	Bacteriophage HP1 str	1.14e+01
15	15	71.4	36087	26	CELZC21	C. elegans cosmid ZC2	1.14e+01
16	15	71.4	338234	28	CEUJ31961	Drosophila melanogast	1.14e+01
17	14	66.7	228	4	TB18324	Trypanosoma brucei sm	5.77e+01
18	14	66.7	360	4	TB18329	Trypanosoma brucei sm	5.77e+01
19	14	66.7	360	31	TBUI8329	Trypanosoma brucei sm	5.77e+01
20	14	66.7	661	79	HSITRA	Herpes simplex virus	5.77e+01
21	14	66.7	684	36	HEFIGLAAB	H.francisci Ig rearra	5.77e+01
22	14	66.7	810	72	SYNBRDGG	Synthetic Halobacteri	5.77e+01
23	14	66.7	2400	95	HEHS08	Herpes simplex type 1	5.77e+01
24	14	66.7	3259	37	XELKCFB	Xenopus laevis mRNA f	5.77e+01
25	14	66.7	3384	36	HELI122	Heterodontus francisc	5.77e+01
26	14	66.7	3513	47	SCYKR086W	S.cerevisiae chromoso	5.77e+01
27	14	66.7	3939	49	YSCSL2A	Saccharomyces cerevis	5.77e+01
28	14	66.7	3955	49	YSCRAD25A	Saccharomyces cerevis	5.77e+01
29	14	66.7	4733	74	CRTV1	Cymbidium ringspot to	5.77e+01
30	14	66.7	14526	19	ECUNC	E. coli origin of rep	5.77e+01
31	14	66.7	18002	47	SCUNORE1	S. cerevisiae HBS1, MR	5.77e+01
32	14	66.7	21914	25	CEF20B10	Caenorhabditis elegans	5.77e+01
33	14	66.7	26245	95	HSIUS	HSV1 (strain 17) comp	5.77e+01
34	14	66.7	26245	15	HEHSIUS	HSV1 (strain 17) comp	5.77e+01
35	14	66.7	26245	79	HSIUS	HSV1 (strain 17) comp	5.77e+01
36	14	66.7	37093	48	SPAC56F8	S.pombe chromosome I	5.77e+01
37	14	66.7	38661	46	SC9582X	S.cerevisiae chromoso	5.77e+01
38	14	66.7	75317	46	SC4357	S.cerevisiae chromoso	5.77e+01
39	14	66.7	97015	17	BSEGNR	B.subtilis genomic re	5.77e+01
40	14	66.7	124884	75	HEVZVXX	Varicella-Zoster viru	5.77e+01
41	14	66.7	136254	18	ECUUM82	E. coli; the region f	5.77e+01
42	14	66.7	144861	15	HH43400	Human herpesvirus-7 (	5.77e+01
43	14	66.7	152260	15	HEICG	Herpes simplex virus	5.77e+01
44	14	66.7	439885	46	SCCHRX	S. cerevisiae chromos	5.77e+01
45	14	66.7	439885	2	SCCHRIX	S. cerevisiae chromos	5.77e+01

## ALIGNMENTS

RESULT 1  
LOCUS ECPPSGENE 3312 bp DNA  
DEFINITION E.coli pps gene for phosphoenolpyruvate synthase.  
ACCESSION X59381  
NID 942480  
KEYWORDS phosphoenolpyruvate synthase; pps gene; pyruvate.  
SOURCE Escherichia coli.  
ORGANISM Escherichia coli  
Prokaryota; Bacteria; Gracilicutes; Scotobacteria; Facultatively

REFERENCE 1 (bases 1 to 3312)  
AUTHORS Hirsch,H.J.  
TITLE Direct Submission  
JOURNAL Submitted (03-APR-1991) to the EMBL/GenBank/DBJ databases. H.J.,  
Hirsch, Institut fuer Biologie I, RWTH, Worrringer Weg, 5100 Aachen,  
FRG

REFERENCE 2 (bases 1 to 3312)  
AUTHORS Nierbach,M., Kreuzaler,F., Geersee,R.H., Postma,P.W. and  
Hirsch,H.J.

TITLE Cloning and nucleotide sequence of the *Escherichia coli* K-12 *ppsA*  
gene, encoding PEP synthase  
JOURNAL Mol. Gen. Genet. 231 (2), 332-336 (1992)  
MEDLINE 92140374

REFERENCE 3 (bases 1 to 3312)  
AUTHORS Ramseier,T.M., Negre,D., Cortay,J.C., Scarabel,M., Cozzzone,A.J. and  
Saler,M.H. Jr.

TITLE In vitro binding of the pleiotropic transcriptional regulatory  
protein, FruR, to the fru, *pps*, ace, pts and icd operons of  
*Escherichia coli* and *Salmonella typhimurium*

JOURNAL J. Mol. Biol. 234 (1), 28-44 (1993)  
MEDLINE 94047069

## FEATURES

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/note="putative"  
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/EC\_number="2.7.9.2"  
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## CDS

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terminator 3041...3065

BASE COUNT 809 a 803 c 886 g 814 t  
ORIGIN

Query Match 76.2%; Score 16; DB 18; Length 3312;  
Best Local Similarity 94.4%; Pred. No. 2.09e+00;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 769 tccggaatgggtgtttcc 786

||||| |||||||

Qy 4 TCCGGTATGGGTGTTCC 21

RESULT 2  
LOCUS ECOPEPSYN 3662 bp DNA BCT 11-JUN-1991  
DEFINITION *E. coli* phosphoenolpyruvate synthase (*pps*) gene, complete cds.  
ACCESSION M69116  
NID g147145  
KEYWORDS phosphoenolpyruvate synthase.  
SOURCE *Escherichia coli* (sub strain W3110, strain K-12) (library: Sau3AI  
library in pBR322) DNA.

ORGANISM *Escherichia coli*

Prokaryote; Gram-negative facultatively anaerobic rods;  
Enterobacteriaceae.

REFERENCE 1 (bases 1 to 3662)

AUTHORS Holzschu,D.L., McEliver,J.A., Liao,C.C. and Berry,A.

TITLE The cloning and sequence of the *E. coli* *pps* gene

JOURNAL Unpublished (1991)

FEATURES

## source

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/organism="Escherichia coli"

/sub\_strain="W3110"

/strain="K-12"

/sequenced\_mol="DNA"

/tissue\_lib="Sau3AI library in pBR322"

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/map="37 minutes"

/note="putative; putative"

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575..580

/gene="pps"

/map="37 minutes"

/note="putative; putative"

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/map="37 minutes"

646...3027

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/db\_xref="PID:g147146"

/translation="MSNNGSSPLVLWNQLGMNDVDRVGGKNASLGEMITNLSGMGVS  
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VFITSAFLGEMVQGVANPDDEFYVHKPTLAANRPAIVRRTMGSKKIRMYVAPTQEH  
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ECEAVKVRNDNGLTNWEIMIPFVRTDQAKAVVEELARQGLKRGCKIKIMCEIP  
SNALLAEQFLEYDFGFSIGNSMDTQALGLDRDSDGVVSELEDERNDVAKLLSMAIRA  
AKKQKGYVGCQGFSDHEDFAAWLMEEGDSLSINPDTVVQTWLSLAEKK"

BASE COUNT 891 a 902 c 960 g 907 t 2 others  
ORIGIN

Query Match 76.2%; Score 16; DB 18; Length 3662;  
Best Local Similarity 94.4%; Pred. No. 2.09e+00;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 760 tccggaatgggtgtttcc 777

||||| |||||||

Qy 4 TCCGGTATGGGTGTTCC 21

Mar 19 08:39

US-08-612-929-54.rge

5

RESULT 3  
LOCUS S75897 438 bp mRNA ROD 14-JUN-1995  
DEFINITION Ig VH=IgG heavy chain variable region [mice, Ric45.14 U1 hybridoma, secondary variant DMK, mRNA Partial, 438 nt].  
ACCESSION S75897  
NID g861529  
KEYWORDS  
SOURCE mice Ric45.14.U1 hybridoma secondary variant DMK.  
ORGANISM Mus sp.  
REFERENCE 1 (bases 1 to 438)  
AUTHORS Kobrin,B.J., Schiffr,C., Zivion,D., Scharff,M.D. and Spira,G.  
TITLE In vitro activation of a nonproductive immunoglobulin allele by a single base pair insertion  
JOURNAL Hybridoma 13 (4), 257-261 (1994)  
MEDLINE 95104873  
REMARK GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 161740] from the original journal article.  
COMMENT Insertion of a single A converts nonproductive allele to productive one.

FEATURES  
source Location/Qualifiers  
1..438 /organism="Mus sp."  
/note="mice"  
307..438  
/partial  
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/note="Method: conceptual translation supplied by author.  
This sequence comes from Fig. 3."  
/product="IgG heavy chain variable region"  
/db\_xref="PID:g861530"  
/translation="KNFYGSADFYWGQGTTLTVSAKTTPPSVYPLAPGSAQAQNSMVT"

BASE COUNT 100 a 131 c 99 g 108 t  
ORIGIN

Query Match 71.4%; Score 15; DB 70; Length 438;  
Best Local Similarity 94.1%; Pred. No. 1.14e+01;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Db 100 acctctggtatgggtgt 116  
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QY 1 ACCTCCGGTATGGGTGT 17

RESULT 4  
LOCUS S77714S2 1661 bp DNA ROD 26-SEP-1995  
DEFINITION Ifi56-interferon-alpha regulated gene [mice, Genomic, 1661 nt, segment 2 of 2].  
ACCESSION S77715  
NID g998618  
KEYWORDS  
SEGMENT 2 of 2  
SOURCE mice.  
ORGANISM Mus sp.  
REFERENCE 1 (bases 1 to 1661)  
AUTHORS Bluyssen,H.A., Vlietstra,R.J., Faber,P.W., Smit,E.M., Hagemeijer,A. and Trapman,J.  
TITLE Structure, chromosome localization, and regulation of expression of

Mar 19 08:39

US-08-612-929-54.rge

6

the interferon-regulated mouse Ifi54/Ifi56 gene family  
JOURNAL Genomics 24 (1), 137-148 (1994)  
MEDLINE 95203869  
REMARK GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 166055] from the original journal article.  
This sequence comes from Fig. 2B.  
Map location: 19D1.

FEATURES  
source Location/Qualifiers  
1..1661 /organism="Mus sp."  
/note="mice"  
Join(S77714:320..324,66..1452)  
/gene="Ifi56"  
/note="Mismatch(94[1->T]); Description: interferon-alpha regulated gene; Method: conceptual translation supplied by author. This sequence comes from Fig. 2B. Author-given protein sequence is in conflict with the conceptual translation."  
/codon\_start=1  
/db\_xref="PID:g998619"  
/translation="MGENADGQVMEHLQLRCHFTWKLFFENNDDPDEVRISEQVQ FIDIKNPLGMNVLAYVRHLKQQDEALQSEALIQSEQLSKRSIAWNCAMLIH YHRGSLAEAQYVDIKVERVKESFSPRYRLECAEMDCGHALKCGGNYKQAMAC FAKALKVEPENPYNTGYAVAYRQDLDNFIISLEPRKAVRLNPEDPYLKVLLAKL QDLGEHVEAEAHIEALSQSVIRYAAKYFRKRVKALHLNRLAQLASPSGC YLHYQKGLCYKQIISLRTSRNQPRQDNLQALAIHEFQETLKLRTFEMATVC MAEQVETIHQYEEAEAFKALNNKTLVAHIQDILHRYGRFLQFHQSEDKAITLYL KCLVKEKSFARWKLITALEKVAERVQNVHLVESTLLGLVYKLKQEKNAIFYE KALRLTGEWNPAF"

BASE COUNT 463 a 382 c 401 g 415 t  
ORIGIN

Query Match 71.4%; Score 15; DB 70; Length 1661;  
Best Local Similarity 85.7%; Pred. No. 1.14e+01;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Db 1169 acctccgctatgccgtttcc 1189  
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QY 1 ACCTCCGGTATGGGTGTTC 21

RESULT 5  
LOCUS HSU45983 1953 bp DNA PRI 02-APR-1996  
DEFINITION Human G protein-coupled receptor GPR-CY6 gene, complete cds.  
ACCESSION U45983  
NID g1245056  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo. 1 (bases 1 to 1953)  
REFERENCE 1 (bases 1 to 1953)  
AUTHORS Lautens,L.L., Tiffany,H.L., Gao,J.-L., Modi,W., Murphy,P.M. and Bonner,T.I.  
TITLE Cloning, Tissue Distribution and Chromosomal Localization of two potential G-Protein-Linked Chemokine Receptors  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 1953)  
AUTHORS Bonner,T.I.  
TITLE Direct Submission  
JOURNAL Submitted (16-JAN-1996) Tom I. Bonner, Lab of Cell Biology, NIMH, Bldg 36, Rm 3A-17, MSC 4090, Bethesda, MD 20892-4090, USA  
FEATURES  
source Location/Qualifiers  
1..1953



Mar 19 08:39

US-08-612-929-54.rge

9

CKALQCCFINITNSHVSILQERPPLENRLVTGMLNDGLGSLQWAREALQTGTLV  
ALLLVLTAGPCILQRHLPSRVRYPHYSLINPESSL"

BASE COUNT 697 a 1168 c 544 g 812 t 12 others  
ORIGIN

Query Match 71.4%; Score 15; DB 79; Length 3233;  
Best Local Similarity 26.7%; Pred. No. 1.14e+01;  
Matches 4; Conservative 11; Mismatches 0; Indels 0; Gaps 0;

Db 1701 tccdddddiddt 1715  
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Qy 4 TCCGGTAGGGTGT 18

RESULT 8 PFINAW 4657 bp DNA BCT 12-SEP-1993  
LOCUS Pseudomonas fluorescens ice nucleation gene (inaW)  
DEFINITION Pseudomonas fluorescens ice nucleation gene (inaW).  
ACCESSION X04501  
KEYWORDS g45507  
NID  
SOURCE Pseudomonas fluorescens.  
ORGANISM Pseudomonas fluorescens  
Eubacteria; Proteobacteria; gamma subdivision; Pseudomonas.

ice nucleation activity; inaW gene; inverted repeat.

REFERENCE 1 (bases 1 to 4657)  
AUTHORS Warren, G., Corotto, L. and Wolber, P.  
TITLE Conserved repeats in diverged ice nucleation structural genes from two species of Pseudomonas  
JOURNAL Nucleic Acids Res. 14 (20), 8047-8060 (1986)  
MEDLINE 87040772  
COMMENT Data kindly reviewed (21-JUL-1987) by Warren G.

FEATURES  
Location/Qualifiers  
1..4657  
/organism="Pseudomonas fluorescens"  
misc\_feature 649...664  
/note="extragenic homology with inaZ sequence"  
RBS 677..680  
/note="put. rRNA binding site"  
CDS 690..4322  
/note="inaW gene product ( AA 1-1210) "  
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/db\_xref="PID:g45508"  
/translation="MKSEKVLVLTTCANNTHDCLVMPILGLVECKFWEPTIKLENG  
LTGALWQGSQAQLSMNAKWKVCEVTGCDLIFLENNEGKPEPRAEVHVGTRSSAL  
GYISDNVSKHEKCSNLIIEKFTFDVKSETRNISLPALPTVDNMENGVNRSTVNTQ  
TLEAVYGLTIGANQSLIAGYSTAGDSSTLIAGYSTGTSCGDSIIAGYGST  
GTAGDSIIAGYSTGTAGDSSTLIAGYSTGTQTAQVGNLTAGYSTGTAGPDSLLI  
AGYSTGTAGDSSTLIAGYSTGTQTAQVGNLTAGYSTGTAGDSSTLIAGYSTGTAG  
GDSSTLIAGYSTGTQTAQVGNLTAGYSTGTAGDSSTLIAGYSTGTAGDSSTLIAG  
STQTAQVGNLTAGYSTGTAGDSSTLIAGYSTGTAGDSSTLIAGYSTGTAGDSSTLI  
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EQSWLTGYSTGTAGDSSTLIAGYSTGTQTAQVGNLTAGYSTGTAGDSSTLIAGYSTGT  
STTAGYSTGTAGDSSTLIAGYSTGTQTAQVGNLTAGYSTGTAGDSSTLIAGYSTGTAG  
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QSQIQP"

Mar 19 08:39

US-08-612-929-54.rge

10

repeat\_unit 4386..4399  
/note="imp. inverted repeat A"  
terminator 4386..4419  
/note="put. stem-loop structure; pot. transcription  
terminator"  
repeat\_unit 4406..4419  
/note="imp. inverted repeat A"  
terminator 4425..4433  
/note="T-rich segment; put. transcriptional termination  
signal"

BASE COUNT 1124 a 1221 c 1325 g 986 t 1 others  
ORIGIN

Query Match 71.4%; Score 15; DB 22; Length 4657;  
Best Local Similarity 85.7%; Pred. No. 1.14e+01;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 3303 ggaagcaccagacagcaggt 3323  
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Cp 21 GGAACACCCATACCGAGGT 1

RESULT 9  
LOCUS CEU02289 4824 bp mRNA INV 11-JUN-1994  
DEFINITION Caenorhabditis elegans Bristol N2 GTPase-activating protein (CEGAP)  
mRNA, partial cds.  
ACCESSION U02289  
NID g437180  
KEYWORDS  
SOURCE Caenorhabditis elegans.  
ORGANISM Caenorhabditis elegans  
Eucaryotae; Metazoa; Nematoda; Secernentea; Rhabditida;

REFERENCE 1 (bases 1 to 4824)  
AUTHORS Chen, W., Blanc, J. and Lim, L.  
TITLE Characterization of a promiscuous GTPase-activating protein that has a bcr-related domain from Caenorhabditis elegans  
JOURNAL J. Biol. Chem. 269, 820-823 (1994)  
MEDLINE 94117490  
REFERENCE 2 (bases 1 to 4824)  
AUTHORS Chen, W.  
TITLE Direct Submission  
JOURNAL Submitted (29-SEP-1993) Chen W., National University of Singapore, Institute of Molecular & Cell Biology, 10 Kent Ridge Crescent, Singapore 0511

FEATURES  
Location/Qualifiers  
1..4824  
/clone\_lib="lambda ZAP cDNA library"  
/strain="Bristol N2"  
/organism="Caenorhabditis elegans"  
/sex="hermaphrodite"  
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<1..4322  
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/product="GTPase-activating protein"  
/db\_xref="PID:g437181"  
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PSEDGHDDPEETQETISETP IRRSRNRNAS LNRQSSRLGGIDFEKLRLGTARVGD  
NEATAENGTSSSSRKSRDDGLTSPPTVAGPVTTTSTSTSTISGASSTAVAAAA  
ACGVAATTSRQTSSNSVDNSNINEMKMKIRRAPKSYVLATASASWEDVLSSIIANE



QSSSIHDTTSGRELPSSLMGTSIMEMSGCASSATTTTNSGQTSRSINAPHP  
PATRIHQRF TALFNSSKTS DSGEHHKSRMKSRSTS PASRFALP GTTILQROGVARQT  
WYHQEITALGKSGKRNWEDRAVLCCRSLYLCSVPAYTTKTEITELGSHTRVDVCNA  
IVD JAYDMLSSSESKQRHVVRIVTONSEHILTELNTESEMLSWI SVLQSSSEDIATG  
SSVDENELSTGRNNHNAVNSALLHNSQSIAS LASSCSCTATTSEFIANSQHTLQOQ  
QQOQTNQKQOQMETDPSVTPSSSQWATTTSSFFHHHSQACPSRD JENCEAPTATATP  
QLOQSP TANKMETDPSVTPSSSQWATTTSSFFHHHSQACPSRD JENCEAPTATATP  
KSGRRKKSKAAKQSGGSGSGSSGSGSQOQGAAPQVLCVRIADCP TSCEDHVPK  
IVQACVCLVETGYMDTVGTYRIPGNTAAVNALKESLNRGFSDVLSKVESLDPRWD  
VNVSVLWELKRLPELPTDKLYPFFIDANRI STHNRLHKLRLNLRKLPRHYDT  
LFLVLHSELSTKSDVNMKRNALALMFPSIVRPSDDNMATWTHMSDQCKLIELI  
IHYLNMFTDESSTEDVPEQHPADQGNPLEFGYGVGVP TGVSAASFNDMHNLRKA  
NEDQAAAMNEGKQKIKNMLRNSRRKSKLKIESTAPAAVNPRTQPTPSNTS  
AASVESAF CNQVEDRDAIEIESRQTVSPQTS GSNACASSTLQDQSPSLESSLIP  
DTSRTEPIGSSGVDDEKAEARQVQSEMYARRIF IAGAGAAAAATADAEKA  
AIDALANHQSILHLASSPAFEVLSEETREKIRMOKQSHDTKELASGELLKTSPT  
KDLTDALSCTSYDSTTSAPLSTNPP LAVACADQPNSSDYASSDP SPICARNPSTPA  
SRPNSLAI PAOLHATSSGSHQPMRSOKILRLKLSRDPARRHTLSVDVDTLKEG  
RLDKLARWFGIRKSPDVSDEVDSEKHNQEA PPLPAAA PVPVIRTSNLTPTVSGD  
ELL"

3' UTR 4323..4824  
BASE COUNT 1469 a 1121 c 991 g 1243 t  
ORIGIN

Query Match 71.4%; Score 15; DB 26; Length 4824;  
Best Local Similarity 100.0%; Pred. No. 1.14e+01;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 4643 acctccggtatgggt 4657  
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QY 1 ACCTCCGATGGGT 15

RESULT 10  
ID MYHPIORF standard; DNA; PHG; 8204 BP.  
AC M12911;  
DT 16-JUL-1998 (Rel. 16, Created)  
DT 22-APR-1990 (Rel. 23, Last updated, Version 1)  
DE Bacteriophage HP1 (mutant cl) from H.influenzae, partial cds.  
KW Bacteriophage HP1  
OS Bacteriophage HP1  
OC Viridae; ds-DNA nonenveloped viruses; Myoviridae.  
RN [1]  
RP 1-8204  
RX MEDLINE; 85128433.  
RA Benjamin R.C., Fitzmaurice W.P., Huang P.C., Scocca J.J.;  
RT "Nucleotide sequence of cloned DNA segments of the Haemophilus  
influenzae bacteriophage HP1c1";  
RL Gene 31:173-185(1984).  
CC Nine open reading frames (orf's) corresponding to presumed  
CC polypeptides of longer than 90 amino acids have been identified.  
CC All share a common orientation which suggests a probable direction  
CC of transcription.  
FH Key Location/Qualifiers  
FH source 1..8204  
FH /organism="Bacteriophage HP1"  
SQ Sequence 8204 BP; 2682 A; 1536 C; 1840 G; 2146 T; 0 other;

Query Match 71.4%; Score 15; DB 96; Length 8204;  
Best Local Similarity 89.5%; Pred. No. 1.14e+01;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 2830 ggaacacccataacgtag 2848

|||||  
Cp 21 GGAACACCCATACCGAG 3  
RESULT 11  
LOCUS DROUBXX2 11215 bp DNA INV 11-MAY-1994  
DEFINITION Drosophila melanogaster (clone DS05563), centromeric to Ubx gene,  
DNA sequence.  
ACCESSION L32750  
NID 9485331  
KEYWORDS bichorax complex.  
SOURCE Drosophila melanogaster (library: Pl) DNA.  
ORGANISM Drosophila melanogaster  
Eukaryota; Animalia; Metazoa; Arthropoda; Uniramia; Insecta;  
Pterygota; Neoptera; Holometabola; Diptera; Brachycera;  
Cyclorhapha; Schizophora; Drosophiloidea; Drosophilidae.  
REFERENCE 1 (bases 1 to 11215)  
AUTHORS Martin, C.H., Bondoc, M.M., Chiang, A., Cloutier, T., Davis, C.A.,  
Ericsson, C.L., Jaklevic, M.A., Kim, R.J., Lee, M.T., Li, M.,  
Mayeda, C.A., Steiert-El Kheir, A. and Palazzolo, M.J.  
TITLE Sequencing of the antennapedia complex of Drosophila melanogaster  
JOURNAL Unpublished (1994)  
COMMENT Sequence submitted by:  
Human Genome Center and  
Drosophila Genome Center  
Lawrence Berkeley Laboratory  
Berkeley, CA 94720  
e-mail: seq@genome.lbl.gov.  
Location/Qualifiers  
1..11215  
/organism="Drosophila melanogaster"  
/sequenced\_mol="DNA"  
/tissue\_lib="Pl"

misc\_feature 1..11215  
/gene="Ubx"  
/note="Description: Ultrabithorax"  
/db\_xref="FlyBase:FBgn0003944"

BASE COUNT 3034 a 2457 c 2515 g 3209 t  
ORIGIN

Query Match 71.4%; Score 15; DB 29; Length 11215;  
Best Local Similarity 85.7%; Pred. No. 1.14e+01;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 9765 accaccgtctctgggtttcc 9785  
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QY 1 ACCTCCGATGGGTGTTTCC 21

RESULT 12  
LOCUS DMCCTGGEN 11216 bp DNA INV 19-FEB-1996  
DEFINITION D.melanogaster Cctg gene.  
ACCESSION X95602  
NID g1199815  
KEYWORDS CCT-gamma protein; Cctg gene.  
SOURCE fruit fly.  
ORGANISM Drosophila melanogaster  
Eukaryota; mitochondrial eukaryotes; Metazoa; Arthropoda;  
Tracheata; Insecta; Pterygota; Diptera; Brachycera; Muscomorpha;  
Ephydroidea; Drosophilidae; Drosophila; Sophophora.  
REFERENCE 1 (bases 1 to 11216)  
AUTHORS Walkley, N.A. and Malik, A.N.  
TITLE Drosophila melanogaster Pl genomic clone DS05563 contains the  
chaperonin-encoding gene Cctg

JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 11216)  
AUTHORS Walkley,N.A.  
TITLE Direct Submission  
JOURNAL Submitted (09-FEB-1996) N.A. Walkley, School of Molecular & Medical  
Bioscience, University of Wales, College of Cardiff, PO Box 911,  
Cardiff CF1 3US, UK  
COMMENT Related sequence L32750, FLYBASE FBgn0003944.  
FEATURES Location/Qualifiers

source  
1..11216  
/organism="Drosophila melanogaster"  
complement(join(534..1572,1639..2138,2224..2284,  
2340..2377))  
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/codon\_start=1  
/product="CCT-gamma protein"  
/db\_xref="PID:g119816"  
/translation="MFGGQPIVLISDNTKRESGRKVOLENIQAKIAIDVIRTCLG  
PQAMKMLDPMGGIVMNDGNALIREITVQHPAKSMIEIARTODEVGDGTTTSVIV  
LAGELAAAEPLAQQIHPTVITIRYREALEIVHLSQSLQIDVDRKAKWADVK  
ACVCTKEIGKNSDLAKIALDAVETVLSNGRLEVDIKRYAKVEKIPGGAIEESCVL  
KGMINKDVTHKMRRLIENPRIVLDCSLEYKKGESQTNVELIGEQDFTRMLQIEE  
FVQRICADIIAVKQDILVFTKGVSDLAQHYLLKAGITAIRLRKTDNLRIRACGATI  
VNRTEELTEKQVGTGAGLEEVKKIGDEYFVTECKEPAKCTILLRGASKDIINETER  
NLQDLHARNVILVLEPLVAGGVAVEMASQLLRKQKGYTVAVAHLEIIPRTLQ  
NCGANTRALTRAKHSHITGDGVCAGIDGESGETVMNVNITWEP LAVKIQTYKT  
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complement(534..1572)  
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intron complement(1573..1638)  
/gene="Cctg"  
/number=3  
exon complement(1639..2138)  
/gene="Cctg"  
/number=3  
intron complement(2139..2223)  
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exon complement(2224..2284)  
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intron complement(2285..2339)  
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exon complement(2340..2377)  
/gene="Cctg"  
/number=1

BASE COUNT 3034 a 2457 c 2515 g 3209 t 1 others  
ORIGIN  
Query Match 71.4%; Score 15; DB 27; Length 11216;  
Best Local Similarity 85.7%; Pred. No. 1.14e+01;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 9766 accaccgtctgggtgttcc 9786  
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QY 1 ACCTCGGTATGGGTGTTCC 21

RESULT 13  
LOCUS CELK03C7 29989 bp DNA INV 09-NOV-1995  
DEFINITION Caenorhabditis elegans cosmid K03C7.  
ACCESSION U40059

NID g1055170  
KEYWORDS  
SOURCE  
ORGANISM  
Caenorhabditis elegans strain=Bristol N2.  
Eukaryotae; mitochondrial eukaryotes; Metazoa; Nematoda;  
Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea;  
Rhabditidae; Caenorhabditis.

REFERENCE 1 (bases 1 to 29989)  
AUTHORS Wilson,R., Ainscough,R., Anderson,K., Baynes,C., Berks,M.,  
Bonfield,J., Burton,J., Connell,M., Copsey,T., Cooper,J.,  
Coulson,A., Craxton,M., Dear,S., Du,Z., Durbin,R., Favello,A.,  
Fulton,L., Gardner,A., Green,P., Hawkins,T., Hillier,L., Jier,M.,  
Johnston,L., Jones,M., Kershaw,J., Kirsten,J., Laister,N., B.,  
Latreille,P., Lightning,J., Lloyd,C., McMurray,A., Mortimore,B.,  
O'Callaghan,M., Parsons,J., Percy,C., Rifken,L., Roopra,A.,  
Saunders,D., Showkeen,R., Smaldon,N., Smith,A., Sonnhammer,E.,  
Staden,R., Sulston,J., Thierry-Mieg,J., Thomas,K., Vaudin,M.,  
Vaughan,K., Waterston,R., Watson,A., Weinstock,L.,  
Wilkinson-Sproat,J. and Wohldman,P.  
2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
elegans

JOURNAL Nature 368 (6466), 32-38 (1994)  
MEDLINE 94150718  
REFERENCE 2 (bases 1 to 29989)  
AUTHORS Leimbach,D.  
TITLE The sequence of C. elegans cosmid K03C7  
JOURNAL Unpublished (1995)  
REFERENCE 3 (bases 1 to 29989)  
AUTHORS Waterston,R.  
TITLE Direct Submission  
JOURNAL Submitted (05-NOV-1995) Robert Waterston

Submitted by:  
Genome Sequencing Center  
Department of Genetics, Washington University,  
St. Louis, MO 63110, USA, and  
Sanger Centre, Hinxton Hall  
Cambridge CB10 1RQ, England  
e-mail: tw@nematode.wustl.edu and jess@sanger.ac.uk  
NEIGHBOR COSMID INFORMATION:  
The 5' cosmid is F35A5, 400 bp overlap; 3' cosmid is 2C64, 500 bp  
overlap. Actual start of this cosmid is at base position 397 of  
CELK03C7; actual end is at 6975 of CEL2C64

NOTES:  
Coding sequences below are predicted from computer analysis, using  
the program GeneFinder(P. Green and L. Hillier, ms in preparation).

FEATURES Location/Qualifiers  
source 1..29989  
/organism="Caenorhabditis elegans"  
join(190..715,1068..2436,2479..2540,2585..2778,3325..3411,  
3456..3590,3913..4110)  
/evidence=not\_experimental  
/gene="K03C7.1"  
/map="X"  
/codon\_start=1  
/db\_xref="PID:g1055171"  
/translation="MPAPKKPSDEPADSLGGPKPKDKPLASKAPAKKPSSETPKPEV  
PKELPKAEPKPAAPKKWRPWEDDPEPEEADFTWAPKKPDTEDPADSLGEPK  
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PAPKKPTEDLADPEPKPAAPKKWRPWEDDPEPEEADYTMPAPKKPDTEDPA  
DP1GGPKPKLAKAPAKKPTDKPKSKDVPEAPKPAEPKPAAPKKWRPWEDD  
DEPEEADFTWAPKKPDTEDPADP1GGPKPKDKLAKKAPSKPTDKPKDKLPKE  
EPKPAEPKPAAPKKWRPWEDDPEPEEADFTWAPKKPDTEDPADP1GGPKKKD  
PKLAKAPAKKPTDKPKKDAFKDAKPTPEEPKPAVPKWKWPWEEDDPEPEEAD

FTMPAKKPDTEADPADLGGCNKKPKLAKKAPTCKPADKPKSEEPKPVAPKKWRP  
PWEEDPDDEPADTVP IKPGEDEDEPADDEEPEDEAEDEPKKKPKKRRKRP  
KKKPVPEKKEPTPEVPVPKAPKWIAP IKKPEEP IPMPKPKTIAENKEERIPALR  
YAKKRELEVTPVPVPEQVTAALITQEGMAGFSRAANVEVNF GDRP IVQAVDSK  
TVPI LNDKSKANRSGMTAFCAPREIDONVVDHKKSGOIIPI LAKGTIVVPHGEY  
GTIRQTDVYKDGKPKGMSHSGEISRQFIANSKERAAGSNLLDKRRITIIISDALPQ  
SKECEAMPIAMFDRGAVETREGSEFSRFLPVNTWATCGYILMSYADEMKCKNIIPQVN  
\*

CDS complement (join (6883..7232, 8236..8374, 9093..9314,  
9874..9969))

/evidence=not experimental

/gene="K03C7.2"

/map="X"

/note="contains similarity to the fork-head DNA binding

domain"

/codon\_start=1

/db\_xref="PID:g1055172"

/translation="MTTECKLIEFVLYQSAVMPFEPSPOLPPKKNMOLLRSPIQIPS  
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ELSDKQTLRRNRQPPALAKKSDAGTTLRRDRDSSGSGETSPSPQSPISPPNENP  
MPSVQALNVLELLSGMNDYKGTFLFQNNYRTSELKQSIYVILLHFTNVLFQI"  
complement (join (15975..16084, 17527..17753, 17806..18044))  
/evidence=not experimental

/gene="K03C7.3"

/map="X"

/codon\_start=1

/db\_xref="PID:g1055173"

/translation="MSTCPMRGLQKRLSDGKKDASFECVTLKLSVFCARKKKRFFL  
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RFSFLSHQHNVSXKHLAPLGIFYRFFFLRHCFALFETENGEMWNCGQCEPPVA  
ALALFQDPDEQETIANQKSNDFFLGACPA"

BASE COUNT 10357 a 5252 c 6025 g 8355 t  
ORIGIN

Query Match 71.44; Score 15; DB 26; Length 29989;

Best Local Similarity 89.54; Pred. No. 1.14e+01;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 1019 gaacacccaacccgaagg 1037

||||| ||||| ||||| |||

Cp 20 GAAACACCCATACCGAGG 2

RESULT 14

LOCUS BRU24159 32355 bp DNA PHG 01-NOV-1995

DEFINITION Bacteriophage HP1 strain HP1cl, complete genome.

ACCESSION U24159 006847 M28366 M12911 M22941 M12910 M15313

NID g1046235

KEYWORDS

SOURCE Bacteriophage HP1.

ORGANISM Bacteriophage HP1

REFERENCE 1 Viruses; deDNA viruses, no RNA stage; Tailed phages; Myoviridae.

1 (bases 1 to 32355)

Esposito, D., Fitzmaurice, W.P., Benjamin, R.C., Goodman, S.D. and

Scocca, J.J.

TITLE The complete nucleotide sequence of the genome of Bacteriophage

HP1, a temperate phage of Haemophilus influenzae

JOURNAL Unpublished (1995)

REFERENCE 2 (bases 1 to 6506)

Esposito, D. and Scocca, J.J.

AUTHORS Identification of an HP1 phage protein required for site-specific

TITLE excision

JOURNAL Mol. Microbiol. 13 (4), 685-695 (1994)

MEDLINE 95089704

REFERENCE 3 (bases 1 to 2363)

AUTHORS Goodman, S.D. and Scocca, J.J.

TITLE Nucleotide sequence and expression of the gene for the

site-specific integration protein from bacteriophage HP1 of

Haemophilus influenzae

JOURNAL J. Bacteriol. 171 (8), 4232-4240 (1989)

MEDLINE 89327135

REFERENCE 4 (bases 17471 to 25675)

AUTHORS Benjamin, R.C., Fitzmaurice, W.P., Huang, P.C. and Scocca, J.J.

TITLE Nucleotide sequence of cloned DNA segments of the Haemophilus

influenzae bacteriophage HP1cl

Gene 31 (1-3), 173-185 (1984)

JOURNAL MEDLINE 85128433

REFERENCE 5 (bases 1 to 2357; 32265 to 32355)

AUTHORS Fitzmaurice, W.P., Waldman, A.S., Benjamin, R.C., Huang, P.C. and

Scocca, J.J.

TITLE Nucleotide sequence and properties of the cohesive DNA termini from

bacteriophage HP1cl of Haemophilus influenzae Rd

Gene 31 (1-3), 197-203 (1984)

MEDLINE 85128435

REFERENCE 6 (bases 1 to 858)

AUTHORS Waldman, A.S., Goodman, S.D. and Scocca, J.J.

TITLE Nucleotide sequences and properties of the sites involved in

lysogenic insertion of the bacteriophage HP1cl genome into the

Haemophilus influenzae chromosome

J. Bacteriol. 169 (1), 238-246 (1987)

MEDLINE 87083373

REFERENCE 7 (bases 1 to 32355)

AUTHORS Esposito, D., Fitzmaurice, W.P., Benjamin, R.C., Goodman, S.D. and

Scocca, J.J.

TITLE Direct Submission

JOURNAL Submitted (04-APR-1995) Dominic Esposito, Biochemistry, The Johns

Hopkins University School of Public Health, 615 North Wolfe Street,

Baltimore, MD 21205, USA

FEATURES

source

1..32355

/organism="Bacteriophage HP1"

/strain="HP1cl"

misc\_feature

1..9

/note="cosL; left cohesive end"

251..694

/note="attP; bacterial attachment site"

complement (698..1711)

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NAKIFADYRRRLDGEFSVKNKPPKATVNRHAYLRVFNELKSLRKWTENPLDG

VALKEKETELAFYERDIYRLIAECDNSNPDLGLIVRICALATGARWSEATLTQSQ

VMPKTIPTWTKSKNRITVPISKELFDMLPKRGLFNDAYESFNNAVIRAEITLPKG

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LTVNQRRHANDYLRD ILDRVLRQVFSQYNVNVDF LQAFINTPQWLLSVKDEHQARVQ
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RFQDCDSHFLKNGIEKNEDIGQYFYQLYKWCIEIAFSAGEFKIPHEKIENDKRIKA
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Note: remainder of annotations omitted.

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Best Local Similarity 89.5%; Pred. No. 1.14e+01;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 20301 ggaaacaccataacgtag 20319

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Cp 21 GGAAACACCATACCGGAG 3

RESULT 15  
LOCUS CELZC21 36087 bp DNA INV 22-OCT-1993  
DEFINITION C. elegans cosmid ZC21.  
ACCESSION L16685 L18807  
NID 9289729  
KEYWORDS breakpoint cluster region protein; dual bar protein;  
transient receptor potential protein.  
SOURCE Caenorhabditis elegans (strain Bristol N2) hermaphrodite mixed  
whole animal DNA.  
ORGANISM Caenorhabditis elegans  
Eukaryota; Animalia; Eumetazoa; Nematoda; Secernentea; Rhabditida;  
Rhabditina; Rhabditidae; Rhabditidae.  
REFERENCE 1 (bases 1 to 36087)  
AUTHORS Sulston, J., Du, Z., Thomas, K., Wilson, R., Hillier, L., Staden, R.,  
Halloran, N., Green, P., Thierry-Mieg, J., Qiu, L., Dear, S.,  
Coulson, A., Craxton, M., Durbini, R., Berks, M., Metzstein, M.,  
Hawkins, T., Ainscough, R. and Waterston, R.  
TITLE The C.elegans genome sequencing project: A beginning  
JOURNAL Nature 356, 37-41 (1992)  
MEDLINE 92168156  
REFERENCE 2 (bases 1 to 36087)  
AUTHORS Du, Z. and Waterston, R.  
TITLE Sequence of the C. elegans cosmid ZC21  
JOURNAL Unpublished (1993) see COMMENT for author address  
COMMENT Submitted by:  
Nematode Sequencing Project  
Department of Genetics, Washington University,  
St. Louis, MO 63110, USA, and  
MRC Laboratory of Molecular Biology,  
Cambridge CB2 2QH, England  
e-mail: rwenematode.wustl.edu and jes@cele.mrc-lmba.cam.ac.uk NOTE:  
Coding sequences below are predicted from computer analysis, using  
the program Genefinder (P. Green and L. Hillier, in preparation)  
Neighboring cosmid information:  
This sequence is the entire sequence of C. elegans cosmid ZC21.  
Bases 1 to 200 of this cosmid correspond to bases 10234 to 10433 of  
the C. elegans cosmid C04D8 entry (GenBank: L16687). Bases 1 to  
200 of the GenBank entry for cosmid C02D5 (GenBank: CELC02D5)  
correspond to bases 35888 to 36087 of this entry.  
The end of the actual sequence of the C04D8 cosmid is at 7298 of  
this entry.  
The beginning of the actual C02D5 cosmid sequence is at 22573 of  
this entry.  
The beginning of the actual K10C7 cosmid sequence is at 30071 of  
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/note="putative"  
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exon

CDS

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2360..2456  
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FLRKLPEPLLDKLYPFFIDANRISTHNRLLKRLNLRKLPHPHYDTLRLFLVHSE  
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5854..6064  
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14870..15023  
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exon

CDS

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Note: remainder of annotations omitted.
Query Match      71.4%; Score 15; DB 26; Length 36087;
Best Local Similarity 100.0%; Pred. No. 1.14e+01;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 ACCTCCGGTATGGGT 15
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Search completed: Wed Mar 19 08:40:58 1997
Job time : 64 secs.
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\*\*\*\*\*

WATERMAN

(TM)

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Release 2.1D John F. Collins, BioComputing Research Unit.  
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MPPerch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed Mar 19 08:45:22 1997; MasPar time 68.40 Seconds  
309.508 Million cell updates/sec

Tubular output not generated.

Title: >US-08-612-929-55

Description: (1-48) from US08612929.seq

Perfect Score: 48

N.A. Sequence: 1 CACATCTACTGGGACGACGACAAACGTTACACCGAGCTCAATCC 48

Comp: GTGTAGATGACCTGCTGCTGTTGCAATGTTGGCTCGGACTTAGG

Scoring table: TABLE default

Gap 10

Nmatch STD : Dbase 0; Query 0

Searched: 630489 seqs, 220513910 bases x 2

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

EST-STS  
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9:EST9 10:EST10 11:EST11 12:EST12 13:EST13 14:EST14  
15:EST15 16:EST16 17:EST17 18:EST18 19:EST19 20:EST20  
21:EST21 22:EST22 23:EST23 24:EST24 25:EST25 26:EST26  
27:EST27 28:EST28 29:EST29 30:EST30 31:EST31 32:EST32  
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120:EST120 121:EST121 122:EST122 123:EST123 124:EST124  
125:EST125 126:EST126 127:EST127 128:EST128 129:EST129

Database:

EST-STS-TWO  
100:EST100 101:EST101 102:EST102 103:EST103 104:EST104  
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120:EST120 121:EST121 122:EST122 123:EST123 124:EST124  
125:EST125 126:EST126 127:EST127 128:EST128 129:EST129

130:STS2 131:STS3 132:STS4 133:STS5 134:STS6 135:STS7  
136:STS8 137:STS9 138:STS10 139:STS11 140:STS12  
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151:STS23 152:STS24 153:STS25 154:STS26 155:STS27  
156:STS28 157:STS29 158:STS30 159:STS31 160:STS32  
161:STS33 162:STS34 163:STS35 164:STS36 165:STS37  
166:STS38 167:STS39 168:STS40 169:STS41 170:STS42  
171:STS43 172:STS44 173:STS45 174:STS46

Statistics: Mean 7.317; Variance 1.357; scale 5.393

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	18	37.5	490	56	N31150	yx52q08.r1 Homo sapie	1.35e-05
2	17	35.4	208	102	R1C50764A	Rice cDNA, partial se	3.42e-04
3	17	35.4	291	38	HSB14G121	H. sapiens partial cD	3.42e-04
4	17	35.4	346	4	CELK059EXR	C.elegans cDNA clone	3.42e-04
5	17	35.4	352	9	H08860	y193e06.s1 Homo sapie	3.42e-04
6	17	35.4	422	162	HS06309	yw32d12.r1 Homo sapie	3.42e-04
7	17	35.4	422	68	N71506	yw32d12.r1 Homo sapie	3.42e-04
8	17	35.4	422	140	N71506	yw32d12.r1 Homo sapie	3.42e-04
9	17	35.4	435	126	T93063	ye24a06.s1 Homo sapie	3.42e-04
10	17	35.4	484	21	H48330	yq77g02.r1 Homo sapie	3.42e-04
11	17	35.4	485	8	H04977	y174a10.s1 Homo sapie	3.42e-04
12	16	33.3	234	61	N49145	yy84a10.r1 Homo sapie	7.63e-03
13	16	33.3	273	46	HUM029C04B	Human fetal brain cDN	7.63e-03
14	16	33.3	296	127	T94533	ye36f07.r1 Homo sapie	7.63e-03
15	16	33.3	312	10	H14807	ym24h12.s1 Homo sapie	7.63e-03
16	16	33.3	342	103	T01202	wEST01923 Caenorhabdi	7.63e-03
17	16	33.3	342	106	T18128	0685c3 Plasmodium fal	7.63e-03
18	16	33.3	368	142	N82994	TgESTzy54g12.r1 Toxop	7.63e-03
19	16	33.3	368	172	TG9944	TgESTzy54g12.r1 Toxop	7.63e-03
20	16	33.3	393	124	T84470	yd47d11.r1 Homo sapie	7.63e-03
21	16	33.3	409	102	R1C511735A	Rice cDNA, partial se	7.63e-03
22	16	33.3	409	127	T96203	ye48b07.r1 Homo sapie	7.63e-03
23	16	33.3	447	15	H29906	yn81a05.r1 Homo sapie	7.63e-03
24	16	33.3	472	160	HS303326	y293f09.r1 Soares mel	7.63e-03
25	16	33.3	472	146	W01303	y293f09.r1 Soares mel	7.63e-03
26	16	33.3	474	12	H20990	yn66a01.r1 Homo sapie	7.63e-03
27	16	33.3	503	103	T02613	0260C3 Plasmodium fal	7.63e-03
28	16	33.3	603	53	N21564	yx60d02.s1 Homo sapie	7.63e-03
29	16	33.3	604	17	H36309	14831 Arabidopsis tha	7.63e-03
30	16	33.3	909	153	W20903	mb95b10.r1 Soares mou	7.63e-03
31	16	33.3	909	171	MM90312	mb95b10.r1 Soares mou	7.63e-03
32	15	31.3	164	172	TC3502	TgESTzy31d10.r1 Toxop	1.48e-01
33	15	31.3	200	8	H07817	khtj009 Brassica napu	1.48e-01
34	15	31.3	246	1	ATTS2648	A. thaliana transcrib	1.48e-01
35	15	31.3	248	38	HSC01A071	H. sapiens partial cD	1.48e-01
36	15	31.3	307	65	N61678	TgESTzy28b04.r1 Toxop	1.48e-01
37	15	31.3	307	140	N61678	TgESTzy28b04.r1 Toxop	1.48e-01
38	15	31.3	348	148	W08966	ma69a01.r1 Soares mou	1.48e-01
39	15	31.3	348	171	MM9662	ma69a01.r1 Soares mou	1.48e-01
40	15	31.3	412	161	HS348324	zcl7a10.s1 Soares par	1.48e-01
41	15	31.3	442	166	HS914305	za47b12.s1 Homo sapie	1.48e-01
42	15	31.3	472	75	R13621	yf60a06.r1 Homo sapie	1.48e-01





4  
RESULT CELK059EXR 346 bp mRNA EST 11-DEC-1995  
LOCUS C.elegans cDNA clone yK59e10 : 3' end, single read.  
DEFINITION D45581  
ACCESSION g1115748  
NID  
KEYWORDS EST (expressed sequence tag).  
SOURCE Caenorhabditis elegans (strain CB1489 him-8(e1489), ) (library:  
Yuji kohara unpublished cDNA) Hermaphrodite, male varied whole  
animal cDNA to mRNA.  
ORGANISM Caenorhabditis elegans  
Eukaryotes; mitochondrial eukaryotes; Metazoa; Nematoda;  
Secernentea; Rhabditia; Rhabditidae; Rhabditina; Rhabditoidea;  
Rhabditidae; Caenorhabditis.  
REFERENCE 1 (bases 1 to 346)  
AUTHORS Kohara,Y., Motohashi,T., Tabara,H., Sugimoto,A., Watanabe,H. and  
Nishigaki,A.  
TITLE Toward an expression map of the C.elegans genome  
JOURNAL Unpublished (1995)  
COMMENT Submitted (23-Aug-1995) to DDBJ by:  
Yuji Kohara  
Gene Library Lab.  
National Institute of Genetics  
Yata 1111, Mishima Shizuoka  
411 Japan  
Phone: 0559-81-6854  
Fax : 0559-81-6855  
Email:ykohara@dbi.nig.ac.jp.

```

FEATURES
  source
    Location/Qualifiers
      1..346
        /organism="Caenorhabditis elegans"
        /strain="CB1489 him-8(e1489)"
        /dev stage="varied"
        /sequenced mol="cDNA to mRNA"
        /sex="Hermaphrodite, male"
        /tissue_type="whole animal"
        /clone lib="Yuji kohara unpublished cDNA"
BASE COUNT      128 a   66 c   48 g   96 t   8 others
ORIGIN

Query Match      35.4%; Score 17; DB 4; Length 346;
Best Local Similarity 69.0%; Pred. No. 3.42e-04;
Matches 29; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Db 163 catctaaggacagataagaattacncccaagatgaa 204
      ||||| ||||| | | | | | | | | | | | | | | | |
QY 3 CATCTACGGGACGACGACAAACGTTACAACCGAGCCTGAA 44

RESULT 5
LOCUS H08860 352 bp mRNA EST 23-JUN-1995
DEFINITION Y193e06.s1 Homo sapiens cDNA clone 45751 3'.
ACCESSION H08860
NID 9873682
KEYWORDS EST.
SOURCE
  human clone=45751 library=Soares infant brain LNB vector=Lafmid BA
  host=DH10B (ampicillin resistant) primer=Pr omega -2lm13 Reitel=Not
  I Rsite2=Hind III Whole brain from a 73 days post natal female. 1st
  strand cDNA was primed with a Not I - oligo(df) primer [5'
  AACTCGAACAATTCGCGCGCCGAGGAATTTTTTTTTTTT 3']; double-stranded
  cDNA was ligated to Hind III adaptors (Pharmacia), digested with
  Not I and directionally cloned into the Not I and Hind III sites of
  the Lafmid BA vector. Library went through one round of
  normalization. Library constructed by Bento Soares and M.Fatima
  Bonaldo.
ORGANISM Homo sapiens
  Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata;
  Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
  Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;
  Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
  1 (bases 1 to 352)
    Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
    Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
    Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
    Trevasakis,E., Waterston,R., Williamson,A., Wohlmann,P. and
    Wilson,R.
  The WashU-Merck EST Project
  Unpublished (1995)
GDB: G00-418-292
Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@waton.wustl.edu
High quality sequence stops: 234
Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES
  Location/Qualifiers

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Mar 19 08:44

US-08-612-929-55.rst

7

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source      1..352
            /organism="Homo sapiens"
            /clone="45751"
            /note="human"
BASE COUNT  99 a 83 c 83 g 83 t 4 others
ORIGIN
Query Match 35.4%; Score 17; DB 9; Length 352;
Best Local Similarity 84.0%; Pred. No. 3.42e-04;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 216 gaagacgtcaaacggttacaccaga 240
|| |||| ||||||||| |||
QY 13 GAGCAGCAGCAACGTTACACCGA 37

RESULT 6
ID H8506309 standard; RNA; EST; 422 BP.
AC N71506;
DT 20-MAR-1996 (Rel. 47, Created)
DT 13-APR-1996 (Rel. 47, Last updated, Version 2)
DE yw32d12.r1 Homo sapiens cDNA clone 253943 5'.
KW EST.
OS Homo sapiens (human)
OC Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
OC Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominoidea.
RN [1]
RP 1-422
RA Hillier L., Clark N., Dubouque T., Elliston K., Hawkins M.,
RA Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M.,
RA Parsons J., Rifkin L., Rohlfing T., Tan F., Trevasakis E.,
RA Waterston R., Williamson A., Wohlmann P., Wilson R.;
RT "WashU-Merck EST Project";
RL Unpublished.
CC Contact: Wilson RK WashU-Merck EST Project Washington University
CC School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,
CC MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email:
CC est@watson.wustl.edu High quality sequence stops: 150 Source: IMAGE
CC Consortium, L1NL This clone is available royalty-free through L1NL
CC ; contact the IMAGE Consortium (info@image.llnl.gov) for further
CC information. NCBI gi: 1228218
FH Key Location/Qualifiers
FT source 1..422
FT /organism="Homo sapiens"
FT /clone="253943"
FT /note="human"
FT <1..>422
SQ Sequence 422 BP; 136 A; 94 C; 96 G; 91 T; 5 other;

Query Match 35.4%; Score 17; DB 162; Length 422;
Best Local Similarity 83.3%; Pred. No. 3.42e-04;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 228 ggngtgacgacaaacggtgcaacc 251
||| ||||||||| |||||
QY 11 GGCAGCAGCAACGTTACACCC 34

RESULT 7
LOCUS N71506 422 bp mRNA EST 15-MAR-1996
DEFINITION yw32d12.r1 Homo sapiens cDNA clone 253943 3'.
ACCESSION N71506
NID g1228218

```

Mar 19 08:44

US-08-612-929-55.rst

8

```

KEYWORDS EST.
SOURCE human clone=253943 primer=m13 -40 forward library=Morton Fetal
Cochlea vector=pBluescript SK- host-SOLR cells (kanamycin
resistant) Raitel=EcoRI Raitel2=XhoI The cDNA was oligo (dT) primed
with an XhoI restriction enzyme recognition site and an 18 base
poly dT sequence. For the 5' end, the synthesized cDNA termini
were treated with T4 DNA polymerase and EcoRI adaptors were ligated
to the blunt ends. adaptor linker: GAATTCGGCAGCAG.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 422)
AUTHORS Hillier L., Clark N., Dubouque T., Elliston K., Hawkins M.,
Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M.,
Parsons J., Rifkin L., Rohlfing T., Tan F., Trevasakis E.,
Waterston R., Williamson A., Wohlmann P. and Wilson, R.
WashU-Merck EST Project
Unpublished (1995)

TITLE Contact: Wilson RK
JOURNAL WashU-Merck EST Project
COMMENT Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 150
Source: IMAGE Consortium, L1NL
This clone is available royalty-free through L1NL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES
source
Location/Qualifiers
1..422
/organism="Homo sapiens"
/clone="253943"
/note="human"
mRNA <1..>422
BASE COUNT 136 a 94 c 96 g 91 t 5 others
ORIGIN
Query Match 35.4%; Score 17; DB 68; Length 422;
Best Local Similarity 83.3%; Pred. No. 3.42e-04;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 228 ggngtgacgacaaacggtgcaacc 251
||| ||||||||| |||||
QY 11 GGCAGCAGCAACGTTACACCC 34

RESULT 8
LOCUS N71506 422 bp mRNA EST 02-APR-1996
DEFINITION yw32d12.r1 Homo sapiens cDNA clone 253943 5'.
ACCESSION N71506
NID g1228218
KEYWORDS EST.
SOURCE human clone=253943 primer=reverse ET library=Morton Fetal Cochlea
vector=pBluescript SK- host-SOLR cells (kanamycin resistant)
Raitel=EcoRI Raitel2=XhoI The cDNA was oligo (dT) primed with an
XhoI restriction enzyme recognition site and an 18 base poly dT
sequence. For the 5' end, the synthesized cDNA termini were
treated with T4 DNA polymerase and EcoRI adaptors were ligated to
the blunt ends. adaptor linker: GAATTCGGCAGCAG.
Homo sapiens
ORGANISM Homo sapiens

```

Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS

1 (bases 1 to 422)  
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevaakis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.

TITLE  
JOURNAL  
COMMENT

WashU-Merck EST Project  
Unpublished (1995)  
Contact: Wilson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
High quality sequence stops: 150  
Source: IMAGE Consortium, LLNL

This clone is available royalty-free through LML ; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES  
source

NCBI gi: 1228218  
Location/Qualifiers  
1..422  
/organism="Homo sapiens"  
/clone="253943"  
/note="human"

BASE COUNT  
ORIGIN

mRNA  
136 a 94 c 96 g 91 t 5 others  
<1..>422

Query Match  
Best Local Similarity 83.3%; Score 17; DB 140; Length 422;  
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 228 ggggtgacgacaaacgggtgcaacc 251

Qy 11 GGGACGACGACACGTTACACC 34

RESULT  
LOCUS

T93063 435 bp mRNA EST 22-MAR-1995  
DEFINITION ye24a06.s1 Homo sapiens cDNA clone 118642 3'.

ACCESSION  
NID

T93063  
g724976

KEYWORDS  
SOURCE

EST.  
human clone=118642 library=Stratagene lung (#937210)

vector=pBluescript SK- host=SOIR cells (kanamycin resistant)  
primer=-21m13 RseI=EcoRI RseI2=XhoI Normal lung tissue from a 72  
year old male. Cloned unidirectionally. Primer: Oligo dT. Average  
insert size: 1.0 kb; Uni-ZAP XR Vector; 5' adaptor sequence:  
5'-GAATTCGGCAGCAG-3'; 3' adaptor sequence:  
5'-CTCGAGTTTCTTTTCTTTTCTTTT-3'.

## ORGANISM

Homo sapiens  
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;  
Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS

1 (bases 1 to 435)  
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevaakis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.

TITLE  
JOURNAL  
COMMENT

WashU-Merck EST Project  
Unpublished (1995)

## CONTACT

Contact: Wilson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
High quality sequence stops: 370  
Source: IMAGE Consortium, LLNL  
This clone is available royalty-free through LML ; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES  
source

Location/Qualifiers  
1..435  
/organism="Homo sapiens"  
/clone="118642"  
/note="human"

BASE COUNT  
ORIGIN

120 a 107 c 101 g 95 t 12 others  
Query Match  
Best Local Similarity 84.0%; Score 17; DB 126; Length 435;  
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 208 gaagcgtcaaacggtacagccaga 232

Qy 13 GAGCAGCAGACGTTACACCGCA 37

RESULT  
LOCUS

10 H48330 484 bp mRNA EST 14-SEP-1995  
DEFINITION yq77g02.r1 Homo sapiens cDNA clone 201842 5' similar to SP:S40207  
S40207 RAB12 PROTEIN - ;.

ACCESSION  
NID

H48330  
g986717

KEYWORDS  
SOURCE

EST.  
human clone=201842 primer=M13RP1 library=Soares fetal liver spleen  
INFLS vector=PT73D (Pharmacia) with a modified polylinker  
host=DH10B (ampicillin resistant) RseI=Pac I RseI2=Eco RI Liver  
and spleen from a 20 week-post conception male fetus. 1st strand  
cDNA was primed with a Pac I - oligo(dT) primer [5'  
AACTGGAAGATTAAATTAAGATCTTTTCTTTTCTTTTCTTTT 3'], double-stranded  
cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac  
I and cloned into the Pac I and Eco RI sites of the modified pT7T3  
vector. Library went through one round of normalization. Library  
constructed by Bento Soares and M.Fatima Bonaldo.

## ORGANISM

Homo sapiens  
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;  
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;  
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;  
Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS

1 (bases 1 to 484)  
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaakis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.

TITLE  
JOURNAL  
COMMENT

The WashU-Merck EST Project  
Unpublished (1995)  
Contact: Wilson RK  
WashU-Merck EST Project

Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu

High quality sequence stops: 362

Source: IMAGE Consortium, LNL

This clone is available royalty-free through LNL ; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.

## FEATURES

source  
i..484  
/organism="Homo sapiens"  
/clone="201842"  
/note="human"

BASE COUNT 144 a 87 c 112 g 136 t 5 others  
ORIGIN  
Query Match 35.4%; Score 17; DB 21; Length 484;  
Best Local Similarity 86.4%; Pred. No. 3.42e-04;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 281 cgttacaccagcgtgagat 302

||||||| || ||||||| ||

Qy 25 CGTTACACCGGCGCTCAAT 46

## RESULT 11

LOCUS H04977 485 bp mRNA EST 21-JUN-1995  
DEFINITION y174a10.s1 Homo sapiens cDNA clone 43636 3' similar to contains Alu  
repetitive element;

ACCESSION H04977

NID 9868529

KEYWORDS EST.

SOURCE human clone=43636 library=Soares infant brain lNIB vector=lafmid BA  
host=DH10B (ampicillin resistant) primer=Promega -21mi3 Rsite1=Not  
I Rsite2=Hind III Whole brain from a 73 days post natal female. 1st  
strand cDNA was primed with a Not I - oligo(dT) primer [5'  
AAGTCAGAAATTCGGCGCCGAGAAATTTTTTTTTT 3']; double-stranded  
cDNA was ligated to Hind III adaptors (Pharmacia), digested with  
Not I and directionally cloned into the Not I and Hind III sites of  
the lafmid BA vector. Library went through one round of  
normalization. Library constructed by Bento Soares and M.Fatima  
Bonaldo.

## ORGANISM

Homo sapiens  
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;  
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;  
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;  
Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.

## REFERENCE

AUTHORS 1 (bases 1 to 485)  
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,  
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,  
Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P. and  
Wilson, R.

TITLE The WashU-Merck EST Project

JOURNAL

COMMENT Unpublished (1995)

GDB: G00-416-177

Contact: Wilson RK

WashU-Merck EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810  
Email: est@watson.wustl.edu  
High quality sequence stops: 395  
Source: IMAGE Consortium, LNL

This clone is available royalty-free through LNL ; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.

## FEATURES

Location/Qualifiers  
source  
i..485  
/organism="Homo sapiens"  
/clone="43636"  
/note="human"

BASE COUNT 93 a 120 c 136 g 132 t 4 others  
ORIGIN

Query Match 35.4%; Score 17; DB 8; Length 485;  
Best Local Similarity 73.0%; Pred. No. 3.42e-04;  
Matches 27; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Db 292 ttccagctgggtgttagttttttatcatcacccag 328

||||| || ||||||| || || || || || || ||

Cp 45 TTTGAGGCTGGGTTGTAAAGCTTTGTCGTCGCCAG 9

## RESULT 12

LOCUS N49145 234 bp mRNA EST 14-FEB-1996  
DEFINITION yy84a10.r1 Homo sapiens cDNA clone 280218 5'.  
ACCESSION N49145

NID q1190311

KEYWORDS EST.

SOURCE human clone=280218 primer=T7 library=Soares multiple sclerosis  
2NHMSP vector=pT73D (Pharmacia) with a modified polylinker  
V\_TYPE: phagemid host=DH10B (ampicillin resistant) Rsite1=Not I  
Rsite2=Eco RI 46 year old male. 1st strand cDNA was primed with a  
Not I - oligo(dT) primer

[5'-TGTACCAATCTGAAGTGGAGCGCCGCAATTTTTTTTTTTTTTTT-3'],  
double-stranded cDNA was size selected, ligated to Eco RI adapters  
(Pharmacia), digested with Not I and cloned into the Not I and Eco  
RI sites of a modified pT7 vector (Pharmacia). Library went  
through one round of normalization to a Cot = 5. Library  
constructed by Bento Soares and M.Fatima Bonaldo. RNA from 4  
multiple sclerosis lesions from one patient was kindly provided by  
Dr. Kevin G. Becker (NINDS/NIH).

## ORGANISM

Homo sapiens  
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;  
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;  
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;  
Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.

## REFERENCE

AUTHORS 1 (bases 1 to 234)  
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,  
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,  
Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P. and  
Wilson, R.

TITLE The WashU-Merck EST Project

JOURNAL

COMMENT Unpublished (1995)

Contact: Wilson RK

WashU-Merck EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence stops: 208

Mar 19 08:44

US-08-612-929-55.rst

13

Source: IMAGE Consortium, LNL  
This clone is available royalty-free through LNL ; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.

# FEATURES

## source

1..234  
/organism="Homo sapiens"  
/clone="280218"  
/note="human"  
<1..>234

BASE COUNT 78 a 37 c 57 g 61 t 1 others  
ORIGIN

Query Match 33.3%; Score 16; DB 61; Length 234;  
Best Local Similarity 83.3%; Pred. No. 7.63e-03;  
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 178 caaacgttacacccgcagcagaa 201

Qy 21 CAAACGTTACACCCGAGCTGAA 44

# RESULT 13

LOCUS HUM029G04B 273 bp mRNA EST 26-AUG-1995  
DEFINITION Human fetal brain cDNA 5'-end GEN-029G04.

ACCESSION D59416

NTD 9960522

KEYWORDS EST (expressed sequence tag); Human fetal brain;  
similar to none (May 29, 1995).

SOURCE Homo sapiens (library: Clontech human fetal brain polyA+ mRNA  
(#6535)) cDNA to mRNA.

## ORGANISM

Eukaryota; Eukaryotes; Metazoa; Chordata;  
Vertebrata; Sarcopterygia; Mammalia; Eutheria; Primates;  
Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 273)

AUTHORS Fujiwara, T., Hirano, H., Katagiri, T., Kawai, A., Kuga, Y., Nagata, M.,  
Okuno, S., Ozaki, K., Shimizu, F., Shimada, Y., Shinomiya, H.,  
Takaichi, A., Takeda, S., Watanabe, T., Takahashi, E.-I., Hirai, Y.,  
Maekawa, H., Shin, S. and Nakamura, Y.

TITLE Unpublished (101)

JOURNAL Unpublished (1995)

COMMENT Submitted (30-May-1995) to DDBJ by:

Tsutomu Fujiwara  
Otsuka GEN Research Institute  
Otsuka Pharmaceutical Co., Ltd  
463-10 Kagasuno Kawauchi-cho  
Tokushima, Tokushima  
771-01

Japan

Phone: 0886-65-2888

Fax : 0886-37-1035.

# FEATURES

## source

1..273  
/organism="Homo sapiens"  
/sequenced\_mol="cDNA to mRNA"  
/clone\_lib="Clontech human fetal brain polyA+ mRNA  
(#6535)"

BASE COUNT 68 a 51 c 67 g 62 t 25 others  
ORIGIN

Query Match 33.3%; Score 16; DB 46; Length 273;  
Best Local Similarity 77.3%; Pred. No. 7.63e-03;  
Matches 17; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Mar 19 08:44

US-08-612-929-55.rst

14

Db 108 atcvtbttggacgacgacac 129

Qy 4 ATCTACTGGGACGACGACAAAC 25

# RESULT 14

LOCUS T94533 296 bp mRNA EST 24-MAR-1995  
DEFINITION ye36f07.r1 Homo sapiens cDNA clone 119845 5'.

ACCESSION T94533

NTD 9728021

KEYWORDS EST.

SOURCE human clone=119845 library=Stratagene lung (#937210)  
vector=pBluescript SK- host-SOLR cells (kanamycin resistant)  
primer=M13RP1 Reitel=EcoRI Reitel=XhoI Normal lung tissue from a 72  
year old male. Cloned unidirectionally. Primer: Oligo dT. Average  
insert size: 1.0 kb; Uni-ZAP XR Vector; 5' adaptor sequence:  
5'-GAATTCGGCAGAG-3'; 3' adaptor sequence:  
5'-CTCGAGTTTTTTTTTTTTTTTT-3'.

# ORGANISM

Homo sapiens  
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;  
Eutheria; Primates; Catarrhini; Homnidae; Homo.

# REFERENCE

1 (bases 1 to 296)

AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,  
Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevas, E.,  
Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.

TITLE WashU-Merck EST Project

JOURNAL Unpublished (1995)

# COMMENT

Contact: Wilson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
High quality sequence stops: 202  
Source: IMAGE Consortium, LNL

This clone is available royalty-free through LNL ; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.

# FEATURES

## source

1..296  
/organism="Homo sapiens"  
/clone="119845"  
/note="human"

BASE COUNT 66 a 75 c 83 g 70 t 2 others  
ORIGIN

Query Match 33.3%; Score 16; DB 127; Length 296;  
Best Local Similarity 86.4%; Pred. No. 7.63e-03;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 34 ggatttctggcagcagctgtaa 55

Cp 48 GGATTTAGGTCGGGTGTAA 27

# RESULT 15

LOCUS H14807 312 bp mRNA EST 27-JUN-1995  
DEFINITION ym24h12.s1 Homo sapiens cDNA clone 49118 3'.

ACCESSION H14807

NTD 9879627

KEYWORDS EST.

SOURCE human clone=49118 library=Soares infant brain 1NIB vector=Lafmid BA

Mar 19 08:44

US-08-612-929-55.rst

15

host=DH10B (ampicillin resistant) primer=Promega -21m13 Rsite1=Not  
I Reite2=Hind III Whole brain from a 73 days post natal female. 1st  
strand cDNA was primed with a Not I - oligo(dT) primer [5'  
AACTGAGAAATTCGGCGCCGACGAAATTTTTTTTTT 3']; double-stranded  
cDNA was ligated to Hind III adaptors (Pharmacia), digested with  
Not I and directionally cloned into the Not I and Hind III sites of  
the LfaIid BA vector. Library went through one round of  
normalization. Library constructed by Bento Soares and M.Fatima  
Bonaldo.

ORGANISM

Homo sapiens  
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;  
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;  
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;  
Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 312)

REFERENCE

AUTHORS

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,  
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,  
Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P. and  
Wilson, R.

TITLE

The WashU-Merck EST Project

JOURNAL

COMMENT

Unpublished (1995)

GDB: G00-421-659

Contact: Wilson RK

WashU-Merck EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence stops: 200

Source: IMAGE Consortium, LIND

This clone is available royalty-free through LIND; contact the

IMAGE Consortium (info@image.lind.gov) for further information.

FEATURES

source

1..312

/organism="Homo sapiens"

/clone="49118"

/note="human"

BASE COUNT 87 a 62 c 72 g 90 t 1 others

ORIGIN

Query Match 33.3%; Score 16; DB 10; Length 312;  
Best Local Similarity 83.3%; Pred.No. 7.63e-03;  
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 199 aaaccttaccatccgagactaaaa 222

||||| ||||| ||||| ||||| |||||

Qy 22 AAACGTTACAAACCGAGCGCTGAA 45

Search completed: Wed Mar 19 08:46:41 1997

Job time : 79 secs.

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(TM)

\*\*\*\*\*

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Distribution rights by IntelliGenetics, Inc.

MPSrch nn n.a. - n.a. database search, using Smith-Waterman algorithm

```
Run on: Wed Mar 19 08:44:46 1997; MasPar time 12.52 Seconds
334,509 Million cell updates/sec
```

**Tabular output not generated.**

Title: >US-08-612-929-55

Description: (1-48) from US08612929.seq

Perfect Score: 48

N.A. Sequence: 1 CACATCTACTGGACGACGACAAACGTTACAAACCGAGCCTGAAATCC 48  
Comp: GTGTAGATGACCCCTGCTGCTGTTTGCAATGTTGGGCTCGGACTTAGG

Scoring table: TABLE default

Gap 10

Nmatch STD : Dbase 0; Query 0

Searched: 113505 seqs. 43611913 bases x 2

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: n-genes25

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13  
14:part14 15:part15 16:part16 17:part17 18:part18  
19:part19 20:part20 21:part21 22:part22

**Statistics:** Mean 6.056; Variance 3.431; scale 1.765

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query		DB	ID	Description	Pred. No.
		Match	Length				
1	48	100.0	120	14	Q83499	Heavy chain variable	1.12e-19
2	48	100.0	423	14	Q83493	Humanized antibody 3B	1.12e-19
3	33	68.8	91	9	Q51746	Oligonucleotide probe	9.91e-10
4	26	54.2	423	14	Q83492	Chimeric antibody 3B9	2.41e-05
5	26	54.2	483	14	Q83491	Mouse Mab 3B9 heavy c	2.41e-05
6	24	50.0	39	7	Q51787	Mixed oligonucleotide	3.87e-04
7	24	50.0	204	1	N81164	Base substituted E.co	3.87e-04
8	24	50.0	738	12	Q70612	1l-6 binding inhibito	3.87e-04





PT and IgE-mediated allergic conditions  
 PS Disclosure; Fig.3; 97pp; English.  
 CC A human/mouse chimeric antibody heavy chain variable region was  
 CC constructed (given in R70191) that contained the mouse anti-human  
 CC IL-4 Mab 3B9 variable region including 3 CDRs (R70198-200) and a  
 CC human antibody signal peptide (R70193). The construct was used  
 CC for humanized antibody production.  
 SQ Sequence 423 BP; 87 A; 115 C; 110 G; 111 T;

Query Match 54.2%; Score 26; DB 14; Length 423;  
 Best Local Similarity 79.5%; Pred. No. 2.41e-05;  
 Matches 35; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Db 214 cacattactggatgatgacagcgctataaccatccctgaa 257  
 ||||| ||||| || ||||| || ||||| ||||| |||||  
 Qy 1 CACATCTACTGGGACGACGACAAACGTTACACCCGCGCTGAA 44

## RESULT 5

ID Q83491 standard; cDNA; 483 BP.  
 AC Q83491;  
 DT 20-SEP-1995 (first entry)  
 DE Mouse Mab 3B9 heavy chain.  
 KW Chimeric antibody; humanized antibody; antibody engineering;  
 KW monoclonal antibody; Mab; interleukin-4; IL-4; allergy; ds.  
 OS Mus sp.

FH Key Location/Qualifiers

FT CDS 64..483

FT /\*tag= a

FT sig\_peptide 64..120

FT /\*tag= b

FT mat\_peptide 121..483

FT /\*tag= c

FN W09507301-A.

PD 16-MAR-1995.

PF 07-SEP-1994; U10308.

PR 07-SEP-1993; US-117366.

PR 14-OCT-1993; US-136783.

PA (SMIK ) SMITHKLINE BEECHAM CORP.

PA (SMIK ) SMITHKLINE BEECHAM PLC.

PI Gross MS, Holmes SD, Sylvester DR;

DR WPI; 95-123387/16.

DR P-PSDB; R70190.

PT Chimeric and humanised IL-4 monoclonal antibodies (mabs), derived  
 PT from high affinity mabs - useful in treatment of IL-4-mediated

PT and IgE-mediated allergic conditions

PS Disclosure; Fig.2; 97pp; English.

CC Spleen cells from mice immunized with human IL-4 were used to prepare  
 CC hybridomas, which were screened for anti-IL-4 Mab secretion. Only

CC clone 3B9 was positive. cDNA clones of the 3B9 light and heavy

CC chains were cloned into pCEM7f and transformed into E. coli

CC DH5-alpha. The clones were sequenced (Q83490-91), and used for

CC antibody engineering.

SQ Sequence 483 BP; 108 A; 130 C; 124 G; 121 T;

Query Match 54.2%; Score 26; DB 14; Length 483;  
 Best Local Similarity 79.5%; Pred. No. 2.41e-05;  
 Matches 35; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Db 274 cacattactggatgatgacagcgctataaccatccctgaa 317  
 ||||| ||||| || ||||| || ||||| ||||| |||||  
 Qy 1 CACATCTACTGGGACGACGACAAACGTTACACCCGCGCTGAA 44

## RESULT 6

ID Q51787 standard; DNA; 39 BP.  
 AC Q51787;  
 DT 20-DEC-1993 (first entry)  
 DE Mixed oligonucleotide #19 encodes ballast constituent.  
 KW Fusion protein; ballast constituent; pro-insulin production;  
 KW recombinant protein production; HMG CoA reductase;  
 KW human 3-hydroxy-3-methylglutaryl-coenzyme A-reductase;  
 KW mixed oligonucleotide; ss.

OS Synthetic.

FH Key Location/Qualifiers

FT repeat\_unit 4..6

FT /\*tag= a

FT /rpt\_type= tandem

FT /note= "can be repeated y times, where y is 4-11,

FT provided that y+z is 6-12"

FT repeat region 4..36

FT /\*tag= b

FT /note= "(DCD)11"

FT repeat\_unit 36..38

FT /\*tag= c

FT /rpt\_type= tandem

FT /note= "can be repeated z times, where z is 1-4,

FT provided that y+z is 6-12; N stands for

FT identical or different nucleotides,

FT excluding stop codons"

PN U85227293-A.

PD 13-JUL-1993.

PF 29-AUG-1989; 399874.

PR 29-AUG-1989; US-399874.

PR 23-APR-1992; US-838221.

PA (GEHO ) GEN HOSPITAL CORP.

PA (FARH ) HOECHST AG.

PI Habermann P, Seed B, Stengelin S, Uhlmann E, Ulmer W;

DR WPI; 93-235119/29.

PT Fusion proteins for prodn. of e.g. pro-insulin - comprise gene

PT for desired protein and oligo-nucleotide (a) encoding ballast

PT protein

PS Claim 9; Column 30; 22pp; English.

CC This preferred mixed oligonucleotide encodes a ballast constituent

CC and is inserted between a regulatory region and the structural gene

CC encoding a desired protein, esp. pro-insulin. The short ballast

CC component improves protease resistance of the fusion protein while

CC still allowing the desired protein to adopt its correct conformation

CC prior to cleavage of the ballast constituent.

SQ Sequence 39 BP; 1 A; 11 C; 1 G; 1 T;

Query Match 50.0%; Score 24; DB 7; Length 39;  
 Best Local Similarity 25.0%; Pred. No. 3.87e-04;  
 Matches 8; Conservative 20; Mismatches 4; Indels 0; Gaps 0;

Db 4 dcd 35  
 :||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

Qy 2 ACATCTACTGGGACGACGACAAACGTTACAC 33

## RESULT 7

ID N81164 standard; DNA; 204 BP.  
 AC N81164;  
 DT 08-NOV-1990 (first entry)  
 DE Base substituted E.coli beta-galactosidase alpha-fragment.  
 KW E.coli beta galactosidase alpha-fragment; base substitutions; ss.  
 OS Escherichia coli.

FH Key Location/Qualifiers

FT misc feature 19..69  
FT /\*tag= a  
FT /function= multiple cloning site  
FT primer\_bind 187..204  
FT /\*tag= b  
PN EP-285123-A.  
PD 05-MAY-1988.  
PF 30-MAR-1988; 105163.  
PR 03-APR-1987; US-034819.  
PA (SUSO) SUOMEN SOKERI OY.  
PI Lehtovaara P, Knowles J, Koivula A, Bamford J, Reinikainen T;  
DR WPI; 88-27927/40.  
PT Introducing random point mutations into nucleic acids -  
PT by prepn of single stranded template, annealing a primer, elongation,  
PT misincorporation, completion of molecules and screening.  
PS Disclosure; p; English.  
CC Random point mutations were introduced into the alpha fragment of  
CC E.coli beta-galactosidase. The wild type sequence was obtained as a  
CC single stranded template and an oligonucleotide was hybridised to  
CC it to generate a popn of DNA molecules which terminate at all  
CC possible nucleotide positions within a specified region. The  
CC variable 3' ends generated in this way are used as primers for  
CC reverse transcriptase. Nucleotides are misincorporated by the  
CC transcriptase and the molecules are completed to forms that can be  
CC amplified and then expressed in a suitable host-vector system.  
CC The sequence covers all 176 diff base substitutions, most of which  
CC occurred singularly in any given mutant.  
CC See also P80575.  
SQ Sequence 204 BP; 21 A; 47 C; 17 G; 11 T; 108 Others;  
  
Query Match 50.0%; Score 24; DB 1; Length 204;  
Best Local Similarity 6.7%; Pred. No. 3.87e-04;  
Matches 3; Conservative 26; Mismatches 16; Indels 0; Gaps 0;  
  
Db 131 hhdhdyvbbvynvnhnnccebnhvchvnhvbnhrnwayv 175  
::: ::::: :: | :: ::::: ::  
QY 3 CATCTACTGGGACGACGACAAAGTTACACCGCGCTGAATC 47

RESULT 8  
ID Q70612 standard; DNA; 738 BP.  
AC Q70612;  
DT 28-APR-1995 (first entry)  
DE IL-6 binding inhibitor DNA.  
KW Human interleukin-6 binding inhibitor; IL-6; rheumatoid arthritis;  
KW septic shock; multiple myeloma; ss.  
OS Homo sapiens.  
PN EP-617126-A.  
PD 28-SEP-1994.  
PF 16-FEB-1994; 102346.  
PR 17-FEB-1993; JP-028173.  
PA (AJIN) AJINOMOTO KK.  
PI Hamuro J, Nakazawa H, Shimamura T;  
DR WPI; 94-295777/37.  
DR P-PSDB; R58612.  
PT Polypeptide inhibiting binding of human interleukin-6 (IL-6) to  
PT its receptor - useful for treating auto:immune disease induced  
PT or aggravated by IL-6  
PS Claim 9; Page 19; 26pp; English.  
CC Q70612 codes for human interleukin-6 binding inhibitor, the  
CC polypeptide described in R58612. This polypeptide inhibits the  
CC binding of human IL-6 to its receptor, and can therefore be  
CC useful in the treatment of a variety of autoimmune diseases;  
CC specifically in the treatment of rheumatoid arthritis, septic

CC shock due to bacterial infection and multiple myeloma.  
SQ Sequence 738 BP; 187 A; 189 C; 180 G; 182 T;  
  
Query Match 50.0%; Score 24; DB 12; Length 738;  
Best Local Similarity 77.3%; Pred. No. 3.87e-04;  
Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;  
  
Db 520 cacattattggatgatgacaaacactataaccatccctgaa 563  
||||| || ||||| || ||||| || ||||| |||||  
QY 1 CACATCTACTGGGACGACGACAAAGTTACACCGCGCTGAAG 44  
  
RESULT 9  
ID Q51746 standard; cDNA; 91 BP.  
AC Q51746;  
DT 31-MAY-1994 (first entry)  
DE Oligonucleotide probe MK14-A  
KW Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;  
KW ss.  
OS Synthetic.  
PN EP-571911-A.  
PD 01-DEC-1993.  
PF 24-MAY-1993; 108325.  
PR 26-MAY-1992; US-889651.  
PA (BECT) BECTON DICKINSON CO.  
PI Shank DD, Spears PA;  
DR WPI; 93-378844/48.  
PT New oligonucleotide probes specific for Mycobacteria - used for  
PT detection and amplification of Mycobacteria nucleic acid in  
PT samples  
PS Claim 3; Page 14; 23pp; English.  
CC Oligonucleotide probe MK14-A consists of nucleotides 5-95 of MK14  
CC (Q51735). It hybridized to all spp. of mycobacteria tested, but  
CC cross reacted to a few non-mycobacterial spp. The probe may  
CC be useful as an initial screen for mycobacterial infection.  
CC See also Q51735-45 and Q51747-59.  
SQ Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;  
  
Query Match 47.9%; Score 23; DB 9; Length 91;  
Best Local Similarity 0.0%; Pred. No. 1.51e-03;  
Matches 0; Conservative 28; Mismatches 5; Indels 0; Gaps 0;  
  
Db 24 hhhsvhhvhhvhhvavvvvhhvhhvhhvhhvhyv 56  
::: ::::: :: ::::: ::::: ::::: ::  
Cp 43 TCAGGCTCGGGTTGTAAAGCTTTGTCGTGCTGCC 11  
  
RESULT 10  
ID Q11195 standard; DNA; 36 BP.  
AC Q11195;  
DT 05-JUN-1991 (first entry)  
DE Ballast Constituent coding sequence #2.  
KW ballast constituent; fusion protein; oligonucleotide library; ss.  
OS Synthetic.  
FH Key Location/Qualifiers  
FT repeat\_unit 7..9  
FT /\*tag= a  
FT /note= "can be present 4 to 8 times"  
PN W09103550-A.  
PD 21-MAR-1991.  
PF 28-AUG-1990; U04840.  
PR 29-AUG-1989; US-399874.  
PA (FARH) HOECHST AG.  
PA (GEMO-) GEN HOSPITAL CORP.



PT for desired protein and oligo-nucleotide(s) encoding ballast  
 PT protein  
 PS Claim 4; Column 29; 22pp; English.  
 CC This preferred mixed oligonucleotide encodes a ballast constituent  
 CC and is inserted between a regulatory region and the structural gene  
 CC encoding a desired protein. The short ballast component improves  
 CC protease resistance of the fusion protein while still allowing the  
 CC desired protein to adopt its correct conformation prior to cleavage  
 CC of the ballast constituent. Proteins which can be produced as fusion  
 CC proteins with a ballast region include pro-insulin and HMG CoA  
 CC reductase.  
 SQ Sequence 33 BP; 1 A; 10 C; 3 G; 1 T;

Query Match	41.7%	Score 20;	DB 7;	Length 33;
Best Local Similarity	27.3%	Pred. No. 8.14e-02;		
Matches	6;	Conservative	15;	Mismatches 1; Indels 0; Gaps 0;
DB	7	cdcdcdcdcdcdcdcdcdcdcd	28	
ov	2	ACATCTACTGTCGACGACAA	23	

Human; mouse; murine; heavy; light; chain; monoclonal; antibody;  
 KW complementarity determining region; CDR; IgG; kappa; IIB; IIMN; ds.  
 KW Chimeric - Mus musculus.  
 OS

PN	J06141885-A.
PD	24-MAY-1994.
PP	05-NOV-1992; 322476.
PR	05-NOV-1992; JP-322476.
RPA	(KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
DR	WPI; 94-205040/25.

DR WIPI; 94-205040/25.  
DR P-PSDB; R54101.  
DR Recombinant anti-HIV monoclonal antibody - capable of  
PPT neutralising strains which can not be neutralised by anti-IIIB  
PPT and IIIM antibodies  
PT Disclosure; Page 13; 23pp; Japanese.  
CC The sequences given in Q68709-10 encode the heavy and light chains  
CC respectively of the humanised monoclonal antibody (MAB) of the  
CC invention. The antibody has the ability to neutralise human  
CC immunodeficiency virus. The antibody is classified as IgG kappa and  
CC has the sequence RIGRGR or RVGPER in the principal neutralising  
CC domain. The antibody may be used to neutralise the clinically  
CC separate strains which cannot be neutralised by the neutralising  
CC antibodies against IIIB and IIIM strains.  
SQ Sequence 366 BP; 85 A; 98 C; 99 T;

CC has the sequence RIGPCR or RVGPCR in the principal neutralising  
 CC domain. The antibody may be used to neutralise the clinically  
 CC separate strains which cannot be neutralised by the neutralising  
 CC antibodies against IIIB and IIIMN strains.  
 SQ Sequence 366 BP; 85 A; 98 C; 84 G; 99 T;

Query Match 41.7%; Score 20; DB 11; Length 366;  
 Best Local Similarity 72.7%; Pred. No. 8.14e-02;  
 Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Search completed: Wed Mar 19 08:45:02 1997  
Job time : 16 secs.

PT Fusion proteins for prodn. of e.g. pro-insulin - comprise gene

(TM)

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## ORGANISM

Mus musculus

Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Sarcophrygii; Mammalia; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Mus.

## REFERENCE

1 (bases 1 to 345)

## AUTHORS

Yamanaka, H.I., Kirii, Y. and Ohmoto, H.

## TITLE

An improved phage display antibody cloning system using newly designed PCR primers optimized for Pfu DNA polymerase

## JOURNAL

J. Biochem. 117 (6), 1218-1227 (1995)

## MEDLINE

96104992

## COMMENT

Submitted (21-Apr-1995) to DDBJ by:

Hachiro Yamanaka

New Drug Research Laboratories

Kanebo Ltd.

1-5-90 Tomobuchi-cho Miyakojima-ku

Osaka, Osaka 534

Japan

Phone: 06-921-1281 x3609

Fax: 06-923-3381.

Location/Qualifiers

1..345

/organism="Mus musculus"

/strain="BALB/c"

/sub species="domesticus"

/cell\_line="KSE1"

/cell\_type="hybridoma producing anti-human procollagenase antibody"

## primer\_bind

1..11

/note="PCR primer"

## V\_region

/product="immunoglobulin heavy chain variable region"

## BASE COUNT

79 a 95 c 80 g 91 t

## ORIGIN

## Query Match

58.3%; Score 28; DB 67; Length 345;

Best Local Similarity 81.8%; Pred. No. 9.03e-08;

Matches 36; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Db 142 cacattactggatgatgacaaagcgtataaccatccctgaa 185

||||| ||||||| || ||||||| || ||||||| |||||||

Qy 1 CACATCTACTGGACGACGACAAACGTTACACCCGAGCCTGAA 44

## RESULT 2

## LOCUS

MMU23024

286 bp DNA

Mus musculus C57BL/6

clone CB17H-8, partial cds.

U23024

g780650

house mouse.

Mus musculus

## ORGANISM

Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcophrygii; Chaoanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Mus.

## REFERENCE

1 (bases 1 to 286)

## AUTHORS

Young, D.C. and Kearney, J.F.

## TITLE

Sequence analysis and antigen binding characteristics of immunoglobulins from SCID Ig<sup>+</sup> mice

## JOURNAL

Int. Immunol. 7 (1995) In press

## REFERENCE

2 (bases 1 to 286)

## AUTHORS

Young, D.C.

## TITLE

Direct Submission

## JOURNAL

Submitted (17-MAR-1995) David C. Young, University of Texas Health Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137, Houston, TX 77030, USA

## FEATURES

Location/Qualifiers

source

1..286

/clones="CB17H-8"

/strain="C57BL/6"

/organism="Mus musculus"

/sub species="domesticus"

/germline

/tissue\_type="Liver"

&lt;1..&gt;286

/note="7183 Vh gene family"

/codon\_start=2

/product="immunoglobulin heavy chain"

/db\_xref="PID:g780651"

/translation="QVTLKESGPGILASSQTLISLTCFSGFSINTSGHVSIRQPSG KGLEWLAHYDWDKRYNPSIAKSLTISKDTSRNQVFLKITSVDADTATY"

## BASE COUNT

68 a 77 c 69 g 72 t

## ORIGIN

## Query Match

54.2%; Score 26; DB 65; Length 286;

Best Local Similarity 79.5%; Pred. No. 3.73e-06;

Matches 35; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Db 155 cacattactggatgatgacaaagcgtataaccatccctgaa 198

||||| ||||||| || ||||||| || ||||||| |||||||

Qy 1 CACATCTACTGGACGACGACAAACGTTACACCCGAGCCTGAA 44

## RESULT 3

## LOCUS

MMU23019

286 bp DNA

Mus musculus C57BL/6

clone CB17H-1, partial cds.

U23019

g780640

house mouse.

Mus musculus

## ORGANISM

Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcophrygii; Chaoanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Mus.

## REFERENCE

1 (bases 1 to 286)

## AUTHORS

Young, D.C. and Kearney, J.F.

## TITLE

Sequence analysis and antigen binding characteristics of immunoglobulins from SCID Ig<sup>+</sup> mice

## JOURNAL

Int. Immunol. 7 (1995) In press

## REFERENCE

2 (bases 1 to 286)

## AUTHORS

Young, D.C.

## TITLE

Direct Submission

## JOURNAL

Submitted (17-MAR-1995) David C. Young, University of Texas Health Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137, Houston, TX 77030, USA

## FEATURES

Location/Qualifiers

source

1..286

/clones="CB17H-1"

/strain="C57BL/6"

/organism="Mus musculus"

/sub species="domesticus"

/germline

Mar 19 08:42

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5

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CDS
/tissue_type="liver"
<1..>286
/note="7183 Vh gene family"
/codon_start=2
/product="immunoglobulin heavy chain"
/db_xref="PID:g780641"
/translation="QVTLKESFGILQSSQTLSTLTCFSFGSLTSGMGVSWIRQPSG
KGLEWLAHYWDDKRYNPSIKSLRTISKDTSRNQVFLKITSVDADTATY"
BASE COUNT      67 a   77 c   70 g   72 t
ORIGIN
Query Match      54.2%; Score 26; DB 65; Length 286;
Best Local Similarity 79.5%; Pred. No. 3.73e-06;
Matches 35; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Db 155 cacattactgggatgacgaagcgctataaaccatccctgaa 198
||||| ||||||| || ||||||| || ||||||| |||||||
Qy 1 CACATCTACTGGGACGACGACAAACGTTACACCCGAGCCTGAA 44

RESULT 4
LOCUS MUSB 306 bp mRNA ROD 14-MAR-1994
DEFINITION Mus musculus immunoglobulin heavy chain (Igh) mRNA, VDJ4 region,
partial cds.
ACCESSION L22743
NID g348959
KEYWORDS Ig heavy chain; diversity region; immunoglobulin; joining region;
variable region.
SOURCE Mus musculus (strain BALB/cByJ) female adult spleen cDNA to mRNA.
ORGANISM Mus musculus
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE 1 (bases 1 to 306)
AUTHORS Sheehan,K.M., Mainville,C.A., Willert,S. and Brodeur,P.H.
TITLE The utilization of individual VH exons in the primary repertoire of
adult BALB/c mice
JOURNAL J. Immunol. 151 (10), 5364-5375 (1993)
MEDLINE 94044761
FEATURES
source
location/Qualifiers
1..306
/organism="Mus musculus"
/strain="BALB/cByJ"
/cell_type="B-lymphocyte"
/dev_stage="adult"
/sequenced_mol="cDNA to mRNA"
/sex="female"
/tissue_type="spleen"
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/gene="Igh"
/map="chromosome 12"
<1..>306
/gene="Igh"
/map="chromosome 12"
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/product="immunoglobulin heavy chain"
/db_xref="PID:g348960"
/translation="LTCSFGSLTSGMGVSWIRQPSGKLEWLAHYWDDKRYNP
SIKSLRTISKDTSRNQVFLKITSVDADTATYTCARAWLLRDYAMDYWGQGSVTVSS"
BASE COUNT      72 a   80 c   75 g   79 t
ORIGIN
Query Match      54.2%; Score 26; DB 66; Length 306;
Best Local Similarity 79.5%; Pred. No. 3.73e-06;
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Mar 19 08:42

US-08-612-929-55.rge

6

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Matches 35; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Db 97 cacattactgggatgacgaagcgctataaaccatccctgaa 140
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Qy 1 CACATCTACTGGGACGACGACAAACGTTACACCCGAGCCTGAA 44

RESULT 5
LOCUS MUSIGHAEO 328 bp mRNA ROD 14-NOV-1991
DEFINITION Mouse Ig heavy-chain mRNA V region, partial cds. L2-5D2HV.
ACCESSION M36234
NID g194851
KEYWORDS V-region; immunoglobulin heavy chain; processed gene.
SOURCE Mouse (strain BALB/c), cDNA to mRNA, from hybridoma L2-5D2.
ORGANISM Mus musculus
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE 1 (bases 1 to 328)
AUTHORS Kavalier,J., Caton,A.J., Staudt,L.M., Schwartz,D. and Gerhard,W.
TITLE A set of closely related antibodies dominates the primary antibody
response to the antigenic site CB of the A/PR/8/34 influenza virus
hemagglutinin
JOURNAL J. Immunol. 145, 2312-2321 (1990)
MEDLINE 90375932
COMMENT Draft entry and computer-readable sequence for [J. Immunol. (1990)
In press] kindly submitted
by J.Kavalier, 06-JUL-1990.
FEATURES
source
location/Qualifiers
1..328
/organism="Mus musculus"
/strain="BALB/c"
/sub_species="domesticus"
/cell_line="L2-5D2"
/sequenced_mol="cDNA to mRNA"
/tissue_type="hybridoma"
<1..>328
/gene="Igh"
/map="chromosome 12"
/codon_start=2
/product="immunoglobulin heavy chain V-region"
/db_xref="PID:g194852"
/translation="PGILQPSQTLSTLTCFSFGSLTSGMGXSWIRQPSGKLEWLAH
IYWDDKRYNPSIKSLRTISKDTSRNQVFLKITSVDADTATYTCARSYGNGDYAMD
YWGQGS"
BASE COUNT      76 a   85 c   82 g   83 t   2 others
ORIGIN
Query Match      54.2%; Score 26; DB 66; Length 328;
Best Local Similarity 79.5%; Pred. No. 3.73e-06;
Matches 35; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Db 131 cacattactgggatgacgaagcgctataaaccatccctgaa 174
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Qy 1 CACATCTACTGGGACGACGACAAACGTTACACCCGAGCCTGAA 44

RESULT 6
LOCUS MMHCIVR4 348 bp RNA ROD 23-FEB-1994
DEFINITION M.musculus (A.SW) mRNA for ASWP1 antibody heavy chain variable
region.
ACCESSION X75098
NID g414167
KEYWORDS antibody; variable region; VH region.
SOURCE house mouse.
```

ORGANISM Mus musculus  
Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 348)  
AUTHORS Monestier, M.  
TITLE Direct Submission  
JOURNAL Submitted (09-SEP-1993) to the EMBL/GenBank/DBJ databases. M. Monestier, Center for Molecular Medicine and Immunology, one Bruce Street, Newark, NJ 07103-2763, USA

REFERENCE 2 (bases 1 to 348)  
AUTHORS Monestier, M., Iosman, M.J., Novick, K.E. and Arie, J.P.  
TITLE Molecular analysis of mercury-induced antinuclear antibodies in H-2S mice  
JOURNAL J. Immunol. 152 (2), 667-675 (1994)  
MEDLINE 94110621

FEATURES  
source Location/Qualifiers  
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/chromosome="12"  
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V\_region /gene="VH ASW1"  
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/product="ASW1 heavy chain variable region"  
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/product="ASW1 heavy chain variable region"  
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BASE COUNT 81 a 95 c 85 g 85 t 2 others  
ORIGIN  
Query Match 54.2%; Score 26; DB 63; Length 348;  
Best Local Similarity 79.5%; Pred. No. 3.73e-06;  
Matches 35; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
Db 154 cacattactggatgatgacagcgctataaccctccctgaa 197  
||||| ||||||| || ||||| || ||||| |||||  
Qy 1 CACATCTACTGGGACGACGACAAAGCTTACACCGGCGCTGAA 44

RESULT 7  
LOCUS MMU23007 359 bp mRNA ROD 26-APR-1995  
DEFINITION Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA, clone 45-4h, partial cds.  
ACCESSION U23007  
NID 9780616  
KEYWORDS house mouse.  
SOURCE Mus musculus  
ORGANISM Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 359)  
AUTHORS Young, D.C. and Kearney, J.F.  
TITLE Sequence analysis and antigen binding characteristics of immunoglobulins from SCID Ig+ mice  
JOURNAL Int. Immunol. 7 (1995) In press  
REFERENCE 2 (bases 1 to 359)  
AUTHORS Young, D.C.  
TITLE Direct Submission  
JOURNAL Submitted (17-MAR-1995) David C. Young, University of Texas Health Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137, Houston, TX 77030, USA

AUTHORS Young, D.C. and Kearney, J.F.  
TITLE Sequence analysis and antigen binding characteristics of immunoglobulins from SCID Ig+ mice  
JOURNAL Int. Immunol. 7 (1995) In press  
REFERENCE 2 (bases 1 to 359)  
AUTHORS Young, D.C.  
TITLE Direct Submission  
JOURNAL Submitted (17-MAR-1995) David C. Young, University of Texas Health Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137, Houston, TX 77030, USA

FEATURES  
source Location/Qualifiers  
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/clone="45-4h"  
/strain="CB17 SCID"  
/organism="Mus musculus"  
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/cell\_type="lymphocyte"  
/tissue\_type="spleen"  
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/db\_xref="PID:g780617"  
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BASE COUNT 83 a 97 c 87 g 92 t  
ORIGIN  
Query Match 54.2%; Score 26; DB 65; Length 359;  
Best Local Similarity 79.5%; Pred. No. 3.73e-06;  
Matches 35; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
Db 153 cacattactggatgatgacagcgctataaccctccctgaa 196  
||||| ||||||| || ||||| || ||||| |||||  
Qy 1 CACATCTACTGGGACGACGACAAAGCTTACACCGGCGCTGAA 44

RESULT 8  
LOCUS MMU22988 360 bp mRNA ROD 26-APR-1995  
DEFINITION Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA, clone 45-23h, partial cds.  
ACCESSION U22988  
NID 9780578  
KEYWORDS house mouse.  
SOURCE Mus musculus  
ORGANISM Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 360)  
AUTHORS Young, D.C. and Kearney, J.F.  
TITLE Sequence analysis and antigen binding characteristics of immunoglobulins from SCID Ig+ mice  
JOURNAL Int. Immunol. 7 (1995) In press  
REFERENCE 2 (bases 1 to 360)  
AUTHORS Young, D.C.  
TITLE Direct Submission  
JOURNAL Submitted (17-MAR-1995) David C. Young, University of Texas Health Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137, Houston, TX 77030, USA

FEATURES  
source Location/Qualifiers  
1..360



Mar 19 08:42

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9

/clone="45-23h"  
/strain="CB17 SCID"  
/organism="Mus musculus"  
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AITFDYWGQGTTLTVSG"

BASE COUNT 82 a 101 c 87 g 90 t

ORIGIN

Query Match 54.2%; Score 26; DB 65; Length 360;  
Best Local Similarity 79.5%; Pred. No. 3.73e-06;  
Matches 35; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Db 154 cacatttactggatggcagaagcgctataaccctccctgaa 197

||||| ||||||| | |||||| | || ||||| |||||||  
QY 1 CACATCTACTGGGACGACGACAAACGTTACACCCGAGCCTGAA 44

RESULT 9

ID MM22979 standard; RNA; ROD; 360 BP.  
AC U22979;  
DT 29-APR-1995 (Rel. 43, Created)  
DT 09-APR-1996 (Rel. 47, Last updated, Version 2)  
DE Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA,  
DE clone 45-12h, partial cds.  
KW Mus musculus (mouse)  
OC Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;  
OC Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.  
RN [1]  
RP 1-360  
RA Young D., Kearney J.F.;  
RT "Sequence analysis and antigen binding characteristics of Ig SCID  
Ig+ mice";  
RL Int. Immunol. 7:807-819(1995).  
RN [2]  
RP 1-360  
RA Young D.C.;

Submitted (17-MAR-1995) to the EMBL/GenBank/DBJ databases.  
RL David C. Young, University of Texas Health Science Center, Houston,  
RL Pathology, 6431 Fannin, MSMB 2.137, Houston, TX 77030, USA  
CC NCBI gi: 780560  
FH Key Location/Qualifiers

source 1..360  
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/strain="CB17 SCID"  
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CDS  
Query Match 54.2%; Score 26; DB 91; Length 360;  
Best Local Similarity 79.5%; Pred. No. 3.73e-06;  
Matches 35; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Db 154 cacatttactggatggcagaagcgctataaccctccctgaa 197

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10

K GLEWLAHIYWDGKRNPSIKSRLTISKDTSRQVFLKITSVDTAUTATYYCARRALG  
S SYFDYWGQGTTLTVSS"  
SQ Sequence 360 BP; 84 A; 98 C; 87 G; 91 T; 0 other;

Query Match 54.2%; Score 26; DB 12; Length 360;  
Best Local Similarity 79.5%; Pred. No. 3.73e-06;  
Matches 35; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Db 154 cacatttactggatggcagaagcgctataaccctccctgaa 197

||||| ||||||| | |||||| | || ||||| |||||||  
QY 1 CACATCTACTGGGACGACGACAAACGTTACACCCGAGCCTGAA 44

RESULT 10

LOCUS MMU22988 360 bp mRNA ROD 09-APR-1996  
DEFINITION Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA,  
clone 45-23h, partial cds.

ACCESSION U22988

NID g780578

KEYWORDS house mouse.  
SOURCE Mus musculus

ORGANISM Eukaryota; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;  
Vertebrata; Murinae; Mus.  
REFERENCE 1 (bases 1 to 360)  
AUTHORS Young,D. and Kearney,J.F.  
TITLE Sequence analysis and antigen binding characteristics of Ig SCID  
Ig+ mice  
JOURNAL Int. Immunol. 7 (5), 807-819 (1995)  
MEDLINE 96053543  
REFERENCE 2 (bases 1 to 360)  
AUTHORS Young,D.C.  
TITLE Direct Submission  
JOURNAL Submitted (17-MAR-1995) David C. Young, University of Texas Health  
Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137,  
Houston, TX 77030, USA  
COMMENT NCBI gi: 780578  
FEATURES Location/Qualifiers

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/sub\_species="domesticus"  
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/codon\_start=1  
/product="immunoglobulin heavy chain"  
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AITFDYWGQGTTLTVSG"

CDS

BASE COUNT 82 a 101 c 87 g 90 t  
ORIGIN

Query Match 54.2%; Score 26; DB 91; Length 360;  
Best Local Similarity 79.5%; Pred. No. 3.73e-06;  
Matches 35; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Db 154 cacatttactggatggcagaagcgctataaccctccctgaa 197

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QY 1 CACATCTACTGGGACGACGACAAACGTTTACAAACCGAGCCTGAA 44

RESULT 11
LOCUS MMHCVR3 360 bp RNA ROD 23-FEB-1994
DEFINITION M.musculus (A.SW) mRNA for ASWB1 antibody heavy chain variable
region.
ACCESSION X75097
NID 9414165
KEYWORDS antibody; variable region; VH region.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.
1 (bases 1 to 360)
Monestier,M.
Direct Submission
Submitted (09-SEP-1993) to the EMBL/GenBank/DBJ databases. M.
Monestier, Center for Molecular Medicine and Immunology, one Bruce
Street, Newark, NJ 07103-2763, USA
2 (bases 1 to 360)
Monestier,M., Losman,M.J., Novick,K.E. and Aris,J.P.
Molecular analysis of mercury-induced antinuclear antibodies in
H-2S mice
J. Immunol. 152 (2), 667-675 (1994)
MEDLINE 94110621
FEATURES
source
1..360
Location/Qualifiers
/organism="Mus musculus"
/cell_type="hybridoma"
/cell_line="ASWB1 hybridoma"
/chromosome="12"
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/gene="VH ASWB1"
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/product="ASWB1 heavy chain variable region"
<1..>360
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/codon_start=1
/product="ASWB1 heavy chain variable region"
/db_xref="PID:g414166"
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KGLGLAHLYWDDDKRYPNSLKSRITISKDTSRNQVFLKITSVDATATYYCARRVIG
YDAMDYWGQTSVTSS"
BASE COUNT 82 a 95 c 89 g 94 t
ORIGIN
Query Match 54.2%; Score 26; DB 63; Length 360;
Best Local Similarity 79.5%; Pred. No. 3.73e-06;
Matches 35; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
Db 154 cacattactggatgatgacaggcgtataaccatccctgaa 197
||||| ||||||| || |||||| || |||||| |||||||
QY 1 CACATCTACTGGGACGACGACAAACGTTTACAAACCGAGCCTGAA 44

RESULT 12
ID MM22994
AC MM22994;
DT 29-APR-1995 (Rel. 4.3, Created)
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DT 09-APR-1996 (Rel. 47, Last updated, Version 2)
DE Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA,
DE clone 45-27h, partial cds.
KW .
OS Mus musculus (mouse)
OC Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
OC Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
RN [1]
RP 1-360
RA Young D., Kearney J.F.;
RT "Sequence analysis and antigen binding characteristics of Ig SCID
RT Ig+ mice";
RL Int. Immunol. 7:807-819 (1995).
RN [2]
RP 1-360
RA Young D.C.;
RT ;
RL Submitted (17-MAR-1995) to the EMBL/GenBank/DBJ databases.
RL David C. Young, University of Texas Health Science Center, Houston,
RL Pathology, 6431 Fannin, MSMB 2.137, Houston, TX 77030, USA
CC NCBI gi: 780590
FH Key Location/Qualifiers
FH 1..360
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FT K
FT S
FT SYFDYWGQGTTLTVSS"
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Query Match 54.2%; Score 26; DB 12; Length 360;
Best Local Similarity 79.5%; Pred. No. 3.73e-06;
Matches 35; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
Db 154 cacattactggatgatgacaggcgtataaccatccctgaa 197
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QY 1 CACATCTACTGGGACGACGACAAACGTTTACAAACCGAGCCTGAA 44

RESULT 13
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DEFINITION Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA,
clone 45-27h, partial cds.
ACCESSION U22994
NID g780590
KEYWORDS .
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.
```

REFERENCE 1 (bases 1 to 360)  
AUTHORS Young,D.C. and Kearney,J.F.  
TITLE Sequence analysis and antigen binding characteristics of immunoglobulin from SCID Ig<sup>+</sup> mice  
JOURNAL Int. Immunol. 7 (1995) In press  
REFERENCE 2 (bases 1 to 360)  
AUTHORS Young,D.C.  
TITLE Direct Submission  
JOURNAL Submitted (17-MAR-1995) David C. Young, University of Texas Health Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137, Houston, TX 77030, USA

FEATURES  
source

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/cell_type="lymphocyte"
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KGLEWLAHIYDDDKRNPISIKSLRTISKDTSRNQVFLKITSVDTAUTATYYCARRVL
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ORIGIN

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Matches 35; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Db 154 cacattactgggatgacgaagcgctataaccatccctgaa 197  
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Qy 1 CACATCTACTGGGAGCAGCACAAAGCTTACACCCGAGCCTGAA 44

RESULT 14  
LOCUS MMU22979 360 bp mRNA ROD 26-APR-1995  
DEFINITION Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA, clone 45-12h, partial cds.  
ACCESSION U22979  
NID g780560  
KEYWORDS house mouse.  
SOURCE Mus musculus  
ORGANISM Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia; Sciurognathi; Myomorphae; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 360)  
AUTHORS Young,D.C. and Kearney,J.F.  
TITLE Sequence analysis and antigen binding characteristics of immunoglobulin from SCID Ig<sup>+</sup> mice  
JOURNAL Int. Immunol. 7 (1995) In press  
REFERENCE 2 (bases 1 to 360)  
AUTHORS Young,D.C.  
TITLE Direct Submission  
JOURNAL Submitted (17-MAR-1995) David C. Young, University of Texas Health Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137, Houston, TX 77030, USA

FEATURES  
Location/Qualifiers

source

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CDS

BASE COUNT 84 a 98 c 87 g 91 t  
ORIGIN

Query Match 54.2%; Score 26; DB 65; Length 360;  
Best Local Similarity 79.5%; Pred. No. 3.73e-06;  
Matches 35; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Db 154 cacattactgggatgacgaagcgctataaccatccctgaa 197  
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RESULT 15  
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DEFINITION Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA, clone 45-12h, partial cds.  
ACCESSION U22979  
NID g780560  
KEYWORDS house mouse.  
SOURCE Mus musculus  
ORGANISM Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorphae; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 360)  
AUTHORS Young,D. and Kearney,J.F.  
TITLE Sequence analysis and antigen binding characteristics of Ig SCID Ig<sup>+</sup> mice  
JOURNAL Int. Immunol. 7 (5), 807-819 (1995)  
MEDLINE 96053543  
REFERENCE 2 (bases 1 to 360)  
AUTHORS Young,D.C.  
TITLE Direct Submission  
JOURNAL Submitted (17-MAR-1995) David C. Young, University of Texas Health Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137, Houston, TX 77030, USA  
COMMENT NCBI gi: 780560  
FEATURES Location/Qualifiers

source

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CDS

Mar 19 08:42

US-08-612-929-55 rge

15

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BASE COUNT 84 a 98 c 87 g 91 t  
ORIGIN

Query Match 54.2%; Score 26; DB 91; Length 360;  
Best Local Similarity 79.5%; Pred. No. 3.73e-06;  
Matches 35; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Db 154 cacatttactgggatgacaaagcgctataaaccatccctgaa 197

||||| ||||||| || ||||||| || ||||||| |||||||

Qy 1 CACATCTACTGGGACGACGACAAACGTTACACCCCGACCTGAA 44

Search completed: Wed Mar 19 08:44:28 1997  
Job time : 70 secs.

\*\*\*\*\*

WQESREH (TM)

\*\*\*\*\*

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MPsrch\_nm n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed Mar 19 08:49:17 1997; MasPar time 52.75 Seconds  
275.919 Million cell updates/sec  
Tabular output not generated.

Title: >US-08-612-929-56  
Description: (1-33) from US08612929.seq  
Perfect Score: 33  
N.A. Sequence: 1 CGCGAACCGTTTCTACTGCTGACTGACGTT 33  
Comp: CGCGTTTGCAAGATGACCATGACCTGCA

Scoring table:  
Gap 10

Nmatch STD : Dbase 0; Query 0

Searched: 630489 seqs, 220513910 bases x 2

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: EST-STS  
1:EST1 2:EST2 3:EST3 4:EST4 5:EST5 6:EST6 7:EST7 8:EST8  
9:EST9 10:EST10 11:EST11 12:EST12 13:EST13 14:EST14  
15:EST15 16:EST16 17:EST17 18:EST18 19:EST19 20:EST20  
21:EST21 22:EST22 23:EST23 24:EST24 25:EST25 26:EST26  
27:EST27 28:EST28 29:EST29 30:EST30 31:EST31 32:EST32  
33:EST33 34:EST34 35:EST35 36:EST36 37:EST37 38:EST38  
39:EST39 40:EST40 41:EST41 42:EST42 43:EST43 44:EST44  
45:EST45 46:EST46 47:EST47 48:EST48 49:EST49 50:EST50  
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63:EST63 64:EST64 65:EST65 66:EST66 67:EST67 68:EST68  
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75:EST75 76:EST76 77:EST77 78:EST78 79:EST79 80:EST80  
81:EST81 82:EST82 83:EST83 84:EST84 85:EST85 86:EST86  
87:EST87 88:EST88 89:EST89 90:EST90 91:EST91 92:EST92  
93:EST93 94:EST94 95:EST95 96:EST96 97:EST97 98:EST98  
99:EST99  
EST-STS-TWO  
100:EST100 101:EST101 102:EST102 103:EST103 104:EST104  
105:EST105 106:EST106 107:EST107 108:EST108 109:EST109  
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115:EST115 116:EST116 117:EST117 118:EST118 119:EST119  
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125:EST125 126:EST126 127:EST127 128:EST128 129:EST129

Database:

130:STS2 131:STS3 132:STS4 133:STS5 134:STS6 135:STS7  
136:STS8 137:STS9 138:STS10 139:STS11 140:STS12  
141:STS13 142:STS14 143:STS15 144:STS16 145:STS17  
146:STS18 147:STS19 148:STS20 149:STS21 150:STS22  
151:STS23 152:STS24 153:STS25 154:STS26 155:STS27  
156:STS28 157:STS29 158:STS30 159:STS31 160:STS32  
161:STS33 162:STS34 163:STS35 164:STS36 165:STS37  
166:STS38 167:STS39 168:STS40 169:STS41 170:STS42  
171:STS43 172:STS44 173:STS45 174:STS46

Statistics: Mean 6.934; Variance 1.401; scale 4.951

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result	No.	Score	Query	Match	Length	DB	ID	Description	Pred. No.
c	1	16	48.5	382	129	G01101		fruit fly STS Dml786	5.94e-03
c	2	16	48.5	409	29	H77083		17514 Arabidopsis tha	5.94e-03
c	3	16	48.5	1023	170	MM4651		mb50409.rl Soares mou	5.94e-03
c	4	16	48.5	1023	148	W08465		mb50409.rl Soares mou	5.94e-03
c	5	15	45.5	183	38	HSC02D012		H. sapiens partial cD	1.02e-01
c	6	15	45.5	224	153	W21175		zb57c09.rl Soares fet	1.02e-01
c	7	15	45.5	224	159	HS175387		zb57c09.rl Soares fet	1.02e-01
c	8	15	45.5	250	16	H31942		EST106521 Rattus sp.	1.02e-01
c	9	15	45.5	270	37	HSAL7H021		H. sapiens partial cD	1.02e-01
c	10	15	45.5	290	22	H53129		yq84f06.sl Homo sapie	1.02e-01
c	11	15	45.5	299	30	H80521		yu76c03.sl Homo sapie	1.02e-01
c	12	15	45.5	303	3	CELK032CYR		C.elegans cDNA clone	1.02e-01
c	13	15	45.5	318	6	CELK12903R		C.elegans cDNA clone	1.02e-01
c	14	15	45.5	320	81	R36228		yh91c09.sl Homo sapie	1.02e-01
c	15	15	45.5	354	93	R76012		y122d11.sl Homo sapie	1.02e-01
c	16	15	45.5	357	138	HUMUT147		Human STS UT147.	1.02e-01
c	17	15	45.5	360	5	CELK089AYF		C.elegans cDNA clone	1.02e-01
c	18	15	45.5	409	123	T81859		yd34e02.rl Homo sapie	1.02e-01
c	19	15	45.5	428	49	HUM408F02B		Human fetal brain cDN	1.02e-01
c	20	15	45.5	433	120	T70674		68 Zea mays cDNA clon	1.02e-01
c	21	15	45.5	437	82	R36669		yh89g06.sl Homo sapie	1.02e-01
c	22	15	45.5	443	172	TC5073		TgESTzy55b04.rl Toxop	1.02e-01
c	23	15	45.5	443	142	N82507		TgESTzy55b04.rl Toxop	1.02e-01
c	24	15	45.5	454	10	H12331		yj11f06.sl Homo sapie	1.02e-01
c	25	15	45.5	455	144	N94475		zb80b01.sl Homo sapie	1.02e-01
c	26	15	45.5	455	162	HS475320		zb80b01.sl Homo sapie	1.02e-01
c	27	15	45.5	513	121	T75965		10743 Arabidopsis tha	1.02e-01
c	28	14	42.4	91	34	H93159		yt93b07.rl Homo sapie	1.53e+00
c	29	14	42.4	184	38	HSC02D022		H. sapiens partial cD	1.53e+00
c	30	14	42.4	261	173	HS238VD10		H. sapiens (D8S1770) D	1.53e+00
c	31	14	42.4	292	102	RICR2383A		Rice cDNA, partial se	1.53e+00
c	32	14	42.4	314	17	H35246		EST111446 Rattus sp.	1.53e+00
c	33	14	42.4	315	136	HS4070TH5		H. sapiens DNA segment	1.53e+00
c	34	14	42.4	342	2	BNAF1556		Brassica campestris (	1.53e+00
c	35	14	42.4	349	125	T88344		12040 Arabidopsis tha	1.53e+00
c	36	14	42.4	360	5	CELK096F7F		C.elegans cDNA clone	1.53e+00
c	37	14	42.4	379	172	TC2753		TgESTzy25h12.sl Toxop	1.53e+00
c	38	14	42.4	432	158	HS049310		zb04g01.sl Homo sapie	1.53e+00
c	39	14	42.4	440	75	R12213		yf51h11.rl Homo sapie	1.53e+00
c	40	14	42.4	445	54	N24692		yx91e09.sl Homo sapie	1.53e+00
c	41	14	42.4	462	118	T64969		yd11d03.sl Homo sapie	1.53e+00
c	42	14	42.4	463	165	HS740301		za01f12.sl Homo sapie	1.53e+00

Mar 19 08:49

US-08-612-929-56.rst

3

43 14 42.4 569 1 ATTS0202 A. thaliana transcrib 1.53e+00  
44 14 42.4 604 56 N32182 yy25c11.s1 Homo sapie 1.53e+00  
45 14 42.4 1359 150 W13169 ma93g11.r1 Soares mou 1.53e+00

## ALIGNMENTS

RESULT 1  
LOCUS G01101 382 bp DNA STS 27-FEB-1995  
DEFINITION fruit fly STS Dm1786 clone DS07454 T7.  
ACCESSION G01101  
NID g684505  
KEYWORDS STS sequence; primer; sequence tagged site.  
SOURCE fruit fly vector=PAD105ac11 The PI library was made by D. Smoller  
in D. Hartl's lab (see Smoller et al., Chromosoma 100: 487).  
Chromosomal position was mapped by polytene chromosome in situ  
hybridization in the Hartl lab (see Hartl et al., PNAS 91: 6824).  
STS's were generated by sequencing the ends of the Drosophila  
insert in these PI clones, by the W. Kimmerly, C. Martin, and M.  
Palazzolo lab at LBL.

## ORGANISM

Drosophila melanogaster  
Eucaryotae; Metazoa; Arthropoda; Tracheata; Insecta; Diptera;  
Brachyera; Cyclorhapha; Drosophilidae; Drosophila.

## REFERENCE

1 (bases 1 to 382)

## AUTHORS

Rubin, G.

## TITLE

Drosophila STS

## JOURNAL

Unpublished (1994)

## COMMENT

Contact:

Berkeley Drosophila Genome Project

Primer A: GGGAAAGCTGTACAGGAGG

Primer B: CAAGGACATGTACGAGGAC

STS size: 217

PCR Profile:

Annealing: 58 degrees C

PCR Cycles: 32

Protocol:

Template: P1 Library Pools

Primer: 1 uM each

dNTPs: 250 uM each

Taq Poly: 0.05 units/ul

Total Vol: 15 ul

Buffer:

MgCl2: 1.5mM

KCl: 50 mM

Tris-HCl: 50 mM

pH: 8.3

Gelatin: .001 %

The PI library has been distributed to 16 regional sites. A list  
of these sites is available from FlyBase, via anonymous ftp to  
ftp.bio.indiana.edu in the file  
flybase/allied-data/genome-projects/1bl/1BL.doc.

## FEATURES

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Location/Qualifiers  
/organism="Drosophila melanogaster"  
/note="fruit fly"

28..244

28..47

primer\_bind complement(225..244)

primer\_bind

BASE COUNT 94 a 77 c 117 g 91 t 3 others

ORIGIN

Mar 19 08:49

US-08-612-929-56.rst

4

Query Match 48.5%; Score 16; DB 129; Length 382;  
Best Local Similarity 90.0%; Pred. No. 5.94e-03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 244 gtcgaagtaccagtagctacataa 263

||||| ||||| ||||| ||||| |||||

Cp 30 GTCGAAGTACCAGTAGAGAAA 11

## RESULT

2

LOCUS H77083 409 bp mRNA EST 07-NOV-1995

DEFINITION 17514 Arabidopsis thaliana cDNA clone 203C19T7.

ACCESSION H77083

NID g1054334

KEYWORDS EST.

SOURCE thale cress clone=203C19T7 primer=T7 dye primer library=Lambda-PRL2  
strain=var columbia vector=lambda Zip-Lox Reitel=Sal Reitel=Not  
Lambda PRL2 is a cDNA library derived from equal quantities of 4  
pools of mRNA. The mRNA sources were 1) 7 day germinated etiolated  
seedlings; 2) tissue culture grown roots; 3) staged plants half  
with 24 hour light cycle, half on 16 hr light, 8 hour dark-  
rosettes; 4) same plants as 3 but aerial tissue (stems, flowers  
and siliques). The vector is BRL's Lambda Zip-Lox. The cDNA  
inserts were directionally cloned with Sal-Not arms using oligo dT  
primed cDNA.

## ORGANISM

Arabidopsis thaliana  
Eucaryotae; Embryophyta; Magnoliophyta; Magnoliopsida; Capparales;  
Brassicaceae; Arabidopsis.

## REFERENCE

1 (bases 1 to 409)

## AUTHORS

Newman, T., de Bruijn, F.J., Green, P., Keegstra, K., Kende, H.,

McIntosh, L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomasow, M.,

Retzel, E. and Somerville, C.

Genes galore: a summary of methods for accessing results from

large-scale partial sequencing of anonymous Arabidopsis cDNA clones

Plant Physiol. 106, 1241-1255 (1994)

## JOURNAL

COMMENT

Contact: Thomas Newman

MSU-DOE Plant Research Laboratory

Michigan State University

MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E.

Lansing, MI

Tel: 517-353-0854

Fax: 517-353-9168

Email: 22313tcn@lbn.cl.msu.edu.

## FEATURES

source

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/clone="203C19T7"

/strain="var columbia"

/note="thale cress"

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## BASE COUNT

107 a 92 c 86 g 108 t 16 others

## ORIGIN

Query Match 48.5%; Score 16; DB 29; Length 409;

Best Local Similarity 86.4%; Pred. No. 5.94e-03;

Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 152 gaatccctttttctctgtact 173

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Qy 4 GAATCCGTTTCTACTGTACT 25

Mar 19 08:49

US-08-612-929-56.rst

5

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RESULT 3
ID M44651 standard; RNA; EST; 1023 BP.
AC W08465;
DT 27-APR-1996 (Rel. 47, Created)
DT 27-APR-1996 (Rel. 47, Last updated, Version 1)
DE mb50d09.r1 Soares mouse p3NMF19.5 Mus musculus cDNA clone 332849 5'
DE similar to gb:J00413 Mouse beta-globin major gene (MOUSE);.
KW EST.
OS Mus musculus (mouse)
OC Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
OC Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
RN [1]
RP 1-1023
RA Marra M., Hillier L., Allen M., Bowles M., Dietrich N.,
RA Dubuque T., Geisler S., Kucaba T., Lacy M., Le M., Martin J.,
RA Morris M., Schellenberg K., Steptoe M., Tan F., Underwood K.,
RA Moore B., Theising B., Wylie T., Lennon G., Soares B., Wilson R.,
RA Waterston R.;
RA "The WashU-HHMI Mouse EST Project";
RL Unpublished.
CC Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project
CC Washington University School of MedicineP 4444 Forest Park Parkway,
CC Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810
CC Email: mouseest@wustl.edu This clone is available
CC royalty-free through LNL ; contact the IMAGE Consortium
CC (info@image.llnl.gov) for further information. MGI:214249 Seq
CC primer: ETPRimer High quality sequence stop: 492. NCBI gi: 1282467
FH Key Location/Qualifiers
FH source 1..1023
FH /organism="Mus musculus"
FH /note="Vector: pT73D (Pharmacia) with a modified
FH polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
FH was primed with a Not I - oligo(dT) primer [5'
FH TGTTCACATCTGAAGTCGGAGCGCGCGCATTTTTTTTTTTT 3'],
FH double-stranded cDNA was size selected, ligated to Eco RI
FH adapters (Pharmacia), digested with Not I and cloned into
FH the Not I and Eco RI sites of a modified pT73 vector
FH (Pharmacia). Library went through one round of
FH normalization to a Cot = 5. Library constructed by Bento
FH Soares and M.Fatima Bonaldo."
FH /clone="332849"
FH /clone_lib="Soares mouse p3NMF19.5"
FH /dev_stage="19 weeks"
FH /lab_host="DH10B (ampicillin resistant)"
FH mRNA <1..>1023
SQ Sequence 1023 BP; 209 A; 237 C; 303 G; 266 T; 8 other;

Query Match 48.5%; Score 16; DB 170; Length 1023;
Best Local Similarity 86.4%; Pred. No. 5.94e-03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 684 ccgtttccactggaatacga 705
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Qy 8 CCGTTTCTACTGGTACTCGA 29

RESULT 4
LOCUS W08465 1023 bp mRNA EST 25-APR-1996
DEFINITION mb50d09.r1 Soares mouse p3NMF19.5 Mus musculus cDNA clone 332849 5'
similar to gb:J00413 Mouse beta-globin major gene (MOUSE);.
ACCESSION W08465
NID g1282467
KEYWORDS EST.
```

Mar 19 08:49

US-08-612-929-56.rst

6

```
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
Murinae; Mus.
REFERENCE 1 (bases 1 to 1023)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
TITLE The WashU-HHMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:214249
Seq primer: ETPRimer
High quality sequence stop: 492.

NCBI gi: 1282467 Location/Qualifiers
source 1..1023
/organism="Mus musculus"
/note="Vector: pT73D (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5'
TGTTCACATCTGAAGTCGGAGCGCGCGCATTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M.Fatima Bonaldo."
/clone="332849"
/clone_lib="Soares mouse p3NMF19.5"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
mRNA <1..>1023
BASE COUNT 209 a 237 c 303 g 266 t 8 others
ORIGIN

Query Match 48.5%; Score 16; DB 148; Length 1023;
Best Local Similarity 86.4%; Pred. No. 5.94e-03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 684 ccgtttccactggaatacga 705
| | | | | | | | | | | | | | | | | |
Qy 8 CCGTTTCTACTGGTACTCGA 29

RESULT 5
LOCUS HSC02D012 183 bp RNA EST 28-JAN-1995
DEFINITION H. sapiens partial cDNA sequence; clone c-02d01.
ACCESSION F01388
NID g644945
KEYWORDS partial cDNA sequence; transcribed sequence fragment.
```

## SOURCE

human.

## ORGANISM

Homo sapiens

Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominiidae; Homo.

## REFERENCE

1 (bases 1 to 183)

## AUTHORS

Genexpress.

## TITLE

Direct Submission

## JOURNAL

Submitted (19-JAN-1995) to the EMBL/GenBank/DBJ databases.

Genethon, B.P. 60, 91002 Evry Cedex France and Genetique Moleculaire et Biologie du developpement, CNRS UPR420 B.P. 8, 94801 Villejuif Cedex France. E-mail: genexpress@genethon.fr

## REFERENCE

2 (bases 1 to 183)

## AUTHORS

Genexpress.

## TITLE

The Genexpress cDNA program

## JOURNAL

Unpublished

## REFERENCE

3 (bases 1 to 183)

## AUTHORS

Unpublished

Auffray, C., Behar, G., Bois, F., Boucher, C., da Silva, C., Devignes, M.D., Duprat, S., Houlgatte, R., Jumeau, M.N., Lamy, B., Lorenzo, F., Mitchell, H., Mariage-Samson, R., Pietu, G., Pouliot, Y., Sebastiani-Kabakchis, C. and Tessler, A.

## TITLE

IMAGE: Integrated molecular analysis of the human genome and its expression

## JOURNAL

C.R. Acad. Sci., III, Sci. Vie 318, 263-272 (1995)

## COMMENT

Cloning method: total mRNA was oligo-(dT) primed and directionally cloned 5' -&gt; 3' into the HindIII -&gt; NotI sites of the lsfmid BA vector;

Sequencing method: single read, full automatic;  
Primer: (-21)/M13 universal;  
cDNA sequence complementary to mRNA (3' end)  
Stretch removed: removed at sequence 5' end  
Normalization method: Bento Soares, P.N.A.S in press;  
Genexpress\_library\_id: C;  
Genexpress\_sequence\_id: alc-02d01.

## FEATURES

Location/Qualifiers

1..183

/organism="Homo sapiens"

/clone\_lib="normalized infant brain cDNA from B. Soares, Psychiatry Dept. Columbia University USA"

/sex="female"

/tissue\_type="total brain"

/dev\_stage="3 months old"

/isolates="muscular atrophy patient"

BASE COUNT

64 a 25 c 31 g 54 t 9 others

ORIGIN

Query Match 45.5%; Score 15; DB 38; Length 183;

Best Local Similarity 88.9%; Pred. No. 1.02e-01;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 116 ttctactggtacttcac 133

Qy 13 TTCTACTGGTACTTCAC 30

RESULT 6

LOCUS W21175 224 bp mRNA EST 06-MAY-1996

DEFINITION zb57c09.r1 Soares fetal lung NBHL19W Homo sapiens cDNA clone 307696

5' similar to gb:M88458 ER LUMEN PROTEIN RETAINING RECEPTOR 2

(HUMAN);.

ACCESSION W21175

NID g1298226

## KEYWORDS

EST.

## SOURCE

human.

## ORGANISM

Homo sapiens

Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

## REFERENCE

1 (bases 1 to 224)

## AUTHORS

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawking, M., Holman, M., Hultman, N., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.

## TITLE

The WashU-Merck EST Project

## JOURNAL

Unpublished (1995)

## COMMENT

Contact: Wilson RK

WashU-Merck EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LNL ; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Seq primer: mob.RECA+ET

High quality sequence stop: 211.

## NCBI gi: 1298226

## Location/Qualifiers

1..224

## FEATURES

source

/organism="Homo sapiens"

/notes="Organ: lung; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-TGTTACCAATCTCAAGTGGAGCGCGCAATTTTTTTTTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Patima Bonaldo. This library was constructed from the same fetus as the fetal heart library, Soares fetal heart NBHL19W."

/clone="307696"

/clone\_lib="Soares fetal lung NBHL19W"

/dev\_stage="19 weeks"

/lab\_host="DH10B (ampicillin resistant)"

BASE COUNT

59 a 53 c 49 g 63 t

ORIGIN

Query Match 45.5%; Score 15; DB 153; Length 224;

Best Local Similarity 82.6%; Pred. No. 1.02e-01;

Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 142 aaaccattcttactgtgacttc 164

Qy 5 AAACCGTTTCTACTGTCTTC 27

RESULT 7

ID HSI75387 standard; RNA; EST; 224 BP.

AC W21175;

DT 08-MAY-1996 (Rel. 47, Created)

DT 08-MAY-1996 (Rel. 47, Last updated, Version 1)



DE z657c09.r1 Soares fetal lung NBHL19W Homo sapiens cDNA clone 307696  
 DE 5' similar to gb:M89458 ER LUMEN PROTEIN RETAINING RECEPTOR 2  
 DE (HUMAN);.  
 KW EST.  
 OS Homo sapiens (human)  
 OC Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;  
 OC Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominoidea.  
 RN [1]  
 RP 1-224  
 RA Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M.,  
 RA Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M.,  
 RA Parsons J., Rifkin L., Rohlfing T., Soares M., Tan F.,  
 RA Trevaskis E., Waterston R., Williamson A., Wohlmann P., Wilson R.;  
 RT "The WashU-Merck EST Project";  
 RL Unpublished.  
 CC Contact: Wilson RK WashU-Merck EST Project Washington University  
 CC School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,  
 CC MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email:  
 CC est@watson.wustl.edu This clone is available royalty-free through  
 CC LUNL; contact the IMAGE Consortium (info@image.llnl.gov) for  
 CC further information. Seq primer: mob.REGA+ET High quality sequence  
 CC stop: 211. NCBI gi: 1298226  
 FH Key Location/Qualifiers  
 FH source  
 FT 1..224  
 FT /organism="Homo sapiens"  
 FT /note="Organ: lung; Vector: pT7T3D (Pharmacia) with a  
 FT modified polylinker; Site.1: Not I; Site.2: Eco RI; 1st  
 FT strand cDNA was primed with a Not I - oligo(dT) primer  
 FT [5'-TGTTCAATCTCAAGTCGAGCGCGCAATTTTTTTTTTTT-3']  
 FT double-stranded cDNA was size selected, ligated to Eco RI  
 FT adapters (Pharmacia), digested with Not I and cloned into  
 FT the Not I and Eco RI sites of a modified pT7T3 vector  
 FT (Pharmacia). Library went through one round of  
 FT normalization to a Cot = 5. Library constructed by Bento  
 FT Soares and M.Patima Bonaldo. This library was constructed  
 FT from the same fetus as the fetal heart library, Soares  
 FT fetal heart NBHL19W."  
 FT /clone="307696"  
 FT /clone.lib="Soares fetal lung NBHL19W"  
 FT /dev\_stage="19 weeks"  
 FT /lab\_host="DH10B (ampicillin resistant)"  
 FT <1..>224  
 FT mRNA  
 SQ Sequence 224 BP; 59 A; 53 C; 49 G; 63 T; 0 other;  
 Query Match 45.5%; Score 15; DB 159; Length 224;  
 Best Local Similarity 82.6%; Pred. No. 1.02e-01;  
 Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 Db 142 aaaccattcttactgtgacttc 164  
 ||||| | ||||| |||||  
 QY 5 AAACGGTTTCTACTGGTACTTC 27  
 RESULT 8  
 LOCUS H31942 250 bp mRNA EST 08-SEP-1995  
 DEFINITION EST106521 Rattus sp. cDNA 3' end.  
 ACCESSION H31942  
 NID g977359  
 KEYWORDS EST.  
 SOURCE rat primer=M13 - 21 library=Rat PC-12 cells, untreated  
 vector=pBluescript SK- Rsite=EcoRI Rsite2=XhoI poly(A) + RNA was  
 purified from untreated PC12 cells cultured for 9 days. cDNA was  
 constructed using an oligo-dT primer and directionally cloned using

the Lambda ZAP II Vector Kit by Stratagene.  
 ORGANISM Rattus sp.  
 Eukaryota; Eukaryotes; Metazoa; Chordata;  
 Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Myomorpha;  
 Muridae; Murinae; Rattus.  
 REFERENCE 1 (bases 1 to 250)  
 AUTHORS Lee, N.H., Weinstock, K.G., Kirkness, E.F., Earle-Hughes, J.A.,  
 Fuldner, R.A., Marmaras, S., Glodek, A., Gocayne, J.D., Adams, M.D.,  
 Kerlavage, A.R., Fraser, C.M. and Venter, J.C.  
 TITLE Comparative expressed sequence tag analysis of differential gene  
 expression profiles in PC-12 cells before and after nerve growth  
 factor treatment  
 JOURNAL Proc. Natl. Acad. Sci. USA 92, 8303-8307 (1995)  
 COMMENT Other ESTs: EST106522  
 Contact: Lee NH  
 The Institute for Genomic Research  
 932 Clopper Rd, Gaithersburg, MD 20878  
 Tel: 3018699056  
 Fax: 3018699423  
 Email: nhlee@tigr.org  
 For clone availability please contact the TIGR Database  
 (tcbinfo@db.tigr.org).  
 FEATURES  
 source  
 1..250  
 /organism="Rattus sp."  
 /note="rat"  
 mRNA <1..>250  
 BASE COUNT 72 a 58 c 42 g 75 t 3 others  
 ORIGIN  
 Query Match 45.5%; Score 15; DB 16; Length 250;  
 Best Local Similarity 80.0%; Pred. No. 1.02e-01;  
 Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 Db 116 cgtttcttagtctactttaagtt 140  
 ||||| | ||||| | |||||  
 QY 9 CGTTTCTACTGTACTTCGACGTT 33  
 RESULT 9  
 LOCUS HSA17H021 270 bp RNA EST 04-JUN-1993  
 DEFINITION H. sapiens partial cDNA sequence; clone 17H02; strand (-), single  
 read.  
 ACCESSION Z13017  
 NID g24384  
 KEYWORDS partial cDNA sequence; transcribed sequence fragment.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Eukaryotes; Metazoa; Chordata;  
 Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 REFERENCE 1 (bases 1 to 270)  
 Genexpress.  
 TITLE Direct Submission  
 JOURNAL Submitted (22-JUN-1992) Genethon, B.P. 60, 91002 Evry Cedex France  
 and Genetique Moleculaire et Biologie du developpement, CNRS UPR420  
 B.P. 8, 94801 Villejuif Cedex France.E-mail: genexpress@genethon.fr  
 REFERENCE 2 (bases 1 to 270)  
 Genexpress.  
 AUTHORS The Genexpress cDNA program  
 TITLE Unpublished  
 JOURNAL  
 COMMENT cloning vector is pBluescript SK(+);  
 Genexpress library reference is A.  
 full automatic  
 IMPORTANT: Computer analyses of the total data set derived from

this library indicate a significant proportion of sequences of yeast and bacterial origin. Please contact us if you identify such an entry.

## FEATURES

source Location/Qualifiers  
1..270  
/organism="Homo sapiens"  
/cell\_line="T Lymphoblastoid cell line ATCC#CCL119"  
/clone\_lib="CLONTECH cDNA library CCRF-CEM, cat# HL 1063g"  
BASE COUNT 54 a 57 c 55 g 94 t 10 others  
ORIGIN

Query Match 45.5%; Score 15; DB 37; Length 270;  
Best Local Similarity 94.1%; Pred. No. 1.02e-01;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 41 ttctactggaactcg 57  
||||| ||||| |||||  
Qy 12 TTCTACTGCTACTTCG 28

## RESULT 10

LOCUS H53129 290 bp mRNA EST 20-SEP-1995  
DEFINITION yq94f06.s1 Homo sapiens cDNA clone 202499 3' similar to gb:M64925  
55 KD ERYTHROCYTE MEMBRANE PROTEIN (HUMAN);

ACCESSION H53129  
NID 9993276  
KEYWORDS EST.

SOURCE human clone=202499 primer=Promega -21ml3 library=Soares fetal liver spleen INFUS vector=pfT73D (Pharmacia) with a modified polylinker host=DHI10B (ampicillin resistant) Reitel-Pac I Reite2=Eco RI Liver and spleen from a 20 week-post conception male fetus. 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5' AACTGAGAGTAATTAAGATCTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo.

## ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 290)

## REFERENCE

AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.

TITLE The WashU-Merck EST Project  
JOURNAL Unpublished (1995)  
COMMENT

Contact: Wilson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
High quality sequence starts: 1  
High quality sequence stops: 1  
Source: IMAGE Consortium, LNL  
This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.lnl.gov) for further information.  
Trace considered overall poor quality.

## FEATURES

source Location/Qualifiers  
1..290  
/organism="Homo sapiens"  
/clone="202499"  
/note="human"  
mRNA <1..>290  
BASE COUNT 72 a 61 c 62 g 64 t 31 others  
ORIGIN

Query Match 45.5%; Score 15; DB 22; Length 290;  
Best Local Similarity 72.0%; Pred. No. 1.02e-01;  
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Db 84 aagttcagtnaataaacqcttnc 108  
||||| ||||| ||||| |||||  
Cp 26 AAGTACCAGTAGAAGCGTTCCG 2

## RESULT 11

LOCUS H80521 299 bp mRNA EST 09-NOV-1995  
DEFINITION yu76c03.s1 Homo sapiens cDNA clone 239716 3' similar to gb:M64925  
55 KD ERYTHROCYTE MEMBRANE PROTEIN (HUMAN);

ACCESSION H80521  
NID g1058610  
KEYWORDS EST.

SOURCE human clone=239716 primer=Promega -21ml3 library=Soares fetal liver spleen INFUS vector=pfT73D (Pharmacia) with a modified polylinker host=DHI10B (ampicillin resistant) Reitel-Pac I Reite2=Eco RI Liver and spleen from a 20 week-post conception male fetus. 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5' AACTGAGAGTAATTAAGATCTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo.

## ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 299)

## REFERENCE

AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.

TITLE The WashU-Merck EST Project  
JOURNAL Unpublished (1995)  
COMMENT

Contact: Wilson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
High quality sequence stops: 175  
Source: IMAGE Consortium, LNL  
This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.lnl.gov) for further information.

## FEATURES

source Location/Qualifiers  
1..299  
/organism="Homo sapiens"  
/clone="239716"



Mar 19 08:49

US-08-612-929-56.rst

15

AUTHORS

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaaskie, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.

TITLE

The WashU-Merck EST Project

JOURNAL COMMENT

Unpublished (1995)

Contact: Wilson RK

WashU-Merck EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence stops: 272

Source: IMAGE Consortium, LNL

This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES

source

1..320

/organism="Homo sapiens"

/clone="137104"

/note="human"

BASE COUNT 90 a 45 c 77 g 107 t 1 others

ORIGIN

Query Match 45.5%; Score 15; DB 81; Length 320;

Best Local Similarity 82.6%; Pred. No. 1.02e-01;

Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 108 gaagtaacatttgaaactgttt 130

||||| || ||||| |||||

Cp 27 GAAGTACCAGTAGAAGCGTTT 5

RESULT 15

LOCUS R76012 354 bp mRNA EST 06-JUN-1995

DEFINITION Y122d11.s1 Homo sapiens cDNA clone 158997 3'.

ACCESSION R76012

NID g850694

KEYWORDS EST.

SOURCE human clone=158997 library=Soares breast 2NBH8et vector=ptT73D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) primer=Promega -2lm13 Rsite1=Not I Rsite2=Eco RI Adult female. 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGAGCGCGCCCTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 230. Library constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata;

Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;

Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;

Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 354)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,

Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,

Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,

Trevaaskie, E., Waterston, R., Williamson, A., Wohlmann, P. and

Wilson, R.

The WashU-Merck EST Project

TITLE

Mar 19 08:49

US-08-612-929-56.rst

16

JOURNAL

COMMENT

Unpublished (1995)

Contact: Wilson RK

WashU-Merck EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence stops: 118

Source: IMAGE Consortium, LNL

This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES

source

1..354

/organism="Homo sapiens"

/clone="158997"

/note="human"

BASE COUNT 103 a 80 c 99 g 59 t 13 others

ORIGIN

Query Match 45.5%; Score 15; DB 93; Length 354;

Best Local Similarity 79.2%; Pred. No. 1.02e-01;

Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Db 305 gaagacaagtgganaacgggttc 328

|||| || ||| || ||||| |||

Cp 27 GAAGTACCAGTAGAAGCGTTTC 4

Search completed: Wed Mar 19 08:50:38 1997

Job time : 81 secs.





OS Synthetic.  
 PN EP-571911-A.  
 PD 01-DEC-1993.  
 PF 24-MAY-1993; 108325.  
 PR 26-MAY-1992; US-889651.  
 PA (BECT ) BECTON DICKINSON CO.  
 PI Shank DD, Spears PA;  
 DR WPI; 93-378844/48.  
 PT New oligo:nucleotide probes specific for Mycobacteria - used for  
 PT detection and amplification of Mycobacteria nucleic acid in  
 PT samples  
 PS Claim 3; Page 14; 23pp; English.  
 CC Oligonucleotide probe MK14-A consists of nucleotides 5-95 of MK14  
 CC (Q51735). It hybridized to all spp. of mycobacteria tested, but  
 CC cross reacted to a few non-mycobacterial spp. The probe may  
 CC be useful as an initial screen for mycobacterial infection.  
 CC See also Q51735-45 and Q51747-59.  
 SQ Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;  
  
 Query Match 63.6%; Score 21; DB 9; Length 91;  
 Best Local Similarity 0.0%; Pred. No. 2.06e-02;  
 Matches 0; Conservative 26; Mismatches 5; Indels 0; Gaps 0;

Db 18 vhhvhhvhhvhhvhhvhhvhhvhhv 48  
 QY 1 CGCGAACCCTTTCTACTGCTACTTCGACG 31

## RESULT 5

ID Q51746 standard; cDNA; 91 BP.  
 AC Q51746;  
 DT 31-MAY-1994 (first entry)  
 DE Oligonucleotide probe MK14-A  
 KW Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;  
 KW Synthetic.  
 OS Synthetic.  
 PN EP-571911-A.  
 PD 01-DEC-1993.  
 PF 24-MAY-1993; 108325.  
 PR 26-MAY-1992; US-889651.  
 PA (BECT ) BECTON DICKINSON CO.  
 PI Shank DD, Spears PA;  
 DR WPI; 93-378844/48.  
 PT New oligo:nucleotide probes specific for Mycobacteria - used for  
 PT detection and amplification of Mycobacteria nucleic acid in  
 PT samples  
 PS Claim 3; Page 14; 23pp; English.  
 CC Oligonucleotide probe MK14-A consists of nucleotides 5-95 of MK14  
 CC (Q51735). It hybridized to all spp. of mycobacteria tested, but  
 CC cross reacted to a few non-mycobacterial spp. The probe may  
 CC be useful as an initial screen for mycobacterial infection.  
 CC See also Q51735-45 and Q51747-59.  
 SQ Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;

Query Match 63.6%; Score 21; DB 9; Length 91;  
 Best Local Similarity 0.0%; Pred. No. 2.06e-02;  
 Matches 0; Conservative 27; Mismatches 6; Indels 0; Gaps 0;

Db 28 vhhvhhvhhvhhvhhvhhvhhvhhv 60  
 Cp 33 AACGTCGAGTACACGAGTAAACGGTTCCG 1

RESULT 6  
 ID Q83492 standard; cDNA; 423 BP.  
 AC Q83492;  
 DT 20-SEP-1995 (first entry)  
 DE Chimeric antibody 3B9 heavy chain.  
 KW Chimeric antibody; antibody engineering; monoclonal antibody;  
 KW MAb; interleukin-4; IL-4; allergy; ds.  
 OS Homo sapiens; Mus sp.  
 FH Key Location/Qualifiers  
 FT CDS 1..423  
 FT /tag= a  
 FT sig\_peptide 1..57  
 FT /tag= b  
 FT mat\_peptide 58..423  
 FT /tag= c  
 PN W09507301-A.  
 PD 16-MAR-1995.  
 PR 07-SEP-1993; US-117366.  
 PR 14-OCT-1993; US-136783.  
 PA (SMIK ) SMITHKLINE BEECHAM CORP.  
 PA (SMIK ) SMITHKLINE BEECHAM PLC.  
 PI Gross MS, Holmes SD, Sylvester DR;  
 DR WPI; 95-123387/16.  
 DR P-PSDB; R70191.  
 PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived  
 PT from high affinity mAbs - useful in treatment of IL-4-mediated  
 PT and IgE-mediated allergic conditions  
 PS Disclosure; Fig.3; 97pp; English.  
 CC A human/mouse chimeric antibody heavy chain variable region was  
 CC constructed (given in R70191) that contained the mouse anti-human  
 CC IL-4 MAb 3B9 variable region including 3 CDRs (R70198-200) and a  
 CC human antibody signal peptide (R70193). The construct was used  
 CC for humanized antibody production.  
 SQ Sequence 423 BP; 87 A; 115 C; 110 G; 111 T;

Query Match 63.6%; Score 21; DB 14; Length 423;  
 Best Local Similarity 86.2%; Pred. No. 2.06e-02;  
 Matches 25; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 361 gagactgtgtctactgtactcgaatgt 389  
 QY 4 GAAACCGTTTCTACTGCTACTTCGACGT 32

RESULT 7  
 ID Q83491 standard; cDNA; 483 BP.  
 AC Q83491;  
 DT 20-SEP-1995 (first entry)  
 DE Mouse MAb 3B9 heavy chain.  
 KW Chimeric antibody; humanized antibody; antibody engineering;  
 KW monoclonal antibody; MAb; interleukin-4; IL-4; allergy; ds.  
 OS Mus sp.  
 FH Key Location/Qualifiers  
 FT CDS 64..483  
 FT /tag= a  
 FT sig\_peptide 64..120  
 FT /tag= b  
 FT mat\_peptide 121..483  
 FT /tag= c  
 PN W09507301-A.  
 PD 16-MAR-1995.  
 PR 07-SEP-1994; U10308.  
 PR 07-SEP-1993; US-117366.





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FT      /tag= a
FT      /note= "can be present 3 to 6 times"
PN      W09103550-A.
PD      21-MAR-1991.
PF      28-AUG-1990; U04840.
PR      29-AUG-1989; US-399874.
PA      (FARH ) HOECHST AG.
PA      (GEOH-) GEN HOSPITAL CORP.
PI      Stencelin S, Ulmer W, Habermann P, Uhlmann E, Seed B;
DR      WPI; 91-102070/14.
PT      Prepn. of fusion proteins contg. ballast constituent and protein
PT      - giving prods. which are protease resistant or insoluble
PS      Claim 13; Page 51; 60pp; English.
CC      This oligonucleotide is an example of a member of an oligonucleotide
CC      library encoding ballast constituents. The oligonucleotides are
CC      inserted into a vector, functionally linked to a regulatory region
CC      and to the proinsulin structural gene. Host cells transformed with
CC      such plasmids produce proinsulin-ballast fusion proteins in
CC      high yield. The ballast is short and does not disturb the folding of
CC      the proinsulin. The fusion protein is soluble or easily
CC      solubilised. The oligonucleotide encodes a cleavage site at its 3'
CC      end which allows easy removal of the ballast constituent.
CC      See also Q11194-Q11200 and Q11202.
SQ      Sequence 30 BP; 2 A; 9 C; 4 G; 2 T;

Query Match          57.6%; Score 19; DB 2; Length 30;
Best Local Similarity 34.8%; Pred.No. 2.54e-01;
Matches 8; Conservative 13; Mismatches 2; Indels 0; Gaps 0;

Db      5 cddcdcdcdcdcdcdcdcdcdacg 27
       :::::: :|::|::|
Qy      9 CGTTTCTACTGGTACTGCAGC 31

RESULT 11
ID      Q11197 standard; DNA; 33 BP.
AC      Q11197;
DT      05-JUN-1991 (first entry)
DE      Ballast Constituent coding sequence #4.
KW      Ballast constituent; fusion protein; oligonucleotide library; ss.
OS      Synthetic.
FH      Key Location/Qualifiers
FT      repeat_unit 7..9
FT      /tag= a
FT      /note= "can be present 4 to 7 times"
PN      W09103550-A.
PD      21-MAR-1991.
PF      28-AUG-1990; U04840.
PR      29-AUG-1989; US-399874.
PA      (FARH ) HOECHST AG.
PA      (GEOH-) GEN HOSPITAL CORP.
PI      Stencelin S, Ulmer W, Habermann P, Uhlmann E, Seed B;
DR      WPI; 91-102070/14.
PT      Prepn. of fusion proteins contg. ballast constituent and protein
PT      - giving prods. which are protease resistant or insoluble
PS      Claim 13; Page 50; 60pp; English.
CC      This oligonucleotide is an example of a member of an oligonucleotide
CC      library encoding ballast constituents. The oligonucleotides are
CC      inserted into a vector, functionally linked to a regulatory region
CC      and to a structural gene encoding a desired protein, e.g. proinsulin.
CC      Host cells transformed with such plasmids produce fusion proteins in
CC      high yield. The ballast is short and does not disturb the folding of
CC      the desired protein. The fusion protein is soluble or easily
CC      solubilised. The oligonucleotide encodes a cleavage site at its 3'

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CC end which allows easy removal of the ballast constituent.
CC See also Q11194-6 and Q11198-Q11202.
SQ Sequence 33 BP; 2 A; 10 C; 3 G; 1 T; 0 Gaps 0;
Query Match 57.6%; Score 19; DB 2; Length 33;
Best Local Similarity 26.1%; Pred.No. 2.54e-01;
Matches 6; Conservative 15; Mismatches 2; Indels 0; Gaps 0;

Db 8 cddcdcdcdcdcdcdcdcdcd 30
|:::|::|:::|::|::|::|::|:
QY 9 CGTTTCTACTGCTACTTCGACG 31

RESULT 12
ID Q46603 standard; DNA; 33 BP.
AC Q46603;
DT 20-DEC-1993 (first entry)
DE Mixed oligonucleotide 45 encodes ballast constituent.
KW Fusion protein; ballast constituent; pro-insulin production;
KW recombinant protein production; HMG CoA reductase;
KW human 3-hydroxy-3-methylglutaryl-coenzyme A-reductase;
KW mixed oligonucleotide; ss.
OS Synthetic.
FH Key Location/Qualifiers
FT repeat unit 7..9
FT /*tag= a
FT /rpt_type= tandem
FT /notes= "can be repeated 4-8 times"
FT repeat region 7..30
FT /*tag= b
FT /note= "(OCD)8"
FT FT US5272793-A.
PN 13-JUL-1993. 399874.
PD 29-AUG-1989; 399874.
PF 29-AUG-1989; US-399874.
PR 23-APR-1992; US-838221.
PA (GENO ) GEN HOSPITAL CORP.
PA (FARH ) HOECHST AG.
PI Habermann P, Seed B, Stengelin S, Uhlmann E, Ulmer W;
DR WPI; 93-235119/29.
PT Fusion proteins for prodn. of e.g. pro-insulin - comprise gene
PT for desired protein and oligo-nucleotide(s) encoding ballast
PT protein
PS Claim 4; Column 29; 22pp; English.
CC This preferred mixed oligonucleotide encodes a ballast constituent
CC and is inserted between a regulatory region and the structural gene
CC encoding a desired protein. The short ballast component improves
CC protease resistance of the fusion protein while still allowing the
CC desired protein to adopt its correct conformation prior to cleavage
CC of the ballast constituent. Proteins which can be produced as fusion
CC proteins with a ballast region include pro-insulin and HMG CoA
SQ Sequence 33 BP; 1 A; 10 C; 3 G; 1 T;

Query Match 57.6%; Score 19; DB 7; Length 33;
Best Local Similarity 26.1%; Pred.No. 2.54e-01;
Matches 6; Conservative 15; Mismatches 2; Indels 0; Gaps 0;

Db 8 cddcdcdcdcdcdcdcdcdcd 30
|:::|::|:::|::|::|::|::|:
QY 9 CGTTTCTACTGCTACTTCGACG 31

RESULT 13

```

ID Q46605 standard; DNA; 48 BP.  
 AC Q46605;  
 DT 20-DEC-1993 (first entry)  
 DE Mixed oligonucleotide (9a) encodes ballast constituent.  
 KW Fusion protein; ballast constituent; monkey pro-insulin;  
 KW recombinant protein production; HMG CoA reductase;  
 KW human 3-hydroxy-3-methylglutaryl-coenzyme A-reductase;  
 KW mixed oligonucleotide; *ss*.  
 OS Synthetic.  
 PN US5227293-A.  
 PD 13-JUL-1993.  
 PR 29-AUG-1989; 399874.  
 PR 29-AUG-1989; US-399874.  
 PR 23-APR-1992; US-838221.  
 PA (GENO ) GEN HOSPITAL CORP.  
 PA (FARH ) HOECHST AG.  
 PI Habermann P, Seed B, Stengelin S, Uhlmann E, Ulmer W;  
 PI WPI; 93-235119/29.  
 PT Fusion proteins for prodn. of e.g. pro-insulin - comprise gene  
 PT for desired protein and oligo-nucleotide(s) encoding ballast  
 PT protein  
 PS Example 1; Column 7; 22pp; English.  
 CC Mixed oligonucleotide (9) (Q46604) encodes a ballast constituent  
 CC and forms part of a fusion gene with the monkey pro-insulin gene;  
 CC the double-stranded ballast constituent insert was prepared from  
 CC the synthetic mixed oligonucleotide (9a) (Q46605) which was filled  
 CC in with Klenow polymerase and cut with MluI and Nco. The genebank  
 CC pINT4x contains the resulting plasmid population. After transforming  
 CC E.coli WS310 with the genebank, one clone (pINT41) was found to  
 CC produce, in relatively large quantities, a protein containing an  
 CC insulin constituent. The exact sequence of the pINT41 ballast  
 CC constituent is given in Q51798.  
 SQ Sequence 48 BP; 3 A; 9 C; 16 G; 7 T;

Query Match 57.6%; Score 19; DB 7; Length 48;  
Best Local Similarity 34.8%; Pred. No. 2.54e-01;  
Matches 8; Conservative 13; Mismatches 2; Indels 0; Gaps 0;

**D<sub>b</sub>**     5 cgtghg             |||:||:::||:::||:::||

**C<sub>p</sub>**     31 CGTCGAAGTACCACGTAGAAAACG 9

RESULT	14	
ID	Q46602	standard; DNA; 30 BP.
AC	Q46602;	
DT	20-DEC-1993	(first entry)
DE	Mixed oligonucleotide #4	encodes ballast constituent.
KW	Fusion protein; ballast	constituent; pro-insulin production;
KW	recombinant protein	production; HMG CoA reductase;
KW	human 3-hydroxy-3-methylglutaryl-coenzyme A-reductase;	
KW	mixed oligonucleotide; ss.	
OS	Synthetic.	
FT	Key	Location/Qualifiers
FT	repeat_unit	7..9
FT	/*tag= a	
FT	/rpt_type= tandem	
FT	/note= "can be repeated 4-8 times"	
FT	repeat_region	7..27
FT	/*tag= b	
FT	/note= "(DCD) 7"	
PN	U5527293-A.	
PD	13-JUL-1993.	
PF	29-AUG-1989; 399874.	

PR	29-AUG-1989; US-399874.		
PR	23-APR-1992; US-838221.		
PA	(GEOH) GEN HOSPITAL CORP.		
PA	(FARH) HOECHST AG.		
PI	Habermann P, Seed B, Stangelin S, Uhlmann E, Ulmer W;		
DR	WPI; 93-235119/29.		
PT	Fusion proteins for prodn. of e.g. pro-insulin - comprise gene		
PT	for desired protein and oligo-nucleotide(s) encoding ballast		
PT	protein		
PS	Claim 4; Column 29; 22pp; English.		
CC	This preferred mixed oligonucleotide encodes a ballast constituent		
CC	and is inserted between a regulatory region and the structural gene		
CC	encoding a desired protein. The short ballast component improves		
CC	protease resistance of the fusion protein while still allowing the		
CC	desired protein to adopt its correct conformation prior to cleavage		
CC	of the ballast constituent. Proteins which can be produced as fusion		
CC	proteins with a ballast region include pro-insulin and HMC CoA		
CC	reductase.		
SQ	Sequence 30 BP: 1 A; 9 C; 3 G; 1 T;		

Query Match	54.5%	Score 18;	DB 7;	Length 30;
Best Local Similarity	25.0%;	Pred. No. 8.62e-01;		
Matches	5:	Conservative	14:	Mismatches 1;
				Indels 0;
				Gaps 0;

Db	6	w	c	d	d	d	d	d	d	d	d	d	d	d	d	d	d	25
		:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	
Qv	13	T	T	C	T	A	C	T	G	G	T	A	C	T	T	C	G	32

RESULT 15

ID T12830 standard; cDNA; 363 BP.

AC T12830;

DT 10-OCT-1996 (first entry)

DE Switched VL region kappa-body fragment hZCE-CSVL.

DE Variable region; hZCE-CSVL; in vitro; in vivo;

KW CDR switched variable light chain region; kappa-body fragment;

KW diagnosis; therapy; naked antibody; radioimmunotherapy;

KW radioimmunodiagnostics; radioimmunometric assays; ELISA;

KW immunohistochemical; complementarity determining region; ss.

OS Synthetic.

PN W09606625-A1.

PD 07-MAR-1996.

PF 25-AUG-1995; U10791.

PR 26-AUG-1994; US-296625.

PA (ELIL ) LILLY & CO ELI.

PI Ill CR, Ludwig JR, Rathnachalam R;

PT WPI; 96-160137/16.

PT Recombinant antibody comprising CDR-switched light chain variable

PT region - having VL domain framework and VH domain CDRs, useful in

PT radioimmunotherapy, ELISA assays, etc.

PS Example 11; Page 105; 162pp; English.

CC The present sequence encodes the CDR switched light chain variable

CC (VL) region (CSVL) kappa-body fragment, hZCE-CSVL. A CSVL comprises

CC at least 1 VL region with 3 CDR, where 1 or more of the CDR is

CC derived from the corresponding CDR of a heavy chain variable (VH)

CC region of 1 (donor) Ab, and 4 framework (FW) regions where 1 or more

CC of the regions is derived from the corresponding FW region(s) from

CC the VL region of the same or different (acceptor) Ab.

CC The CSVL Ab, or kappa-body fragment can be used in in vitro and

CC in vivo diagnostic and therapeutic applications, including naked Ab

CC therapy, radioimmunotherapy (i.e. when fused to a chelating peptide

CC incorporating Yttrium-90 as the therapeutic radionuclide), in vivo

CC radioimmunodiagnostics, in vitro radioimmunometric assays, ELISA

CC and immunophistochemical applications.

Mar 19 08:46

US-08-612-929-56.mg

13

SQ Sequence 363 BP; 74 A; 138 C; 86 G; 65 T;

Query Match 54.5%; Score 18; DB 22; Length 363;

Best Local Similarity 100.0%; Pred. No. 8.62e-01;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 315 ctactggctacttcgacgt 332

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Qy 15 CTACTGGCTACTTCGACGT 32

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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Sarcophagii; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 321)  
AUTHORS Brezinschek, H.P.  
TITLE Direct Submission  
JOURNAL Submitted (05-MAY-1995) to the EMBL/GenBank/DBJ databases.  
Brezinschek H.P., Department of Internal Medicine, Harold C. Simmons Arthritis Research Center, University of Texas Southwestern Medical Center, 5323 Harry Hines Blvd., Dallas, TX 75235-8884, USA  
REFERENCE 2 (bases 1 to 321)  
AUTHORS Brezinschek, H.P., Brezinschek, R.I. and Lipsky, P.E.  
TITLE Analysis of the heavy chain repertoire of human peripheral B cells using single-cell polymerase chain reaction  
JOURNAL J. Immunol. 155 (1), 190-202 (1995)  
MEDLINE 95325588  
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Query Match 54.5%; Score 18; DB 52; Length 321;  
Best Local Similarity 100.0%; Pred. No. 2.93e+00;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 294 ttctactggtactctga 311  
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Qy 12 TTCTACTGGTACTTCCA 29

RESULT 4  
LOCUS MUSIHC 414 bp mRNA ROD 05-MAY-1995  
DEFINITION Mus musculus immunoglobulin heavy chain mRNA, 5' end of cds.  
ACCESSION L41877  
NID g798802  
KEYWORDS immunoglobulin heavy chain.  
SOURCE Mus musculus (strain BALB/c, sub\_species domesticus) cDNA to mRNA.  
ORGANISM Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.  
REFERENCE 1 (bases 1 to 414)  
AUTHORS Asakura, K., Miller, D.J., Fogulie, R.J., Pease, L.R. and Rodriguez, M.  
TITLE Oligodendrocyte-specific O1, O4, and HNK-1 monoclonal antibodies are encoded by germ-line immunoglobulin genes  
JOURNAL DNA (1995) In press  
FEATURES  
source  
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1..414  
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Mar 19 08:46

US-08-612-929-56.rge

6

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mRNA  
sig\_peptide  
mat\_peptide

BASE COUNT 99 a 97 c 117 g 101 t  
ORIGIN

Query Match 54.5%; Score 18; DB 67; Length 414;  
Best Local Similarity 95.0%; Pred. No. 2.93e+00;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 361 ttctactggtactctgatg 380  
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Qy 13 TTCTACTGGTACTTGCAGT 32

RESULT 5  
LOCUS ANABCLSA 2169 bp DNA BCT 06-JUL-1993  
DEFINITION Anabaena sp. ribulose 1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) gene, complete cds; ribulose 1,5-bisphosphate carboxylase/oxygenase small subunit (rbcs) gene, complete cds.  
ACCESSION L02520  
NID q142081  
KEYWORDS RUBISCO; large subunit; rbcl gene; rbcs gene; ribulose 1,5-bisphosphate carboxylase/oxygenase; small subunit.  
SOURCE Anabaena sp. (strain PCC 7120) (library: PCC7120) DNA.  
ORGANISM Prokaryota; Gracilicutes; Oxysphobacteria; Cyanobacteria; Nostocales; Nostocaceae.  
REFERENCE 1 (bases 1 to 2169)  
AUTHORS Curtis, S.E. and Haselkorn, R.  
TITLE Isolation and sequence of the gene for the large subunit of ribulose-1,5-bisphosphate carboxylase from the cyanobacterium Anabaena 7120  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 80, 1835-1839 (1983)  
REFERENCE 2 (bases 1 to 2169)  
AUTHORS Nierzwicki-Bauer, S.A., Curtis, S.E. and Haselkorn, R.  
TITLE Cotranscription of genes encoding the small and large subunits of ribulose-1,5-bisphosphate carboxylase in the cyanobacterium Anabaena 7120  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 81, 5961-5965 (1984)  
MEDLINE 85014888  
REFERENCE 3 (bases 1 to 2169)  
AUTHORS Larimer, F.W. and Soper, T.S.  
TITLE Overproduction of Anabaena PCC7120 ribulose-bisphosphate carboxylase/oxygenase in Escherichia coli  
JOURNAL Gene 126, 85-92 (1993)  
MEDLINE 93231541  
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BASE COUNT 600 a 512 c 459 g 598 t
ORIGIN

Query Match 54.5%; Score 18; DB 16; Length 2169;
Best Local Similarity 90.9%; Pred. No. 2.93e+00;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 282 gtcttcctactgtacttgaccg 303
|| ||||| ||||| ||||| |||||
Qy 10 GTTTTCTACTGCTTCTGACG 31

RESULT 6
LOCUS ANARBCLSB 2285 bp DNA BCT 06-JUL-1993
DEFINITION Anabaena sp. ribulose 1,5-bisphosphate carboxylase/oxygenase large
subunit (rbcl) gene, complete cds; ribulose 1,5-bisphosphate
carboxylase/oxygenase small subunit (rbcs) gene, complete cds.
ACCESSION L02521
NID g142084
KEYWORDS RUBISCO; large subunit; rbcl gene; rbcs gene;
ribulose 1,5-bisphosphate carboxylase/oxygenase; small subunit.
SOURCE Anabaena sp. (strain PCC 7120) (Library: PCC7120) DNA.
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ORGANISM Anabaena sp.
Prokaryotae; Gracillitutes; Oxyphotobacteria; Cyanobacteria;
Nostocales; Nostocaceae.
REFERENCE 1 (bases 1 to 2285)
AUTHORS Curtis,S.E. and Haselkorn,R.
TITLE Isolation and sequence of the gene for the large subunit of
ribulose-1,5-bisphosphate carboxylase from the cyanobacterium
Anabaena 7120
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 80, 1835-1839 (1983)
REFERENCE 2 (bases 1 to 2285)
AUTHORS Nierzwicki-Bauer,S.A., Curtis,S.E. and Haselkorn,R.
TITLE Cotranscription of genes encoding the small and large subunits of
ribulose-1,5-bisphosphate carboxylase in the cyanobacterium
Anabaena 7120
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 81, 5961-5965 (1984)
REFERENCE 3 (bases 1 to 2285)
AUTHORS Larimer,F.W. and Soper,T.S.
TITLE Overproduction of Anabaena PCC7120 ribulose-bisphosphate
carboxylase/oxygenase in Escherichia coli
Gene 126, 85-92 (1993)
JOURNAL 93231541
MEDLINE Location/Qualifiers
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KLEGERGITMGEVDLLRENYVEQDKSRGIYFTQDWASIPGWAVASGGIHWHPALV  
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BASE COUNT 637 a 558 c 516 g 574 t  
ORIGIN

Query Match 54.5%; Score 18; DB 16; Length 2285;  
Best Local Similarity 90.9%; Pred. No. 2.93e+00;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 628 gtcttctactgtacttgagc 649  
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Qy 10 GTTTTCTACTGCTACTTCGACG 31

RESULT 7  
LOCUS ANABCLSC 2695 bp DNA BCT 06-JUL-1993  
DEFINITION Anabaena sp. ribulose 1,5-bisphosphate carboxylase/oxygenase large  
subunit (rbcl) gene, complete cds; ribulose 1,5-bisphosphate  
carboxylase/oxygenase small subunit (rbcs) gene, complete cds;  
(rbcx) gene, complete cds.  
ACCESSION L02522  
NID g142087  
KEYWORDS RUBISCO; large subunit; rbcl gene; rbcS gene;  
ribulose 1,5-bisphosphate carboxylase/oxygenase; small subunit.  
SOURCE Anabaena sp. (strain PCC 7120) (Library: PCC7120) DNA.  
ORGANISM Anabaena sp.  
Prokaryotes; Gracillicutes; Oxyphotobacteria; Cyanobacteria;  
Nostocales; Nostocaceae.

REFERENCE 1 (bases 1 to 2695)  
AUTHORS Curtis, S.E. and Haselkorn, R.  
TITLE Isolation and sequence of the gene for the large subunit of  
ribulose-1,5-bisphosphate carboxylase from the cyanobacterium  
Anabaena 7120  
Proc. Natl. Acad. Sci. U.S.A. 80, 1835-1839 (1983)  
REFERENCE 2 (bases 1 to 2695)  
AUTHORS Nierzwickl-Bauer, S.A., Curtis, S.E. and Haselkorn, R.  
TITLE Cotranscription of genes encoding the small and large subunits of  
ribulose-1,5-bisphosphate carboxylase in the cyanobacterium  
Anabaena 7120  
Proc. Natl. Acad. Sci. U.S.A. 81, 5961-5965 (1984)

JOURNAL MEDLINE 85014888  
REFERENCE 3 (bases 1 to 2695)  
AUTHORS Larimer, F.W. and Soper, T.S.  
TITLE Overproduction of Anabaena PCC7120 ribulose-bisphosphate  
carboxylase/oxygenase in Escherichia coli  
Gene 126, 85-92 (1993)  
JOURNAL MEDLINE 93231541  
FEATURES Location/Qualifiers

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BASE COUNT 770 a 628 c 570 g 727 t  
ORIGIN

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Best Local Similarity 90.9%; Pred. No. 2.93e+00;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy 10 GTTTTCTACTGCTACTTCGACG 31





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polyA\_signal 3369..3399  
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BASE COUNT 1430 a 875 c 903 g 1338 t  
ORIGIN

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Best Local Similarity 80.0%; Pred. No. 2.93e+00;  
Matches 24; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Db 4043 gcgaactgtttctgtgggtatttcaacg 4072  
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Qy 2 CGGAACCGTTTTCTACTGCTACTTCGACG 31

RESULT 10 SPU23729 44913 bp DNA PLN 12-APR-1995  
LOCUS Schizosaccharomyces pombe cosmid 855, complete sequence.  
DEFINITION U23729  
ACCESSION g763539  
NID  
KEYWORDS  
SOURCE fission yeast.  
ORGANISM Schizosaccharomyces pombe  
Eukaryotae; mitochondrial eukaryotes; eukaryote crown group;  
Metazoa/Eumycota group; Eumycota; Ascomycotina; Archaeascomycetes;  
Schizosaccharomycetales; Schizosaccharomycetaceae;  
Schizosaccharomycetes.

REFERENCE 1 (bases 1 to 44913)  
AUTHORS CSHL, Advanced Genome Sequencing Course.  
TITLE Sequence of a 44.9 kb cosmid insert determined during a two week course

JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 44913)  
AUTHORS McCombie, W.R.  
TITLE Direct Submission  
JOURNAL Submitted (28-MAR-1995) W. Richard McCombie, Cold Spring Harbor  
Labs, 1 Bungtown Road, Cold Spring Harbor, NY 11724

FEATURES Location/Qualifiers  
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Best Local Similarity 90.9%; Pred. No. 2.93e+00;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 11577 gaattaccagtagtaaacggtt 11598  
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Cp 27 GAAGTACCAGTAGTAAGACGGTT 6

RESULT 11 BACJH642 282700 bp DNA BCT 02-MAY-1996  
LOCUS Bacillus subtilis DNA.  
DEFINITION D84432  
ACCESSION

NID g1303696  
KEYWORDS  
LysA; SpoVAF; SpoVAE; SpoVAD; SpoVAC; SpoVAB; SpoVAA; SpoLIAC;  
spoLIAB; spoLIAB; DacF; YqkQ; YqkN; YqkM; YqkL; SpoIIM; YqkK;  
YqkJ; YqkI; AnsB; AnsA; AnsR; YqkH; YqkG; YqkE; YqkD; YqkC;  
YqkB; YqkA; YqJY; YqJX; YqJW; YqJV; YqJU; YqJT; YqJS; YqJR;  
YqJO; YqJP; YqJO; YqJN; YqJM; YqJL; YqJK; YqJL; YqJL; YqJH; YqJG;  
YqJF; YqJE; YqJD; YqJC; YqJB; YqJA; YqIZ; YqIY; YqIX; YqIW; BarD;  
Bmr; BmrR; BmrB; BmrB; BmrB; YqIV; YqIU; YqIT; YqIS; YqIR;  
YqIQ; YqIP; YqIO; YqIN; YqIM; YqIL; YqIK; YqIU; YqII; YqIH; YqIG;  
Spo0A; SpoIVB; RecN; AhrC; YqIF; YqIE; YqID; YqIC; YqIB; YqIA;  
YqBZ; YqNY; YqNX; YqNW; SpoIIAH; SpoIIAG; SpoIIAF; SpoIIAE;  
SpoIIAD; SpoIIAC; SpoIIAB; SpoIIIAA; YqHV; YqHU; YqHT; YqHS;  
YqHR; YqHQ; YqHP; YqHO; YqHN; YqHM; YqHL; YqHK; YqHJ; YqHI; YqHH;  
YqHG; Sini; SiniR; YqHF; YqHE; YqHD; ComGG; ComGE; ComGD; ComGC;  
ComGB; ComCA; YqHC; YqHB; YqHA; YrKA; YqGZ; YqGY; YqGX; YqGW;  
YqGV; YqGU; YqGT; YqGS; YqGR; YqGQ; YqGP; YqGO; YqGN; YqGM; YqGL;  
YqGK; YqGJ; YqGI; YqGH; YqGF; YqGE; YqGD; YqGC; YqGB; YqGA;  
YqFZ; YqFY; YqFX; YqFW; YqFU; YqFT; YqFS; YqFH; YqFI; YqFI;  
YqFO; YqFN; CcA; RpoD; DnaE; YqFM; YqFL; YqFK; YqFJ; YqFI; YqFI;  
Cdd; DqKA; YqFG; YqFF; YqFE; YqFD; YqFC; YqFB; YqFA; YqE2; YqE1;  
YqE0; YqEW; YqEV; YqEU; YqET; DnaJ; GrpE; YqES; YqER; YqEQ;  
YqEP; SpoIIP; Gori; YqEO; YqEN; ComEC; ComEB; ComEA; YqEM;  
YqEL; YqEK; YqEJ; YqEI; AroD; YqEH; YqEG; YqEF; YqED; YqEC;  
YqEB; NucB; SpoIVCB; SpoIVCA; YqCM; YqCL; YqCK; YqCJ; YqCI; YqCH;  
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YrkS; YrkB; YrkQ; YrkO; YrkK; YrkN; YrkM; YrkL; YrkK; YrkJ; YrkI;  
YrkH; YrkG; YrkF; YrkE; YrkD; YrkC; YrkB; YrkA; BltR; Blt; BltD.  
Bacillus subtilis (strain:JH642(trpc2 PheA1)) DNA.

## ORGANISM

Bacillus subtilis  
Eubacteria; Firmicutes; Low G+C gram-positive bacteria;  
Bacillaceae; Bacillus.

## REFERENCE

1 (bases 1 to 282700)  
Kobayashi, Y.

## AUTHORS

Direct Submission

## TITLE

Submitted (16-APR-1996) to the DDBJ/EMBL/GenBank databases. Yasuo  
Kobayashi, Tokyo University of Agriculture and Technology, Applied  
Biological Science, 3-5-8 Saiwai-cho, Fuchu, Tokyo 183, Japan  
(E-mail:ykobayae@cc.tuat.ac.jp, Tel:81-423-67-5706,  
Fax:81-423-67-5715)

## REFERENCE

2 (bases 1 to 282700)  
Kobayashi, Y., Mizuno, M., Masuda, S., Takemaru, K., Hosono, S., Sato, T.  
and Takeuchi, M.

## TITLE

Systematic sequencing of the 283 Kb region of the Bacillus subtilis  
genome containing the skin element

## JOURNAL

Unpublished (1996)

## COMMENT

NCBI gi: 1303696

## FEATURES

Location/Qualifiers

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/strain="JH642(trpc2 PheA1)"

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complement (811..1284)

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IAF IIVVWAGLGSAYETVESLFDHKFGTTPKDTAAIITISSIVAVIOVLFGKLV  
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complement (2648..2654)

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2757..3578

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VQQYEIDEGYIGGIFAREQIILEKDFYNSYFYIKVKDGAENIYHVRPKGLYAVGYE  
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RBS

CDS

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3748..3894

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RBS

CDS

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4120..4680

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HPNVDOFLRIEQGRGIVKMGSKOHLNFQRNVYDDSAIVVPAGTWHNVINTGNTPLKL  
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CDS

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RBS

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RBS

CDS

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7376..7486

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FT complement(1438..2640)  
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S RILGGVSAFIMPATYAVADITTLKERSKAMGYSAIAISTGFIIGCAGCGIAGCGI  
R MPFFASAIALIAAVTSVFIKESILSTEERHQLSSHTEKSNFIKDLKRSIHPVYFIAP  
I IVFVMAFGLSAYETVFSLESDHKGFTPKDIAAITTSSIVAVIQVLFGLKLVNKLG  
E KRMIQCLITGAILAFVSVTMSGFLTVLLWTCFIFLAFDILLRPALTAHLSNAGNQCG  
F VAGWNSTYTLGNIIFGALGGLIDPIMIHYPFIAGFVMIUGLGLTWVWKEKKNDAAA  
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L QTLIQTKVILTEQALETDFSSISFEYLNESTFWLSRKTIMLPERYVAAISELIEHVQ  
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Q YELDEGYPIGGIFAREQILEKDFYNSYFVIKVDGAENINYHVRPKGLVAVGYEIGG  
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FT /product="YrkB"  
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FT /translation="MLLKNWPSRRIQDKSKRAGIGGTNNRIPYTLILLCYVWQKPPR  
I VDL"  
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S YEDRNLLKDYGPKEFVFNINRATKQNTFRALTWTKHFQVTLMSLIGIGEDIGLEIHH  
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FT NVDQFLRIEQGRGIVRMGSKDHLNFORNVYDDSAIIVVPAGTMHNVINTGNTPLKLYS  
I YAPNHPFGTWHETKADAAED"  
FT 5458..5464  
FT 5473..5664  
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FT /transl\_table=11  
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FT /db\_xref="PID:g1303703"  
FT /translation="MMEQKDCREVVTQLAASRNAIDRANGLIVSTNLEHCRESLEK  
G EDTONLVKEAVDLLVKSR"  
FT 5797..5801  
FT 5809..6291  
FT /codon\_start=1  
FT /transl\_table=11  
FT /product="YrkE"  
FT /db\_xref="PID:g1303704"  
FT /translation="MTEQTKRTTIVLFSGDYDKAMAAAYIIANGAAAYDHEVTIETFEW  
G FNALRKEELIPVKKGFLEKMFCKMMPRGADRMGLSKWNFAGMGPKMIKNVWKKSHVLT  
L POLTEMAQEQGVKLVACTMTMDLLGQEKELDDIDYAGVAAAYLADAEESVNLIPI"  
FT 6464..6471  
FT 6477..7034  
FT /codon\_start=1  
FT /transl\_table=11  
FT /product="YrkF"  
FT /db\_xref="PID:g1303705"  
FT /translation="MKKATIVILDAGLACPMBIVTKTKRMKOLKAGEVLEIHATDKGS  
T ADLEAWAKSTGHEYLTGEAEGEILNHFLLKGGESHSSENASSPEISLEAFKQKVDSDE  
S LNILDVREIEEYKHAHIPGVVHIPLGEVEKRAENELNENDEIYIICHSGRRSEMAARTM  
K KQGFKKVINWVPGMRDWTGKTE"  
FT 7361..7367  
FT 7376..7486  
FT /codon\_start=1  
FT /transl\_table=11  
FT /product="YrkG"  
FT /db\_xref="PID:g1303706"  
FT /translation="MTVKAMTPKEVTKKSLTKNLYLFMMCMVKMILVIGR"  
FT 7597..7605  
FT 7615..8502  
FT /codon\_start=1  
FT /transl\_table=11  
FT /product="YrkH"  
FT /db\_xref="PID:g1303707"  
FT /translation="MVSEMLSEAGHSVSYLKGWKAHSEHLEPVKVGDLKDGGMVQF  
V RIGKGCISYMWISNGEAAIIDATRMVNFIDFAKGGKATTHVFDTHLHADHISGRV  
I AEKTKATYMLPPKDAEEVEFDYQPLEEGNDIIIGNTTIKIQPIYSPGHTIGTSFIVD  
D QYLLSGDILFIDISIGRPDLAGMAEDWVGDLRKTYLSRYKALSNDLIVLPAHFMIIDEL  
N ENGSVQKQLSTLFSENHGINIADETFRHLVTDHLPQPNAYQEIRETNMGKISPDEE  
K QREMEICPNRCAIR"  
FT 8523..8527  
RBS  
...  
Note: remainder of annotations omitted.

Mar 19 08:46

US-08-612-929-56.rge

21

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Query Match          54.5%; Score 18; DB 10; Length 282700;
Best Local Similarity 87.5%; Pred. No. 2.93e+00;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 187816 cgttgaagtattagtagaaacgg 187839
||| ||||| ||||| ||||| |||||
Cp 31 CGTCGAAGTACCAGTACAAAACGG 8

RESULT 13
LOCUS S60819 54 bp DNA ROD 07-JUL-1993
DEFINITION VH7183=immunoglobulin heavy chain V-D-J region (clone FL12,
non-functional rearrangement) [mice, BALB/c, large bone marrow
pre-B cells, Genomic, 54 nt].
ACCESSION S60819
NID g300379
KEYWORDS .
SOURCE mice BALB/c large bone marrow pre-B cells.
ORGANISM Mus sp.
Unclassified.
REFERENCE 1 (bases 1 to 54)
AUTHORS Huetz,F., Carlsson,L., Tornberg,U.C. and Holmberg,D.
TITLE V-region directed selection in differentiating B lymphocytes
JOURNAL EMBO J. 12 (5), 1819-1826 (1993)
MEDLINE 93259123
REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI gibseq 131677] from the original journal article.
This sequence comes from Fig. 4.
FEATURES
source 1..54
/organism="Mus sp."
/note="mice"
misc_feature 1..54
/partial
/feature="VH7183"
/region="
/region"
BASE COUNT 14 a 11 c 14 g 15 t
ORIGIN
Query Match          51.5%; Score 17; DB 70; Length 54;
Best Local Similarity 94.7%; Pred. No. 1.24e+01;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 32 tctactgtacttcgatgt 50
||||| ||||| ||||| ||
Qy 14 TCTACTGGTACTTCGACGT 32

RESULT 14
LOCUS MUSIGHUJ 214 bp DNA ROD 10-SEP-1991
DEFINITION Mouse Ig rearranged heavy-chain gene V-D-J region, isolate 12SP12.
ACCESSION M73852
NID g197806
KEYWORDS D-region; J-region; V-region; immunoglobulin heavy chain;
rearranged gene.
SOURCE Mus musculus adult spleen DNA.
ORGANISM Mus musculus
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE 1 (bases 1 to 214)
AUTHORS Decker,D.J., Boyle,N.E. and Klinman,N.R.
TITLE Predominance of nonproductive rearrangements of V-H8IX gene
segments evidences a dependence of B cell clonal maturation on the
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Mar 19 08:46

US-08-612-929-56.rge

22

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structure of nascent H chains
J. Immunol. 147, 1406-1411 (1991)
MEDLINE 91332457
FEATURES
source 1..214
/organism="Mus musculus"
/dev_stage="adult"
/sequenced_mol="DNA"
/tissue_type="spleen"
BASE COUNT 59 a 57 c 48 g 50 t
ORIGIN chromosome 12.

Query Match          51.5%; Score 17; DB 67; Length 214;
Best Local Similarity 94.7%; Pred. No. 1.24e+01;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 192 tctactgtacttcgatgt 210
||||| ||||| ||||| ||
Qy 14 TCTACTGGTACTTCGACGT 32

RESULT 15
LOCUS MUSIGHAP 229 bp DNA ROD 10-SEP-1991
DEFINITION Mouse Ig rearranged heavy-chain gene V-D-J region, isolate 12SP18.
ACCESSION M73858
NID g197812
KEYWORDS D-region; J-region; V-region; immunoglobulin heavy chain;
rearranged gene.
SOURCE Mus musculus adult spleen DNA.
ORGANISM Mus musculus
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE 1 (bases 1 to 229)
AUTHORS Decker,D.J., Boyle,N.E. and Klinman,N.R.
TITLE Predominance of nonproductive rearrangements of V-H8IX gene
segments evidences a dependence of B cell clonal maturation on the
structure of nascent H chains
J. Immunol. 147, 1406-1411 (1991)
MEDLINE 91332457
FEATURES
source 1..229
/organism="Mus musculus"
/dev_stage="adult"
/sequenced_mol="DNA"
/tissue_type="spleen"
BASE COUNT 62 a 60 c 54 g 53 t
ORIGIN chromosome 12.

Query Match          51.5%; Score 17; DB 67; Length 229;
Best Local Similarity 87.0%; Pred. No. 1.24e+01;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 200 gtctctactgtacttcgatgt 222
||| ||||| ||||| ||||| ||
Qy 10 GTTTTCTACTGGTACTTCGACGT 32

Search completed: Wed Mar 19 08:48:20 1997
Job time : 74 secs.
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3

Qy 2 IYWDKRYNPSIKS 16  
:|||||:|||||

RESULT 2  
ID HV2D HUMAN STANDARD; PRT; 125 AA.  
AC P01817;  
DT 21-JUL-1986 (REL. 01, CREATED)  
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
DE IG HEAVY CHAIN V-II REGION (MCE).  
OS HOMO SAPIENS (HUMAN).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; PRIMATES.  
RN [1]  
RP SEQUENCE.  
RX MEDLINE; 81118242.  
RA GERBER-JENSON B., KAZIN A., KEHOE J.M., SCHEFFEL C., ERICKSON B.W.,  
RA LITMAN G.W.;  
RL J. IMMUNOL. 126:1212-1216(1981).  
CC -/- THIS CHAIN WAS DERIVED FROM A MONOCLONAL IGM CRYOIMMUNOGLOBULIN.  
DR PIR; A02092; MHUMC.  
DR HSP; P01772; IFGV.  
KW IMMUNOGLOBULIN V REGION.  
FT MOD\_RES 1 1  
FT NON\_TER 125 125  
SQ SEQUENCE 125 AA; 13783 MW; 7F897793 CRC32;

Query Match 71.9%; Score 92; DB 4; Length 125;  
Best Local Similarity 73.3%; Pred. No. 6.06e-06;  
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 53 inwdddkrynspslrs 67  
:|||||:|||||

Qy 2 IYWDKRYNPSIKS 16

RESULT 3  
ID HV2B HUMAN STANDARD; PRT; 120 AA.  
AC P01815;  
DT 21-JUL-1986 (REL. 01, CREATED)  
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
DT 21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)  
DE IG HEAVY CHAIN V-II REGION (COR).  
OS HOMO SAPIENS (HUMAN).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; PRIMATES.  
RN [1]  
RP SEQUENCE.  
RX MEDLINE; 70258837.  
RA PRESS E.M., HOGG N.M.;  
RL BIOCHEM. J. 117:641-660(1970).  
CC -/- THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA PROTEIN.  
DR PIR; A02089; GIHUCO.  
DR HSP; P01789; 2FGW.  
KW IMMUNOGLOBULIN V REGION; GLYCOPROTEIN.  
FT MOD\_RES 1 1  
FT DISULFID 22 94  
FT CARBOHYD 62 62  
FT NON\_TER 120 120  
SQ SEQUENCE 120 AA; 13226 MW; D690F656 CRC32;

Query Match 53.9%; Score 69; DB 4; Length 120;  
Best Local Similarity 62.5%; Pred. No. 1.47e-01;

Mar 18 10:13

US-08-612-929-24.fsp

4

Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Db 52 ridwdddkryntslet 67  
:|||||:|||||

Qy 1 HIYWDKRYNPSIKS 16

RESULT 4  
ID YJFC ECOLI STANDARD; PRT; 387 AA.  
AC P33222;  
DT 01-FEB-1994 (REL. 28, CREATED)  
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)  
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)  
DE HYPOTHETICAL 45.0 KD PROTEIN IN VAC-AIDB INTERGENIC REGION (0387).  
GN YJFC.  
OS ESCHERICHIA COLI.  
OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;  
OC ENTEROBACTERIACEAE.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=K12 / MG1655;  
RX MEDLINE; 95334362.  
RA BORLAND V.D., PLUNKETT G. III, SOFIA H.J., DANIELS D.L.,  
RA BLATTNER F.R.;  
RL NUCLEIC ACIDS RES. 23:2105-2119(1995).  
RN [2]  
RP SEQUENCE OF 208-387 FROM N.A.  
RC STRAIN=K12;  
RX MEDLINE; 95050217.  
RA LANDINI P., HAJEC L.I., VOLKERT M.R.;  
RL J. BACTERIOL. 176:6583-6589(1994).  
CC -/- SIMILARITY: STRONG, TO THE N-TERMINAL OF E.COLI GSP AND TO E.COLI  
CC YGIC.  
DR EMBL; U14003; G537027; -.  
DR EMBL; L20915; G304861; -.  
DR ECOGENE; EG11812; YJFC.  
KW HYPOTHETICAL PROTEIN.  
SQ SEQUENCE 387 AA; 45019 MW; 358B5D1B CRC32;

Query Match 52.3%; Score 67; DB 10; Length 387;  
Best Local Similarity 42.9%; Pred. No. 3.28e-01;  
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Db 30 iywdestayrftlr 43  
:|||||:|||||

Qy 2 IYWDKRYNPSIK 15

RESULT 5  
ID HV2H HUMAN STANDARD; PRT; 147 AA.  
AC P04438;  
DT 13-AUG-1987 (REL. 05, CREATED)  
DT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)  
DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)  
DE IG HEAVY CHAIN PRECURSOR V-II REGION (SESS).  
OS HOMO SAPIENS (HUMAN).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; PRIMATES.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 84298107.  
RA TAKAHASHI N., NOMA T., HONJO T.;  
RL PROC. NATL. ACAD. SCI. U.S.A. 81:5194-5198(1984).  
DR PIR; A02090; G2HUCS.



	HSP: P01772; IGBB.	IMMUNOGLOBULIN V REGION; SIGNAL.	IG HEAVY CHAIN V-II REGION (SESS).
OR		1 19	
FW	SIGNAL	20	D SEGMENT.
FT	CHAIN	20	J SEGMENT.
FT	DOMAIN	20	
FT	DOMAIN	119	
FT	DOMAIN	132	
FT	DOMAIN	133	
FT	NON TER	147	
FT	SEQUENCE	147	
SO	SEQUENCE	147 AA; 16323 MM; 0994FF54 CRC32;	

Query Match	50.0%;	Score 64;	DB 4;	Length 147;
Best Local Similarity	56.3%;	Pred. No.	1.07e+00;	
Matches	9;	Mismatches	5;	Indels 0;
	Conservative			Gaps 0;

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Db      71 ridwdddkyygtslet 86
QV      :| | | | | | | :
        1 HIYDDDKRYNPSLKS 16

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RESULT	6	STANDARD;	PR7; 560 AA.
ID	INRI BOVIN		
AC	004730;		
DT	01-OCT-1993 (REL. 27, CREATED)		
DT	01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)		
DT	01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)		
DE	INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC).		
GN	IFNARI OR IFNAR.		
OS	BOS TAURUS (BOVINE).		
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;		
OC	EUTHERIA; ARTIODACTYIA.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=LUNG;		
RC	MEDLINE; 93076908.		
RX	MOUCHEI-VIELH E.; LUTFALLA G.; MOGENSEN K.E.; UZE G.;		
RA	FEBS LETT. 313:255-259(1992).		

RN	{2}	
RP	SEQUENCE FROM N.A.	
RP	MEDLINE; 93305725.	
RX		
RA	LIM J.-K., LANGER J.A.;	
RL	BIOCHIM. BIOPHYS. ACTA 1173:314-319(1993).	
CC	-I- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA.	
CC	-I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.	
CC	-I- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.	
CC	-I- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.	

DR	EMBL; X68443; C432; -.	
DR	EMBL; J06320; G163188; -.	
DR	PIR; S33770; S33770.	
DR	PIR; S27387; S27387.	
KW	RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.	
FT	SIGNAL	1 24
FT	CHAIN	25 560
FT	INTERFERON-ALPHA/BETA RECEPTOR ALPHA. BY SIMILARITY.	

FT	DOMAIN	25	437	CHAIN.
FT	DOMAIN	438	458	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	459	560	POTENTIAL.
FT	DOMAIN	76	84	CYTOPLASMIC (POTENTIAL).
FT	DISULFID	199	220	BY SIMILARITY.
FT	DISULFID	199	220	BY SIMILARITY.
FT	CARBOHYD	47	47	POTENTIAL.
FT	CARBOHYD	55	55	POTENTIAL.
FT	CARBOHYD	85	85	POTENTIAL.
FT	CARBOHYD	109	109	POTENTIAL.
FT	CARBOHYD	172	172	POTENTIAL.
FT	CARBOHYD	254	254	POTENTIAL.

313	CARBOHYD	313	POTENTIAL.
377	CARBOHYD	377	POTENTIAL.
434	CARBOHYD	434	POTENTIAL.
422	CONFLICT	422	F -> V (IN REF. 2).
560	SEQUENCE	560	AA; 63818 MW; 44D98FDF CRC32;

Query Match 49.2%; Score 63; DB 5; Length 560;  
Best Local Similarity 28.6%; Pred. No. 1.57e+00;  
Matches 4; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

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Ddb 317 fwseekefntemkt 330
      :|::|:|:|:
Ov   3 YWDDDKRYNP5LKS 16

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RESULT	7
ID	NDDB RAT STANDARD; PRY; 204 AA.
AC	P06300;
DT	01-JAN-1988 (REL. 06, CREATED)
DT	01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
DT	01-AUG-1990 (REL. 15, LAST ANNOTATION UPDATE)
DE	BETA-NEOENDORPHIN-DYNORPHIN PRECURSOR (PROENKEPHALIN B PRECURSOR) (FRAGMENT).
OS	RATTUS NORVEGICUS (RAT).
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; EUTHERIA; RODENTIA.
RN	[1]
RP	SEQUENCE FROM N.A. TISSUE=HYPOTHALAMUS; MEDLINE; 85216680.
RA	CIVELLI O., DOUGLASS J., GOLDSTEIN A., HERBERT E.; PROC. NATL. ACAD. SCI. U.S.A. 82:4291-4295(1985).
RL	EMBL; M10088; G204040; --
DR	PIR; A01480; DFRTP.
KW	OPIOID PEPTIDE; NEUROTRANSMITTER; HYPOTHALAMUS; NEUROPETIDE; ENDOPHEIN; CLEAVAGE ON PAIR OF BASIC RESIDUES.

FT	NON TER	1	1	
FT	PEPTIDE	122	130	ALPHA-NEOENDORPHIN.
FT	PEPTIDE	122	126	LEU-ENKEPHALIN 1.
FT	PEPTIDE	158	174	DYNORPHIN A.
FT	PEPTIDE	158	162	LEU-ENKEPHALIN 2.
FT	PEPTIDE	177	204	DYNORPHIN B.
FT	PEPTIDE	177	181	LEU-ENKEPHALIN 3.
SQ	SEQUENCE	204 AA;	23386 MW;	3B451063 CRC32;

Query Match	48.4%;	Score 62;	DB 6;	Length 204;
Best Local Similarity	50.0%;	Pred. No. 2.31e+00;		
Matches	6;	Conservative	3;	Mismatches 3;
				Indels 0;
				Gaps 0;

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Db 171 wdnqkryggflr 182
    ||:||| |:
Qv 4 WDDDKRYNPSLK 15
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RESULT	8	
ID	NDDB HUMAN	STANDARD; PRT; 254 AA.
AC	P01213;	
DT	21-JUL-1986	(REL. 01, CREATED)
DT	21-JUL-1986	(REL. 01, LAST SEQUENCE UPDATE)
DT	01-NOV-1990	(REL. 16, LAST ANNOTATION UPDATE)
DE	BETA-NECENDORPHIN-DYNORPHIN PRECURSOR	(PROENKEPHALIN B PRECURSOR).
GN	PDYN.	
OS	GN	
OC	HOMO SAPIENS (HUMAN).	
OC	EUKARYOTA; METAZOA;	
OC	CHORDATA; VERTEBRATA; TETRAPODA;	
OC	MAMMALIA;	

Best Local Similarity 50.0%; Pred. No. 2.31e+00;  
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 222 wdnkryggflr 233  
Qy 4 WDDDKRNPISL 15

RESULT 10

ID GLR1 HUMAN STANDARD; PRT; 906 AA.  
AC P42261;  
DT 01-NOV-1995 (REL. 32, CREATED)  
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)  
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)  
DE GLUTAMATE RECEPTOR 1 PRECURSOR (GLUR-1) (GLUR-A) (GLUR-K1) (GLUTAMATE  
DE RECEPTOR, IONOTROPIC, AMPA 1).  
GN GRIA1 OR GLUR1 OR GLUH1.  
OS HOMO SAPIENS (HUMAN).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; PRIMATES.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 92159065.  
RA SUN W., FERRER-MONTIEL A.V., SCHINDER A.F., MCPHERSON J.P.,  
RA EVANS G.A., MONTAL M.,  
RL PROC. NATL. ACAD. SCI. U.S.A. 89:1443-1447 (1992).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=HIPPOCAMPUS;  
RX MEDLINE; 92329975.  
RA POTIER M.C., SPILLANTINI M.G., CARTER N.P.,  
RL DNA SEQ. 2:211-218 (1992).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 9135207.  
RA PUCKETT C., GOMEZ C.M., KORENBERG J.R., TUNG H., MEIER T.J.,  
RA CHEN X.N., HOOD L.E.;  
RL PROC. NATL. ACAD. SCI. U.S.A. 88:7557-7561 (1991).  
CC -!- FUNCTION: L-GLUTAMATE ACTS AS AN EXCITATORY NEUROTRANSMITTER AT  
CC MANY SYNAPSES IN THE CENTRAL NERVOUS SYSTEM. THE POSTSYNAPTIC  
CC ACTIONS OF GLU ARE MEDIATED BY A VARIETY OF RECEPTORS THAT ARE  
CC NAMED ACCORDING TO THEIR SELECTIVE AGONISTS.  
CC -!- THIS RECEPTOR BINDS AMPA (QUISQUALATE) > GLUTAMATE > KAINATE.  
CC -!- ALTERNATIVE PRODUCTS: THIS RECEPTOR EXISTS IN TWO VERSIONS (FLOP,  
CC SHOWN HERE) AND FLIP, WHICH DIFFER IN A REGION IN FRONT OF TM4.  
CC THE TWO FORMS ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME  
CC GENE.  
CC -!- TISSUE SPECIFICITY: WIDELY EXPRESSED IN BRAIN.  
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.  
DR EMBL; M81886; G179442; -.  
DR EMBL; X58633; G414893; -.  
DR EMBL; M64752; G183281; -.  
DR MIM; 138248; 11TH EDITION.  
KW RECEPTOR; POSTSYNAPTIC MEMBRANE; IONIC CHANNEL; GLYCOPROTEIN; SIGNAL;  
FT SIGNAL 1 18 POTENTIAL.  
FT CHAIN 19 906 GLUTAMATE RECEPTOR A.  
FT DOMAIN 19 536 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 537 557 POTENTIAL.  
FT TRANSMEM 585 605 POTENTIAL.  
FT TRANSMEM 618 638 POTENTIAL.  
FT TRANSMEM 806 826 POTENTIAL.  
FT VARSPLIC 758 758 N -> G (IN FLIP).

OC EUTHERIA; PRIMATES.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 84068211.  
RA HORIKAWA S., TAKAI T., TOYOSATO M., TAKAHASHI H., NODA M.,  
RA KAKIDANI H., KUBO T., HIROSE T., INAYAMA S., HAYASHIDA H., MIYATA T.,  
RA NUMA S.;  
RL NATURE 306:611-614 (1983).  
DR EMBL; X02536; -; NOT ANNOTATED CDS.  
DR EMBL; K02267; -; NOT ANNOTATED CDS.  
DR EMBL; K02268; G182105; -.  
DR EMBL; X00176; G182105; JOINED.  
DR EMBL; X00176; G31155; -.  
DR PIR; A01478; DFHU.  
DR MIM; 131340; 11TH EDITION.  
KW OPIOID PEPTIDE; NEUROTRANSMITTER; HYPOTHALAMUS; NEUROPEPTIDE;  
KW ENDORPHIN; CLEAVAGE ON PAIR OF BASIC RESIDUES; SIGNAL.  
FT SIGNAL 1 20  
FT PEPTIDE 175 183 BETA-NEOENDORPHIN.  
FT PEPTIDE 207 223 DYNORPHIN.  
FT PEPTIDE 226 230 LEO-ENKEPHALIN.  
FT PEPTIDE 226 238 RIMORPHIN.  
FT PEPTIDE 226 254 LEUMORPHIN.  
SQ SEQUENCE 254 AA; 28385 MW; 49A11156 CRC32;

Query Match 48.4%; Score 62; DB 6; Length 254;  
Best Local Similarity 50.0%; Pred. No. 2.31e+00;  
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 220 wdnkryggflr 231  
Qy 4 WDDDKRNPISL 15

RESULT 9

ID NDBB PIG STANDARD; PRT; 256 AA.  
AC P01214;  
DT 21-JUL-1986 (REL. 01, CREATED)  
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)  
DE BETA-NEOENDORPHIN-DYNORPHIN PRECURSOR (PROENKEPHALIN B PRECURSOR).  
OS SUS SCROFA (PIG).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; ARTIODACTYLA.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=HYPOTHALAMUS;  
RX MEDLINE; 82220112.  
RA KAKIDANI H., FURUTANI Y., TAKAHASHI H., NODA M., MORIMOTO Y.,  
RA HIROSE T., ASAI M., INAYAMA S., NAKANISHI S., NUMA S.;  
RL NATURE 298:245-249 (1982).  
DR EMBL; V01362; G1944; -.  
DR PIR; A01479; DFPG.  
KW OPIOID PEPTIDE; NEUROTRANSMITTER; HYPOTHALAMUS; NEUROPEPTIDE;  
KW ENDORPHIN; CLEAVAGE ON PAIR OF BASIC RESIDUES; SIGNAL.  
FT SIGNAL 1 20  
FT PEPTIDE 175 183 BETA-NEOENDORPHIN.  
FT PEPTIDE 209 225 DYNORPHIN.  
FT PEPTIDE 228 232 LEO-ENKEPHALIN.  
FT VARIANT 147 147 G -> E.  
FT VARIANT 197 197 R -> G.  
SQ SEQUENCE 256 AA; 28616 MW; 9427FFC4 CRC32;

Query Match 48.4%; Score 62; DB 6; Length 256;

FT VARSPLIC 768 768 N -> S (IN FLIP).  
 FT VARSPLIC 772 772 L -> V (IN FLIP).  
 FT VARSPLIC 778 778 N -> S (IN FLIP).  
 FT VARSPLIC 790 793 GCGD -> KDSG (IN FLIP).  
 FT CONFLICT 345 345 R -> A (IN REF. 2).  
 FT CONFLICT 375 375 S -> G (IN REF. 2 AND 3).  
 FT CONFLICT 863 863 S -> SA (IN REF. 3).  
 FT CONFLICT 865 867 AGA -> TAP (IN REF. 3).  
 SQ SEQUENCE 906 AA; 101536 MW; 703BEF31 CRC32;

Query Match 47.7%; DB 4; Length 906;  
 Best Local Similarity 36.4%; Pred. No. 3.36e+00;  
 Matches 4; Conservative 2; Indels 0; Gaps 0;

Db 381 yneddkfupa 391  
 ||::|| :: |:  
 Qy 3 YWDDKRYNPS 13

RESULT 11  
 ID GLRI MOUSE STANDARD; PRT; 907 AA.  
 AC P23818;  
 DT 01-NOV-1991 (REL. 20, CREATED)  
 DT 01-NOV-1991 (REL. 20, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)  
 DE GLUTAMATE RECEPTOR 1 PRECURSOR (GLUR-1) (GLUR-A) (GLUR-K1).  
 GN GR1A1 OR GLUR1.  
 OS MUS MUSCULUS (MOUSE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; RODENTIA.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 91032147.  
 RA SAKIMURA K., BOJO H., KUSHIYA E., ARAKI K., YAMAZAKI M., YAMAZAKI M.,  
 RA MEGURO H., WARASHINA A., NUMA S., MISHINA M.;  
 RL FEBS LETT. 272:73-80(1990).  
 CC -|- FUNCTION: L-GLUTAMATE ACTS AS AN EXCITATORY NEUROTRANSMITTER AT  
 CC MANY SYNAPSES IN THE CENTRAL NERVOUS SYSTEM. THE POSTSYNAPTIC  
 CC ACTIONS OF GLU ARE MEDIATED BY A VARIETY OF RECEPTORS THAT ARE  
 CC NAMED ACCORDING TO THEIR SELECTIVE AGONISTS.  
 CC -|- THIS RECEPTOR BINDS AMPA (QUISQUALATE) > GLUTAMATE > KAINATE.  
 CC -|- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
 CC -|- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.  
 DR EMBL; X57497; G51080; -.  
 DR PIR; S12874; S12874.  
 KW RECEPTOR; POSTSYNAPTIC MEMBRANE; IONIC CHANNEL; GLYCOPROTEIN; SIGNAL;  
 KW TRANSMEMBRANE.  
 FT SIGNAL 1 18 POTENTIAL.  
 FT CHAIN 19 907 GLUTAMATE RECEPTOR 1.  
 FT DOMAIN 19 538 EXTRACELLULAR (POTENTIAL).  
 FT TRANSEM 539 558 POTENTIAL.  
 FT TRANSEM 585 603 POTENTIAL.  
 FT TRANSEM 614 632 POTENTIAL.  
 FT TRANSEM 806 826 POTENTIAL.  
 FT CARBOHYD 63 63 POTENTIAL.  
 FT CARBOHYD 249 249 POTENTIAL.  
 FT CARBOHYD 257 257 POTENTIAL.  
 FT CARBOHYD 363 363 POTENTIAL.  
 FT CARBOHYD 401 401 POTENTIAL.  
 FT CARBOHYD 406 406 POTENTIAL.  
 SQ SEQUENCE 907 AA; 101569 MW; D94C24A9 CRC32;

Query Match 47.7%; DB 4; Length 907;  
 Best Local Similarity 36.4%; Pred. No. 3.36e+00;

Matches 4; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Db 381 yneddkfupa 391  
 ||::|| :: |:  
 Qy 3 YWDDKRYNPS 13

RESULT 12  
 ID GLRI RAT STANDARD; PRT; 907 AA.  
 AC P19490;  
 DT 01-FEB-1991 (REL. 17, CREATED)  
 DT 01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)  
 DE GLUTAMATE RECEPTOR 1 PRECURSOR (GLUR-1) (GLUR-A) (GLUR-K1).  
 GN GR1A1 OR GLUR1.  
 OS RATTUS NORVEGICUS (RAT).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; RODENTIA.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=BRAIN;  
 RX MEDLINE; 90341779.  
 RA KEINANEN K., WISDEN W., SOMMER B., WERNER P., HERB A., VERDOORN T.A.,  
 RA SAKMANN B., SEEBURG P.H.;  
 RL SCIENCE 249:556-560(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 90081835.  
 RA HOLLMAN M., O'SHEA-GREENFIELD A., ROGERS S.W., HEINEMANN S.;  
 RL NATURE 342:643-648(1989).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 90371298.  
 RA BOULTER J., HOLLMAN M., O'SHEA-GREENFIELD A., HARTLEY M., DENNERIS E.,  
 RA MARON C., HEINEMANN S.;  
 RL SCIENCE 249:1033-1037(1990).  
 RN [4]  
 RP VARIANTS FLIP/FLOP.  
 RX MEDLINE; 91019421.  
 RA SOMMER B., KEINANEN K., VERDOORN T.A., WISDEN W., BURNASHEV N.,  
 RA HERB A., KOEHLER M., TAKAGI T., SAKMANN B., SEEBURG P.H.;  
 RL SCIENCE 249:1580-1585(1990).  
 CC -|- FUNCTION: L-GLUTAMATE ACTS AS AN EXCITATORY NEUROTRANSMITTER AT  
 CC MANY SYNAPSES IN THE CENTRAL NERVOUS SYSTEM. THE POSTSYNAPTIC  
 CC ACTIONS OF GLU ARE MEDIATED BY A VARIETY OF RECEPTORS THAT ARE  
 CC NAMED ACCORDING TO THEIR SELECTIVE AGONISTS.  
 CC -|- THIS RECEPTOR BINDS AMPA (QUISQUALATE) > GLUTAMATE > KAINATE.  
 CC -|- ALTERNATIVE PRODUCTS: THIS RECEPTOR EXISTS IN TWO VERSIONS (FLOP,  
 CC SHOWN HERE) AND FLIP, WHICH DIFFER IN A REGION IN FRONT OF TM4.  
 CC THE TWO FORMS ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME  
 CC GENE.  
 CC -|- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
 CC -|- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.  
 DR EMBL; M36418; G204394; -.  
 DR EMBL; X17184; G55529; -.  
 DR EMBL; M38060; G202868; -.  
 DR PIR; S07059; ACRTK1.  
 DR PIR; A40170; A40170.  
 KW RECEPTOR; POSTSYNAPTIC MEMBRANE; IONIC CHANNEL; GLYCOPROTEIN; SIGNAL;  
 KW TRANSMEMBRANE; ALTERNATIVE SPLICING.  
 FT SIGNAL 1 18 POTENTIAL.  
 FT CHAIN 19 907 GLUTAMATE RECEPTOR 1.  
 FT DOMAIN 19 538 EXTRACELLULAR (POTENTIAL).  
 FT TRANSEM 539 558 POTENTIAL.

Mar 18 10:13

US-08-612-929-24.fsp

11

FT TRANSEM 585 603 POTENTIAL.  
 FT TRANSEM 614 632 POTENTIAL.  
 FT TRANSEM 806 826 POTENTIAL.  
 FT CARBOHYD 63 63 POTENTIAL.  
 FT CARBOHYD 249 249 POTENTIAL.  
 FT CARBOHYD 257 257 POTENTIAL.  
 FT CARBOHYD 363 363 POTENTIAL.  
 FT CARBOHYD 401 401 POTENTIAL.  
 FT CARBOHYD 406 406 POTENTIAL.  
 FT VARSPLIC 758 758 N -> G (IN FLIP).  
 FT VARSPLIC 768 768 N -> S (IN FLIP).  
 FT VARSPLIC 772 772 L -> V (IN FLIP).  
 FT VARSPLIC 778 778 N -> S (IN FLIP).  
 FT VARSPLIC 789 793 TGGD -> SKDSC (IN FLIP).  
 FT CONFLICT 698 698 L -> R (IN REF. 2 AND 3).  
 FT CONFLICT 710 710 T -> S (IN REF. 2 AND 3).  
 SQ SEQUENCE 907 AA; 101647 MW; 97B082F8 CRC32;

Query Match 47.7%; Score 61; DB 4; Length 907;  
 Best Local Similarity 36.4%; Pred. No. 3.36e+00;  
 Matches 4; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Db 381 ymnedkfcpa 391  
 ||::: ||:  
 Qy 3 YMDDDKRYNS 13

RESULT 13

ID Y16E BPT4 STANDARD; PRT; 70 AA.  
 AC P22977;  
 DT 01-AUG-1991 (REL. 19, CREATED)  
 DT 01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)  
 DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)  
 DE HYPOTHETICAL 8.5 KD PROTEIN IN ASIA-MOTA INTERGENIC REGION.  
 GN Y16E OR MOTA.-2 OR ASIA.5.  
 OS BACTERIOPHAGE T4.  
 OC VIRIDAE; DS-DNA NONENVELOPED VIRUSES; MYOVIRIDAE.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 91141300.  
 RA UZAN M., BRODY E., FAVRE R.;  
 RL MOL. MICROBIOL. 4:1487-1495(1990).  
 DR EMBL; 248569; G695452; -.  
 DR PIR; JVO103; JVO103.  
 KW HYPOTHETICAL PROTEIN.  
 SQ SEQUENCE 70 AA; 8461 MW; 8DA77F8B CRC32;

Query Match 46.9%; Score 60; DB 10; Length 70;  
 Best Local Similarity 50.0%; Pred. No. 4.89e+00;  
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 52 ywdenqky 59  
 ||::: ||:  
 Qy 3 YMDDDKRY 10

RESULT 14

ID RK28 TOBAC STANDARD; PRT; 151 AA.  
 AC P30956;  
 DT 01-JUL-1993 (REL. 26, CREATED)  
 DT 01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)  
 DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)  
 DE 50S RIBOSOMAL PROTEIN L28 CHLOROPLAST PRECURSOR (CL28).  
 GN RPL28.

Mar 18 10:13

US-08-612-929-24.fsp

12

OS NICOTIANA TABACUM (COMMON TOBACCO).  
 OC EUKARYOTA; PLANTA; EMERYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE;  
 OC SOLANALES; SOLANACEAE.  
 RN [1]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 75-95.  
 RC STRAIN=CV. BRIGHT YELLOW 4; TISSUE=LEAF;  
 RX MEDLINE; 92371638.  
 RA YOKOI F., SUGIURA M.;  
 RL FEBS LETT. 308:258-260(1992).  
 CC -/- SIMILARITY: BELONGS TO THE L28P FAMILY OF RIBOSOMAL PROTEINS.  
 DR EMBL; X68078; G20016; -.  
 DR PIR; S24123; R5NT28.  
 KW RIBOSOMAL PROTEIN; TRANSIT PEPTIDE; CHLOROPLAST.  
 FT TRANSIT 1 74 CHLOROPLAST.  
 FT CHAIN 75 151 50S RIBOSOMAL PROTEIN L28.  
 SQ SEQUENCE 151 AA; 16697 MW; B68E598A CRC32;

Query Match 46.9%; Score 60; DB 7; Length 151;  
 Best Local Similarity 50.0%; Pred. No. 4.89e+00;  
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Db 110 riwweagkry 119  
 :||: |||  
 Qy 1 HIYMDDDKRY 10

RESULT 15

ID CRP MOUSE STANDARD; PRT; 225 AA.  
 AC P14867;  
 DT 01-APR-1990 (REL. 14, CREATED)  
 DT 01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)  
 DT 01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)  
 DE C-REACTIVE PROTEIN PRECURSOR.  
 GN CRP.  
 OS MUS MUSCULUS (MOUSE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; RODENTIA.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 89050112.  
 RA OHNISHI S., MAEDA S., NISHICUCHI S., ARAO T., SHIMADA K.;  
 RL BIOCHEM. BIOPHYS. RES. COMMUN. 156:814-822(1988).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CBA/J; TISSUE=LIVER;  
 RX MEDLINE; 90179719.  
 RA WHITEHEAD A.S., ZAHEDI K., RITS M., MORTENSEN R.F., LELIAS J.M.;  
 RL BIOCHEM. J. 266:283-290(1990).  
 CC -/- FUNCTION: CRP DISPLAYS SEVERAL FUNCTIONS ASSOCIATED WITH HOST  
 CC DEFENSE: IT PROMOTES AGGLUTINATION, BACTERIAL CAPSULAR SWELLING,  
 CC PHAGOCYTOSIS, & COMPLEMENT FIXATION THROUGH ITS CALCIUM-DEPENDENT  
 CC BINDING TO PHOSPHORYLCHOLINE.  
 CC -/- INDUCTION: THE CONCENTRATION OF CRP IN PLASMA INCREASES GREATLY  
 CC DURING ACUTE PHASE RESPONSE TO TISSUE INJURY OR INFLAMMATION.  
 CC -/- SUBUNIT: HOMOPENTAMER. PENTAXIN (OR PENTAXIN) HAVE A DISCOID  
 CC ARRANGEMENT OF 5 NONCOVALENTLY BOUND SUBUNITS.  
 CC -/- SIMILARITY: BELONGS TO THE FAMILY OF PENTAXINS.  
 DR EMBL; X13588; G295904; -.  
 DR EMBL; X17496; G50564; -.  
 DR PIR; A31583; A31583.  
 DR PIR; S08286; S08286.  
 DR HSSP; P02743; ISAC.  
 DR PROSITE; P500289; PENTAXIN.  
 KW ACUTE PHASE; PLASMA; CALCIUM; PENTAXIN; SIGNAL.

13

US-08-612-929-24.rsp

Mar 18 10:13

FT SIGNAL 1 19  
FT CHAIN 20 225  
FT DOMAIN 20 225  
FT DISULFID 55 116  
FT CONFLICT 134 134  
SQ SEQUENCE 225 AA; 25361 MB; 3C57F01C CRC32;  
Query Match 46.9%;  
Best Local Similarity 55.6%;  
Matches 5; Conservative  
Db 84 ifwnkdqy 92  
l:l: l:l:  
Qy 2 IYWDDKRY 10

C-REACTIVE PROTEIN.  
PENTAXIN.  
BY SIMILARITY.  
A -> P (IN REF. 2).  
3C57F01C CRC32;

Score 60; DB 2; Length 225;  
Pred. No. 4.89e+00;  
3; Mismatches 1; Indels 0; Gaps 0;

Search completed: Tue Mar 18 10:14:46 1997  
Job time : 6 secs.

Mar 18 10:13

US-08-612 929-24.rpr

1

Mar 18 10:13

US-08-612 929-24.rpr

2

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WAVES (TM)

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MParch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Mar 18 10:15:04 1997; MafPar time 3.17 Seconds  
129.657 Million cell updates/sec

Tabular output not generated.

Title: >US-08-612-929-24  
Description: (1-16) from US08612929.pap  
Perfect Score: 128  
Sequence: 1 HIYDDDKRYNPSLKS 16

Scoring table: PAM 150  
Gap 15

Searched: 82182 seqs, 25727515 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: pir48  
1:ann1 2:ann2 3:ann3 4:unann1 5:unann2 6:unann3 7:unann4  
8:unann5 9:unann6 10:unann7 11:unann8 12:unann9 13:unenc  
14:unrev

Statistics: Mean 27.523; Variance 52.762; scale 0.522

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	128	100.0	122	5	S11740 Ig heavy chain V reg	1.52e-10
2	117	91.4	107	12	A49442 Ig heavy chain V reg	1.46e-08
3	115	89.8	41	11	S26936 Ig heavy chain V reg	3.30e-08
4	115	89.8	138	5	S31513 Ig heavy chain - hum	3.30e-08
5	112	87.5	119	5	S18555 Ig heavy chain - hum	1.12e-07
6	109	85.2	124	5	A49002 rheumatoid factor he	3.75e-07
7	105	82.0	121	2	GIH0HE Ig heavy chain V-II	1.85e-06
8	100	78.1	113	5	S26465 Ig heavy chain V reg	1.33e-05
9	92	71.9	125	2	MHHUMC Ig heavy chain V-II	2.92e-04
10	92	71.9	143	5	PT0174 Ig heavy chain V reg	2.92e-04
11	86	67.2	103	5	B25913 Ig heavy chain V reg	2.78e-03
12	86	67.2	116	12	S26328 Ig heavy chain V reg	2.78e-03

## ALIGNMENTS

RESULT 1  
ENTRY S11740 #type fragment  
TITLE Ig heavy chain precursor V-D-J region - mouse (fragment)  
ORGANISM #formal name Mus musculus #common name house mouse  
DATE 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 22-Apr-1995  
ACCESSIONS S11740  
REFERENCE S11740  
#authors Hayakawa, K.; Carmarck, C.E.; Hyman, R.; Hardy, R.R.  
#submission submitted to the EMBL Data Library, May 1990  
#description Natural autoantibodies to thymocytes: Origin, VH genes, fine specificities, and the role of Thy-1 glycoprotein.  
#accession S11740  
#molecule\_type mRNA  
#residues 1-122 #label EMB  
#cross-references EMBL:X53097  
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology  
SUMMARY #length 122 #checksum 38

Query Match 100.0%; Score 128; DB 5; Length 122;  
Best Local Similarity 100.0%; Pred. No. 1.52e-10;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 59 hiywdddkrynp slks 74

|||||

QY 1 HIYDDDKRYNPSLKS 16

US-08-612-929-24.rpr

Mar 18 10:13

RESULT 4  
ENTRY S31513 #type complete  
TITLE Ig heavy chain - human  
ORGANISM #formal name Homo sapiens #common name man  
DATE 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 12-Apr-1995  
ACCESSIONS S31513  
REFERENCE S31509  
#authors Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.  
#submission Submitted to the EMBL Data Library, December 1992  
#description Dominance of clonotypic patterns and variable gene usage of anti-DNA autoantibodies from patient with lupus.  
#accession S31513  
##status preliminary  
##molecule\_type mRNA  
##residues 1-138 ##label CHA  
##cross-references EMBL:X69861  
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology  
SUMMARY #length 138 #molecular-weight 15115 #checksum 3666

Query Match 89.8%; Score 115; DB 5; Length 138;  
Best Local Similarity 93.3%; Pred. No. 3.30e-08;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 68 iywdddkrypslks 82  
|||||:|||||  
Qy 2 IYWDDDKRYNPSLKS 16

RESULT 5  
ENTRY S18555 #type complete  
TITLE Ig heavy chain - human  
ORGANISM #formal name Homo sapiens #common name man  
DATE 22-Apr-1995  
ACCESSIONS S18555  
REFERENCE S18551  
#authors Shin, E.K.; Mateuda, F.; Nagaoka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, E.; Honjo, T.  
#journal EMBO J. (1991) 10:3641-3645  
#title Physical map of the 3' region of the human immunoglobulin heavy chain locus: clustering of antibody-related variable segments in one haplotype.  
#cross-references WUID:92037524  
#accession S18555  
##status preliminary  
##molecule\_type DNA  
##residues 1-119 ##label SHI  
##cross-references EMBL:X62111  
GENETICS 16/1  
#introns  
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology  
SUMMARY #length 119 #molecular-weight 13230 #checksum 1886

Query Match 87.5%; Score 112; DB 5; Length 119;  
Best Local Similarity 86.7%; Pred. No. 1.12e-07;  
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 72 iywdddkrypslks 86  
|||||:|||||  
Qy 2 IYWDDDKRYNPSLKS 16

RESULT 6

US-08-612-929-24.rpr

Mar 18 10:13

RESULT 2  
ENTRY A49442 #type fragment  
TITLE Ig heavy chain V region (50.1) - mouse (fragment)  
ORGANISM #formal name Mus musculus #common name house mouse  
DATE 21-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 21-Jul-1995  
ACCESSIONS A49442  
REFERENCE A49442  
#authors Stura, E.A.; Stanfield, R.L.; Fieser, G.G.; Silver, S.; Roguska, M.; Hincapie, L.M.; Simmerman, H.K.B.; Profy, A.T.; Wilson, I.A.  
#journal Proteins (1992) 14:499-508  
#title Crystallographic, sequence, and preliminary crystallographic data for an antipeptide Fab 50.1 and peptide complexes with the principal neutralizing determinant of HIV-1 gp120.  
#accession A49442  
##status preliminary; not compared with conceptual translation  
##molecule\_type DNA  
##residues 1-107 ##label STU  
SUMMARY #length 107 #checksum 9363

Query Match 91.4%; Score 117; DB 12; Length 107;  
Best Local Similarity 87.5%; Pred. No. 1.46e-08;  
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 44 hifwddgkrypslks 59  
|||||:|||||  
Qy 1 HIYWDDDKRYNPSLKS 16

RESULT 3  
ENTRY S26936 #type fragment  
TITLE Ig heavy chain V region (DP-76) - human (fragment)  
ORGANISM #formal name Homo sapiens #common name man  
DATE 22-Nov-1993 #sequence\_revision 17-Nov-1995 #text\_change 17-Nov-1995  
ACCESSIONS S26936  
REFERENCE S26885  
#authors Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.  
#journal J. Mol. Biol. (1992) 227:776-798  
#title The repertoire of human germline V(H) sequences reveals about fifty groups of V(H) segments with different hypervariable loops.  
#accession S26936  
##status preliminary  
##molecule\_type DNA  
##residues 1-41 ##label TOM  
##cross-references EMBL:Z14072  
##note the nucleotide sequence was submitted to the EMBL Data Library, July 1992  
##note neither amino acid nor nucleotide sequence is given  
SUMMARY #length 41 #checksum 7016

Query Match 89.8%; Score 115; DB 11; Length 41;  
Best Local Similarity 93.3%; Pred. No. 3.30e-08;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 23 iywdddkrypslks 37  
|||||:|||||  
Qy 2 IYWDDDKRYNPSLKS 16

Mar 18 10:13

US-08-612-929-24 rpr

5

ENTRY A49002 #type fragment  
 TITLE rheumatoid factor heavy chain variable domain, RF H chain V domain-anti-IgM heavy chain variable domain - human (fragment)  
 ORGANISM #formal name Homo sapiens #common name man  
 DATE 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 22-Apr-1995  
 ACCESSIONS A49002  
 REFERENCE A49002  
 #authors Stuber, F.; Lee, S.K.; Bridges Jr., S.L.; Koopman, W.J.; Schroeder, H.W.J.; Gaskin, F.; Fu, S.M.  
 #journal Arthritis Rheum. (1992) 35:900-904  
 #title A rheumatoid factor from a normal individual encoded by VH2 and V kappa II gene segments.  
 #cross-references M01D:92352481  
 #accession A49002  
 #status preliminary  
 #molecule\_type mRNA  
 #residues 1-124 #label STU  
 #cross-references NCBI:110261; NCBI:110262  
 #experimental\_source EBV-transformed lymphoblastoid cell line SSH23  
 #note sequence extracted from NCBI backbone  
 CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology  
 SUMMARY #length 124 #checksum 3208

Query Match 85.2%; Score 109; DB 5; Length 124;  
 Best Local Similarity 80.0%; Pred. No. 3.75e-07;  
 Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 53 iywdddryeps1ks 67  
 |||:||||:||||  
 Qy 2 IYWDDDKRYNPS1KS 16

RESULT 7  
 ENTRY GLHUE #type complete  
 TITLE Ig heavy chain V-II region (He) - human  
 ORGANISM #formal name Homo sapiens #common name man  
 DATE #sequence\_revision 07-May-1981 #text\_change 16-Feb-1996  
 ACCESSIONS A02093  
 REFERENCE A02093  
 #authors Cunningham, B.A.; Pflumm, M.N.; Rutishauser, U.; Edelman, G.M.  
 #journal Proc. Natl. Acad. Sci. U.S.A. (1969) 64:997-1003  
 #title Subgroups of amino acid sequences in the variable regions of immunoglobulin heavy chains.  
 #cross-references M01D:70114712  
 #accession A02093  
 #molecule\_type protein  
 #residues 1-121 #label CUN  
 COMMENT This gamma-1 chain was isolated from a myeloma protein.

GENETICS  
 #gene GDB:IGHV8  
 #map\_position 14q32.33  
 #cross-references GDB:C00-128-528  
 CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology  
 FEATURE 1  
 #modified site blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #status experimental  
 #length 121 #molecular-weight 13483 #checksum 9601

SUMMARY  
 Query Match 82.0%; Score 105; DB 2; Length 121;  
 Best Local Similarity 80.0%; Pred. No. 1.85e-06;  
 Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Mar 18 10:13

US-08-612-929-24 rpr

6

Db 54 lywdddkrfeps1ks 68  
 :|||||:|||||  
 Qy 2 IYWDDDKRYNPS1KS 16

RESULT 8  
 ENTRY S26465 #type complete  
 TITLE Ig heavy chain V region - mouse  
 ORGANISM #formal name Mus musculus #common name house mouse  
 DATE 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 12-Apr-1995  
 ACCESSIONS S26465  
 REFERENCE S26459  
 #authors Kavalier, J.  
 #submission submitted to the EMBL Data Library, April 1991  
 #accession S26465  
 #status preliminary  
 #molecule\_type mRNA  
 #residues 1-113 #label KAV  
 #cross-references EMBL:X59115  
 CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology  
 SUMMARY #length 113 #molecular-weight 12508 #checksum 2993

Query Match 78.1%; Score 100; DB 5; Length 113;  
 Best Local Similarity 87.5%; Pred. No. 1.33e-05;  
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 43 hiwdddkrynp1ks 58  
 |||:||||:|||||  
 Qy 1 HIWDDDKRYNPS1KS 16

RESULT 9  
 ENTRY MHHUMC #type complete  
 TITLE Ig heavy chain V-II region (McE) - human  
 ORGANISM #formal name Homo sapiens #common name man  
 DATE 14-Nov-1983 #sequence\_revision 22-Nov-1983 #text\_change 16-Feb-1996  
 ACCESSIONS A02092  
 REFERENCE A02092  
 #authors Gerbet-Jenson, B.; Kazin, A.; Kehoe, J.M.; Scheffel, C.; Erickson, B.W.; Litman, G.W.  
 #journal J. Immunol. (1981) 126:1212-1216  
 #title Molecular basis for the temperature-dependent insolubility of cryoglobulins. X. The amino acid sequence of the heavy chain variable region of McE.

#cross-references M01D:81118242  
 #accession A02092  
 #molecule\_type protein  
 #residues 1-125 #label GER  
 #note this chain was derived from a monoclonal IgM cryoimmunoglobulin

GENETICS  
 #gene GDB:IGHV8  
 #map\_position 14q32.33  
 #cross-references GDB:C00-128-528  
 CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology  
 KEYWORDS pyroglutamic acid  
 FEATURE 1  
 #modified site pyrrolidone carboxylic acid (Gln) #status experimental

SUMMARY  
 #length 125 #molecular-weight 13783 #checksum 9697



Mar 18 10:13

US-08-612-929-24.rpr

7

Query Match 71.9%; Score 92; DB 2; Length 125;  
 Best Local Similarity 73.3%; Pred. No. 2.92e-04;  
 Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 53 inwdddkrynpals 67  
 |||||:||||:|  
 Qy 2 IYWDKRYNPslks 16

RESULT 10  
 ENTRY PT0174 #type fragment  
 TITLE Ig heavy chain precursor V region (Idb5.7) - mouse (fragment)  
 ORGANISM #formal name Mus musculus #common name house mouse  
 DATE 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change  
 12-Apr-1995

ACCESSIONS PT0174  
 REFERENCE PT0174  
 #authors Perfetti, V.; Borden, P.; Tao, M.H.; Morrison, S.L.; Kabat, E.A.  
 #journal Mol. Immunol. (1991) 28:505-515  
 #title Specificity and variable region cDNA sequence of an isogeneic monoclonal antiidiotype to an anti-alpha (1-6) dextran.  
 #cross-references M01D:9128738  
 #accession PT0174  
 ##molecule\_type mRNA  
 ##residues 1-143 ##label PER  
 ##experimental\_source strain BALB/c  
 ##comment Idb5.7 is an antibody to anti-alpha (1-6) dextran.  
 CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology  
 SUMMARY #length 143 #checksum 3660

Query Match 71.9%; Score 92; DB 5; Length 143;  
 Best Local Similarity 81.3%; Pred. No. 2.92e-04;  
 Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 71 hiswdddkrynpals 86  
 |||||:|||||  
 Qy 1 HIYWDKRYNPslks 16

RESULT 11  
 ENTRY B25913 #type fragment  
 TITLE Ig heavy chain precursor V region (BFL23) - mouse (fragment)  
 ORGANISM #formal name Mus musculus #common name house mouse  
 DATE 16-Aug-1988 #sequence\_revision 16-Aug-1988 #text\_change  
 30-Sep-1993

ACCESSIONS B25913  
 REFERENCE A94148  
 #authors Lawler, A.M.; Lin, P.S.; Gearhart, P.J.  
 #journal Proc. Natl. Acad. Sci. U.S.A. (1987) 84:2454-2458  
 #title Adult B-cell repertoire is biased toward two heavy-chain variable-region genes that rearrange frequently in fetal pre-B cells;  
 #cross-references M01D:87175692  
 #accession B25913  
 ##molecule\_type DNA  
 ##residues 1-103 ##label LAM  
 ##note the authors translated the codon TGT for residue 11 as Ser  
 CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology  
 SUMMARY #length 103 #checksum 957

Query Match 67.2%; Score 86; DB 5; Length 103;  
 Best Local Similarity 68.8%; Pred. No. 2.78e-03;

Mar 18 10:13

US-08-612-929-24.rpr

8

Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Db 56 hilwdddkrynpals 71  
 |||||:|||||  
 Qy 1 HIYWDKRYNPslks 16

RESULT 12  
 ENTRY S26328 #type complete  
 TITLE Ig heavy chain V region - mouse  
 ORGANISM #formal name Mus musculus #common name house mouse  
 DATE 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change  
 13-Jan-1995

ACCESSIONS S26328  
 REFERENCE S26309  
 #authors Stark, S.E.; Caton, A.J.  
 #journal J. Exp. Med. (1991) 174:613-624  
 #title Antibodies that are specific for a single amino acid interchange in a protein epitope use structurally distinct variable regions.  
 #accession S26328  
 ##status preliminary  
 ##molecule\_type mRNA  
 ##residues 1-116 ##label STA  
 ##cross-references EMBL:X59198  
 SUMMARY #length 116 #molecular-weight 12895 #checksum 8145

Query Match 67.2%; Score 86; DB 12; Length 116;  
 Best Local Similarity 68.8%; Pred. No. 2.78e-03;  
 Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Db 48 hilwdddkrynpals 63  
 |||||:|||||  
 Qy 1 HIYWDKRYNPslks 16

RESULT 13  
 ENTRY S09959 #type fragment  
 TITLE Ig heavy chain V-D-J region (31-90) - mouse (fragment)  
 ORGANISM #formal name Mus musculus #common name house mouse  
 DATE 12-Feb-1993 #sequence\_revision 12-Feb-1993 #text\_change  
 23-Mar-1993

ACCESSIONS S09959  
 REFERENCE S09955  
 #authors Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jatón, J.C.; Izui, S.  
 #journal Eur. J. Immunol. (1990) 20:771-777  
 #title Variable region sequences of pathogenic anti-mouse red blood cell autoantibodies from autoimmune NZB mice.  
 #cross-references M01D:90269328  
 #accession S09959  
 ##molecule\_type mRNA  
 ##residues 1-121 ##label REI  
 ##cross-references EMBL:X51847  
 SUMMARY #length 121 #checksum 7852

Query Match 60.2%; Score 77; DB 12; Length 121;  
 Best Local Similarity 62.5%; Pred. No. 7.28e-02;  
 Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 52 niwdddkrynpals 67  
 |||||:|||||  
 Qy 1 HIYWDKRYNPslks 16

US-08-612-929-24 rpt

Mar 18 10:13

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RESULT 14
ENTRY S26922 #type fragment
TITLE Ig heavy chain V region (DP-26) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
10-Nov-1995
ACCESSIONS S26922
REFERENCE S26885
#authors Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.;
Winter, G.
#journal J. Mol. Biol. (1992) 227:776-798
#title The repertoire of human germline V(H) sequences reveals about
fifty groups of V(H) segments with different hypervariable
loops.
#accession S26922
##status preliminary
##molecule_type DNA
##residues 1-96 ##label TOM
##cross-references EMBL:Z12328
SUMMARY #length 96 #checksum 8878

Query Match 59.4%; Score 76; DB 11; Length 96;
Best Local Similarity 56.3%; Pred. No. 1.04e-01;
Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Db 52 hifndekystalks 67
||: ||: ||: ||: ||:
QY 1 HIYDDDKRYNPSLKS 16

RESULT 15
ENTRY S46461 #type complete
TITLE Ig heavy chain V region (YAC-3) - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
26-May-1995
ACCESSIONS S46461
REFERENCE S46460
#authors Cook, G.P.; Tomlinson, I.M.; Walter, G.; Riethman, H.;
Carter, N.P.; Buluwela, L.; Winter, G.; Rabbitts, T.H.
#journal Nature Genet. (1994) 7:162-168
#title A map of the human immunoglobulin V(H) locus completed by
analysis of the telomeric region of chromosome 14q.
#accession S46461
##status preliminary
##molecule_type DNA
##residues 1-78 ##label C00
##cross-references EMBL:Z27502
SUMMARY #length 78 #molecular-weight 8788 #checksum 5329

Query Match 57.8%; Score 74; DB 11; Length 78;
Best Local Similarity 62.5%; Pred. No. 2.09e-01;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 43 ridwdddkfystalkt 58
: || || || || ||: ||: ||:
QY 1 HIYDDDKRYNPSLKS 16

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Search completed: Tue Mar 18 10:15:15 1997  
Job time : 11 secs.

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Mar 18 10:14

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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Mar 18 10:15:33 1997; MaePar time 1.99 Seconds  
82.665 Million cell updates/sec

Tabular output not generated.

Title: >US-08-612-929-24  
Description: (1-16) from US08612929.pep  
Perfect Score: 128  
Sequence: 1 HIWDDDKRYNPILKS 16

Scoring table: PAM 150  
Gap 15

Searched: 88003 seqs, 10495656 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: a-geneseq25  
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13  
14:part14 15:part15 16:part16 17:part17 18:part18

Statistics: Mean 20.200; Variance 65.991; scale 0.306

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.	
SUMMARIES								
1	128	100.0	16	13	R70199	MAB 3B9 heavy chain C	1.07e-06	
2	128	100.0	140	13	R70190	Mouse Mab 3B9 heavy c	1.07e-06	
3	128	100.0	141	13	R70191	Chimeric antibody 3B9	1.07e-06	
4	128	100.0	141	13	R70192	Humanized antibody 3B	1.07e-06	
5	121	94.5	16	10	R54105	Humanised anti-HIV MA	6.87e-06	
6	121	94.5	122	11	R54101	Humanised Mab H-chain	6.87e-06	
7	121	94.5	122	10	R54110	Humanised anti-HIV MA	6.87e-06	
8	121	94.5	246	11	R58612	IL-6 binding inhibito	6.87e-06	
9	115	89.8	139	8	R38315	Sequence of the VH of	3.34e-05	
10	112	87.5	119	12	R62999	Human immunoglobulin	7.32e-05	
11	110	85.9	120	17	R88109	Murine anti-Protein C	1.23e-04	
12	110	85.9	139	17	R88107	Murine anti-Protein C	1.23e-04	

Sequence of mouse VH 5.84e-04  
Mouse anti-human IL-6 1.25e-02  
Anti-human IL-6 chima 1.25e-02  
Mouse heavy chain var 1.25e-02  
Anti-human IL-6 chima 1.25e-02  
CDR-grafted anti-RSV 4.37e-02  
Anti-RSV F glycoprote 4.37e-02  
Human immunoglobulin 6.49e-01  
Rat immunoglobulin H 6.49e-01  
KM50 cell-derived Ig 6.49e-01  
B13/B14 HAVH 1.33e+00  
Partial B13/B14 Ab va 1.33e+00  
Human immunoglobulin 3.44e+00  
Human Cos VH region. 3.44e+00  
Human Cess VH region. 3.44e+00  
Human immunoglobulin 6.93e+00  
Vh 71-4. 6.93e+00  
Human immunoglobulin 6.93e+00  
SpA-reactive IgM heav 1.10e+01  
Anti-human Rhd PAG-1 1.38e+01  
Pig brain thalamus po 1.74e+01  
Anti-HIV gp41 immunog 1.74e+01  
F105 rearranged varia 1.74e+01  
Human glutamate recep 2.18e+01  
Human GluRII receptor 2.18e+01  
Human glutamate recep 2.18e+01  
Human glutamate recep 2.18e+01  
Glutamate receptor i. 2.18e+01  
Human immunoglobulin 2.73e+01  
Human immunoglobulin 2.73e+01  
Human immunoglobulin 2.73e+01  
Mab 1-3-1 variable re 2.73e+01

## ALIGNMENTS

RESULT 1  
ID R70199 standard; Protein; 16 AA.  
AC R70199;  
DT 20-SEP-1995 (first entry)  
DE Mab 3B9 heavy chain CDR.  
KW Chimeric antibody; humanized antibody; antibody engineering;  
KW monoclonal antibody; Mab; interleukin-4; IL-4; allergy; CDR;  
KW complementarity determining region.  
OS Mus sp.  
PN W09507301-A.  
PD 16-MAR-1995.  
PF 07-SEP-1994; U10308.  
PR 07-SEP-1993; US-117366.  
PR 14-OCT-1993; US-136783.  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
PA (SMIK ) SMITHKLINE BEECHAM PLC.  
PA Gross MS, Holmes SD, Sylvester DR;  
PI WPI; 95-123387/16.  
DR Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived  
PT from high affinity mAbs - useful in treatment of IL-4-mediated  
PT and IgE-mediated allergic conditions  
PS Disclosure; Page 57; 91pp; English.  
CC Spleen cells from mice immunized with human IL-4 were used to prepare  
CC hybridomas, which were screened for anti-IL-4 Mab secretion. Only  
CC clone 3B9 was positive. cDNA clones of the 3B9 light and heavy  
CC chains were cloned into pCEN7f and transformed into E. coli  
CC DH5-alpha. A heavy chain cDNA clone was sequenced (Q83491) that

Mar 13 10:14

US-08-612-929-24 mg

3

CC encoded the protein given in R70190. 3 CDRs (R70198-200) were  
 CC identified.  
 SQ Sequence 16 AA;

Query Match 100.0%; DB 13; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 1.07e-06;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 hiywdkrynpelks 16  
 |||  
 Qy 1 HIYWDKRYNPSLKS 16

## RESULT 2

ID R70190 standard; Protein; 140 AA.  
 AC R70190;  
 DT 20-SEP-1995 (first entry)  
 DE Mouse MAb 3B9 heavy chain.  
 KW Chimeric antibody; humanized antibody; antibody engineering;  
 KW monoclonal antibody; MAb; interleukin-4; IL-4; allergy.  
 OS Mus sp. Location/Qualifiers  
 FH Key 1..19  
 FT Peptide 1..19  
 FT /label= Sig\_peptide 50..56  
 FT Region 50..56  
 FT /label= CDR  
 FT /note= "complementarity determining region"  
 FT Region 71..86  
 FT /label= CDR  
 FT /note= "complementarity determining region"  
 FT Region 119..129  
 FT /label= CDR  
 FT /note= "complementarity determining region"  
 PN W09507301-A.  
 PD 16-MAR-1995.  
 PF 07-SEP-1994; U10308.  
 PR 07-SEP-1993; US-117366.  
 PR 14-OCT-1993; US-136783.  
 PA (SMIK ) SMITHKLINE BEECHAM CORP.  
 PA (SMIK ) SMITHKLINE BEECHAM PLC.  
 PI Gross MS, Holmes SD, Sylvester DR;  
 DR WFI; 95-123387/16.  
 DR N-PSDB; Q83491.  
 PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived  
 PT from high affinity mAbs - useful in treatment of IL-4-mediated  
 PT and IgE-mediated allergic conditions  
 PS Disclosure; Fig.2; 97pp; English.  
 CC Spleen cells from mice immunized with human IL-4 were used to prepare  
 CC hybridomas, which were screened for anti-IL-4 MAb secretion. Only  
 CC clone 3B9 was positive. cDNA clones of the 3B9 light and heavy  
 CC chains were cloned into pCEW7f+ and transformed into E. coli  
 CC DH5-alpha. The clones were sequenced (Q83490-91), and used for  
 CC antibody engineering.  
 SQ Sequence 140 AA;

Query Match 100.0%; DB 13; Length 140;  
 Best Local Similarity 100.0%; Pred. No. 1.07e-06;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 71 hiywdkrynpelks 86  
 |||  
 Qy 1 HIYWDKRYNPSLKS 16

Mar 18 10:14

US-08-612-929-24 mg

4

## RESULT 3

ID R70191 standard; Protein; 141 AA.  
 AC R70191;  
 DT 20-SEP-1995 (first entry)  
 DE Chimeric antibody 3B9 heavy chain.  
 KW Chimeric antibody; antibody engineering; monoclonal antibody;  
 KW MAb; interleukin-4; IL-4; allergy.  
 OS Homo sapiens; Mus sp. Location/Qualifiers  
 FH Key 1..19  
 FT Peptide 1..19  
 FT /label= Sig\_peptide 51..57  
 FT Region 51..57  
 FT /label= CDR  
 FT /note= "complementarity determining region"  
 FT Region 72..87  
 FT /label= CDR  
 FT /note= "complementarity determining region"  
 FT Peptide 120..130  
 FT /label= CDR  
 FT /note= "complementarity determining region"  
 PN W09507301-A.  
 PD 16-MAR-1995.  
 PF 07-SEP-1994; U10308.  
 PR 07-SEP-1993; US-117366.  
 PR 14-OCT-1993; US-136783.  
 PA (SMIK ) SMITHKLINE BEECHAM CORP.  
 PA (SMIK ) SMITHKLINE BEECHAM PLC.  
 PI Gross MS, Holmes SD, Sylvester DR;  
 DR WFI; 95-123387/16.  
 DR N-PSDB; Q83492.  
 PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived  
 PT from high affinity mAbs - useful in treatment of IL-4-mediated  
 PT and IgE-mediated allergic conditions  
 PS Disclosure; Fig.3; 97pp; English.  
 CC A human/mouse chimeric antibody heavy chain variable region was  
 CC constructed (given in R70191) that contained the mouse anti-human  
 CC IL-4 MAb 3B9 variable region including 3 CDRs (R70198-200) and a  
 CC human antibody signal peptide (R70193). The construct was used  
 CC for humanized antibody production.  
 SQ Sequence 141 AA;

Query Match 100.0%; DB 13; Length 141;  
 Best Local Similarity 100.0%; Pred. No. 1.07e-06;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 72 hiywdkrynpelks 87  
 |||  
 Qy 1 HIYWDKRYNPSLKS 16

## RESULT 4

ID R70192 standard; Protein; 141 AA.  
 AC R70192;  
 DT 20-SEP-1995 (first entry)  
 DE Humanized antibody 3B9 heavy chain.  
 KW Humanized antibody; antibody engineering; monoclonal antibody;  
 KW MAb; interleukin-4; IL-4; allergy.  
 OS Homo sapiens. Location/Qualifiers  
 FH Key 1..19  
 FT Peptide 1..19  
 FT /label= Sig\_peptide 51..57  
 FT Region 51..57  
 FT /label= CDR  
 FT /note= "complementarity determining region"

Query Match 100.0%; DB 13; Length 141;  
 Best Local Similarity 100.0%; Pred. No. 1.07e-06;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-08-612-929-24.rag

Mar 18 10:14

Query Match 94.5%; Score 121; DB 10; Length 16;  
 Best Local Similarity 93.8%; Pred. No. 6.87e-06;  
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 hiywdkdkhynpslks 16  
 |||||:|||||  
 Qy 1 HIYWDKDKRYNPSLKS 16

## RESULT 6

ID R54101 standard; Protein; 122 AA.  
 AC R54101;  
 DT 08-FEB-1995 (first entry)  
 DE Humanised MAb H-chain.  
 KW Human; mouse; murine; heavy; light; chain; monoclonal; antibody;  
 KW complementarity determining region; CDR; IgG; kappa; IIIB; IIIMN.  
 OS Chimeric - Mus musculus.  
 OS Chimeric - Homo sapiens.  
 FH Key Location/Qualifiers  
 FT Region 31...37  
 FT /label= CDR1  
 FT Region 52..67  
 FT /label= CDR2  
 FT Region 100..111  
 FT /label= CDR3  
 PN J06141885-A.  
 PD 24-MAY-1994.  
 PF 05-NOV-1992; 322476.  
 PR 05-NOV-1992; JP-322476.  
 PA (KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.  
 DR WPI; 94-205040/25.  
 DR N-PSDB; Q68709.  
 PT Recombinant anti-HIV monoclonal antibody - capable of  
 PT neutralising strains which can not be neutralised by anti-IIIB  
 PT and IIIMN antibodies  
 PS Disclosure; Page 13; 23pp; Japanese.  
 CC The sequences given in R54101-02 represent the heavy and light chains  
 CC respectively of the humanised monoclonal antibody (MAB) of the  
 CC invention. The antibody has the ability to neutralise human  
 CC immunodeficiency virus. The antibody is classified as IgG kappa and  
 CC has the sequence RIGPCR or RVGPGR in the principal neutralising  
 CC domain. The antibody may be used to neutralise the clinically  
 CC separate strains which cannot be neutralised by the neutralising  
 CC antibodies against IIIB and IIIMN strains.  
 SQ Sequence 122 AA;

Query Match 94.5%; Score 121; DB 11; Length 122;  
 Best Local Similarity 93.8%; Pred. No. 6.87e-06;  
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 52 hiywdkdkhynpslks 67  
 |||||:|||||  
 Qy 1 HIYWDKDKRYNPSLKS 16

## RESULT 7

ID R54110 standard; Protein; 122 AA.  
 AC R54110;  
 DT 08-FEB-1995 (first entry)  
 DE Humanised anti-HIV MAB fragment #8.  
 KW Human; mouse; murine; heavy; light; chain; monoclonal; antibody;  
 KW complementarity determining region; CDR; IgG; kappa; IIIB; IIIMN;  
 KW polymerase chain reaction; primer; amplify; PCR.

US-08-612-929-24.rag

Mar 18 10:14

FT Region 72..87  
 FT /label= CDR  
 FT /note= "complementarity determining region"  
 FT Region 120..130  
 FT /label= CDR  
 FT /note= "complementarity determining region"

PN W09507301-A.  
 PD 16-MAR-1995.  
 PF 07-SEP-1994; U10308.  
 PR 07-SEP-1993; US-117366.  
 PR 14-OCT-1993; US-136783.  
 PA (SMIK ) SMITHKLINE BEECHAM CORP.  
 PA (SMIK ) SMITHKLINE BEECHAM PLC.  
 PI Gross MS, Holmes SD, Sylvester DR;  
 DR WPI; 95-123387/16.  
 DR N-PSDB; Q83493.  
 PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived  
 PT from high affinity mAbs - useful in treatment of IL-4-mediated  
 PT and IgE-mediated allergic conditions  
 PS Disclosure; Fig. 4; 97pp; English.  
 CC A humanized antibody heavy chain variable region and signal  
 CC sequence is given in R70192. The signal sequence is also  
 CC provided in R70193. The CDR sequences of the construct are  
 CC identical to the native CDRs of mouse anti-human IL-4 MAB  
 CC 389 (R70198-200).  
 SQ Sequence 141 AA;

Query Match 100.0%; Score 128; DB 13; Length 141;  
 Best Local Similarity 100.0%; Pred. No. 1.07e-06;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 72 hiywdkdkhynpslks 87  
 |||||:|||||  
 Qy 1 HIYWDKDKRYNPSLKS 16

## RESULT 5

ID R54105 standard; Protein; 16 AA.  
 AC R54105;  
 DT 08-FEB-1995 (first entry)  
 DE Humanised anti-HIV MAB fragment #3.  
 KW Human; mouse; murine; heavy; light; chain; monoclonal; antibody;  
 KW complementarity determining region; CDR; IgG; kappa; IIIB; IIIMN;  
 KW polymerase chain reaction; primer; amplify; PCR.  
 OS Synthetic.  
 PN J06141885-A.  
 PD 24-MAY-1994.  
 PF 05-NOV-1992; 322476.  
 PR 05-NOV-1992; JP-322476.  
 PA (KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.  
 DR WPI; 94-205040/25.  
 DR Recombinant anti-HIV monoclonal antibody - capable of  
 PT neutralising strains which can not be neutralised by anti-IIIB  
 PT and IIIMN antibodies  
 PS Disclosure; Page 14; 23pp; Japanese.

CC The sequences given in R54103-11 are fragments of the heavy and light  
 CC chains of the humanised monoclonal antibody (MAB) of the invention.  
 CC The antibody has the ability to neutralise human immunodeficiency  
 CC virus. The antibody is classified as IgG kappa and has the  
 CC sequence RIGPCR or RVGPGR in the principal neutralising domain.  
 CC The antibody may be used to neutralise the clinically  
 CC separate strains which cannot be neutralised by the neutralising  
 CC antibodies against IIIB and IIIMN strains.  
 SQ Sequence 16 AA;

Mar 18 10:14 US-08-612-929-24.rag

Qy 1 HIYWDKRYNPSLKS 16

RESULT 9

ID R38315 standard; Protein; 139 AA.

AC R38315;

DT 04-DEC-1993 (first entry)

DE Sequence of the VH of antibody B17X2

KW Variable heavy antibody chain; human subgroup 4 germline.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Region 50..56

FT /label= CDR1 71..86

FT /label= CDR2 119..126

FT /label= CDR3

PN W09312231-A.

PD 24-JUN-1993.

PF 13-DEC-1991; MO-AU0583.

PR 13-DEC-1991; MO-AU0583.

PA (DMC) DOW CHEM AUSTRALIA LTD.

PI Johnson KS, Mezes PS, Richard RA;

DR WPI; 93-214173/26.

DR N-PSDB; Q45597.

DT New composite antibody binding to tumour associated TAG-72

PT antigen - includes light chain variable region from human

PT subgroup 4 germline gene, useful, opt. as conjugate, for

PT diagnosis or treatment of cancer

PS Disclosure; Figure 4; 150pp; English.

CC Cell line B17X2 expresses an antibody utilising a variable light

CC chain encoded by a gene derived from Hum4 VL and a variable heavy

CC chain which makes a stable VL and VH combination.

SQ Sequence 139 AA;

Query Match 89.8%; Score 115; DB 8; Length 139;

Best Local Similarity 93.3%; Pred. No. 3.34e-05;

Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 72 iywdddkrypslks 86

Qy 2 IYWDKRYNPSLKS 16

RESULT 10

ID R66299 standard; Protein; 119 AA.

AC R66299;

DT 07-AUG-1995 (first entry)

DE Human immunoglobulin variable heavy chain #5.

KW Primer; PCR; amplify; human; immunoglobulin; variable; heavy chain;

KW cosmid; placenta; vector; pUB81; E.coli; mammalian.

OS Homo sapiens.

PN W09426895-A.

PD 24-NOV-1994.

PF 10-MAY-1993; J00603.

PR 10-MAY-1993; MO-J00603.

PA (NLSB) JAPAN TOBRACCO INC.

PI Honjo T, Matsuda F;

DR WPI; 95-006791/01.

DR N-PSDB; Q78943.

PT DNA fragment comprising human immunoglobulin Vh genes - for the

PT production of human immunoglobulin in mammalian hosts

PS Disclosure; Page 36-37; 130pp; Japanese.

CC Protein sequences (R66295-51) are novel human immunoglobulin heavy chain

Mar 18 10:14 US-08-612-929-24.rag

OS Synthetic.

PN J06141885-A.

PD 24-MAY-1994.

PF 05-NOV-1992; 322476.

PA (KAGA) ZH KAGAKU & KESSSEI RYOHO KENKYUSHO.

DR WPI; 94-205040/25.

PT Recombinant anti-HIV monoclonal antibody - capable of

PT neutralising strains which can not be neutralised by anti-IIIB

PT and IIIMN antibodies

PS Disclosure; Page 14; 23pp; Japanese.

CC The sequences given in R54103-11 are fragments of the heavy and light

CC chains of the humanised monoclonal antibody (MAb) of the invention.

CC The antibody has the ability to neutralise human immunodeficiency

CC virus. The antibody is classified as IgG kappa and has the

CC sequence RIGPCR or RVGPCR in the principal neutralising domain.

CC The antibody may be used to neutralise the clinically

CC separate strains which cannot be neutralised by the neutralising

CC antibodies against IIIB and IIIMN strains.

SQ Sequence 122 AA;

Query Match 94.5%; Score 121; DB 10; Length 122;

Best Local Similarity 93.8%; Pred. No. 6.87e-06;

Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 52 hiywdkrypslks 67

Qy 1 HIYWDKRYNPSLKS 16

RESULT 8

ID R58612 standard; Protein; 246 AA.

AC R58612;

DT 28-APR-1995 (first entry)

DE IL-6 binding inhibitor.

KW Human interleukin-6 binding inhibitor; IL-6; rheumatoid arthritis;

KW septic shock; multiple myeloma; ss.

OS Homo sapiens.

PN EP-617126-A.

PD 28-SEP-1994.

PF 16-FEB-1994; 102346.

PR 17-FEB-1993; JP-028173.

PA (AJIN) AJINOMOTO KK.

PI Hamuro J, Nakazawa H, Shimamura T;

DR WPI; 94-295777/37.

DR N-PSDB; Q70612.

PT Polypeptide inhibiting binding of human interleukin-6 (IL-6) to

PT its receptor - useful for treating autoimmune disease induced

PT or aggravated by IL-6

PS Claim 5; Page 18; 26pp; English.

CC Q70612 codes for human interleukin-6 binding inhibitor, the

CC polypeptide described in R58612. This polypeptide inhibits the

CC binding of human IL-6 to its receptor, and can therefore be

CC useful in the treatment of a variety of autoimmune diseases;

CC specifically in the treatment of rheumatoid arthritis, septic

CC shock due to bacterial infection and multiple myeloma.

SQ Sequence 246 AA;

Query Match 94.5%; Score 121; DB 11; Length 246;

Best Local Similarity 93.8%; Pred. No. 6.87e-06;

Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 174 hiywdkrypslks 189

10

US-08-612-929-24.rag

Mar 18 10:14

Db 52 hiwdddkrynpvls 67  
 || ||||| ||||| |||||  
 QY 1 HIWDDDKRYNPSLSKS 16

RESULT 12  
 ID R88107 standard; Protein; 139 AA.  
 AC R88107;  
 DT 25-JUL-1996 (first entry)  
 DE Murine anti-Protein C MAb HPC-4 VH gamma protein.  
 KW Epitope; activation; heavy chain; protein C; vitamin K; plasma protein;  
 KW zymogen; cleavage; mouse; humanised antibody; variable region;  
 KW light chain; inhibition; anticoagulant; coagulation; tumour.  
 OS Mus musculus.

Key Location/Qualifiers  
 FT Peptide 1..19  
 FT /note= "signal peptide"  
 FT Peptide 20..139  
 FT /note= "mature peptide"  
 PN W09534652-A1.  
 PD 21-DEC-1995.  
 PF 09-JUN-1995; U07372.  
 PR 10-JUN-1994; US-259321.  
 PA (OKLA-) OKLAHOMA MED RES FOUND.  
 PI Eamon CT, Rezaie A;  
 DR WPI; 96-049681/05.  
 DR N-PSDB; T09299.  
 PT Calcium-binding monoclonal antibody immunoreactive with Protein C -  
 PT inhibits Protein C anticoagulant activation by  
 PT thrombin-thrombomodulin, e.g. for treating tumours  
 PS Claim 2; Page 29; 41pp; English.  
 CC This is the amino acid sequence of the heavy chain variable region from  
 CC the murine anti-protein C monoclonal antibody HPC-4 which recognises  
 CC the activation peptide region (R88106) of the heavy chain of protein C,  
 CC a vitamin K-dependent plasma protein zymogen. Protein C is converted to  
 CC activated protein C (APC) by cleavage between the Arg-Leu amino acid  
 CC contained within the activation peptide sequence. HPC-4 prevents protein  
 CC C activation to APC by binding to this region. The DNA sequences encoding  
 CC the variable regions of the heavy and light chains of the antibody  
 CC (T09299-302) were used to construct humanised antibodies using the PCR  
 CC primers T09303-9. The humanised antibodies are useful as inhibitors of  
 CC coagulation and can be used for the treatment of tumours by inhibiting  
 CC the anticoagulant activity of APC by preventing conversion of protein C  
 CC to APC.  
 SQ Sequence 139 AA;

Query Match 85.9%; Score 110; DB 17; Length 139;  
 Best Local Similarity 87.5%; Pred. No. 1.23e-04;  
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 71 hiwdddkrynpvls 86  
 || ||||| ||||| |||||  
 QY 1 HIWDDDKRYNPSLSKS 16

RESULT 13  
 ID R54092 standard; Protein; 143 AA.  
 AC R54092;  
 DT 29-DEC-1994 (first entry)  
 DE Sequence of mouse VH showing the sequences of recombinant  
 DE anti-FHV-1 antibody CDRs 1, 2 and 3.  
 KW Feline herpes virus; FHV-1; monoclonal antibody; CDR;  
 KW complementarity determining region.  
 OS Mus musculus.

9

US-08-612-929-24.rag

Mar 18 10:14

CC sequences encoded by novel isolated genes. The genes (Q78939-79002) were  
 CC isolated and cloned from a series of cosmid constructs: Y202; Y103; Y21;  
 CC Y6; Y24; 3-31; M84; M118 and M131, by PCR amplification using primers  
 CC Q78917-38. The genes are subdivided into 5 families of Vh genes. The  
 CC fragments cover a region of 800 kb. The DNA fragments were isolated from  
 CC high molecular weight DNA from human placenta. The DNA was partially  
 CC digested with TaqI restriction enzyme. The fragments were separated by  
 CC gel electrophoresis and 35-45 kb fractions were collected. The fragments  
 CC were ligated with ClaI-digested cosmid vector pUB81. The ligation  
 CC products were in vitro packed and infected into E.coli 490A. The  
 CC fragments were then subcloned by colony hybridisation. The Vh genes and  
 CC the DNA fragments encoding them are useful in producing human  
 CC immunoglobulin in mammalian hosts.  
 SQ Sequence 119 AA;

Query Match 87.5%; Score 112; DB 12; Length 119;  
 Best Local Similarity 86.7%; Pred. No. 7.32e-05;  
 Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 72 iywdddkrypsls 86  
 ||||| ||||| ||||| |||||  
 QY 2 IYWDDDKRYNPSLSKS 16

RESULT 11  
 ID R88109 standard; peptide; 120 AA.  
 AC R88109;  
 DT 25-JUL-1996 (first entry)  
 DE Murine anti-Protein C MAb HPC-4 VH gamma mature peptide.  
 KW Epitope; activation; heavy chain; protein C; vitamin K; plasma protein;  
 KW zymogen; cleavage; mouse; humanised antibody; variable region;  
 KW light chain; inhibition; anticoagulant; coagulation; tumour.  
 OS Mus musculus.  
 PN W09534652-A1.  
 PD 21-DEC-1995.  
 PF 09-JUN-1995; U07372.  
 PR 10-JUN-1994; US-259321.  
 PA (OKLA-) OKLAHOMA MED RES FOUND.  
 PI Eamon CT, Rezaie A;  
 DR WPI; 96-049681/05.  
 DR N-PSDB; T09300.  
 PT Calcium-binding monoclonal antibody immunoreactive with Protein C -  
 PT inhibits Protein C anticoagulant activation by  
 PT thrombin-thrombomodulin, e.g. for treating tumours  
 PS Claim 2; Page 29; 41pp; English.

CC This is the amino acid sequence of the mature peptide from the murine  
 CC anti-protein C monoclonal antibody HPC-4 heavy chain variable region.  
 CC HPC-4 recognises the activation peptide region (R88106) of the heavy  
 CC chain of protein C, a vitamin K-dependent plasma protein zymogen.  
 CC Protein C is converted to activated protein C (APC) by cleavage between  
 CC the Arg-Leu amino acid contained within the activation peptide sequence.  
 CC HPC-4 prevents protein C activation to APC by binding to this region.  
 CC The DNA sequences encoding the variable regions of the heavy and light  
 CC chains of the antibody (T09299-302) were used to construct humanised  
 CC antibodies using the PCR primers T09303-9. The humanised antibodies are  
 CC useful as inhibitors of coagulation and can be used for the treatment of  
 CC tumours by inhibiting the anticoagulant activity of APC by preventing  
 CC conversion of protein C to APC.  
 SQ Sequence 120 AA;

Query Match 85.9%; Score 110; DB 17; Length 120;  
 Best Local Similarity 87.5%; Pred. No. 1.23e-04;  
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Mar 18 10:14

US-08-612-929-24.rag

11

FH Key Location/Qualifiers

FT Peptide 1..19  
 FT /label= leader  
 FT Region 20..47  
 FT /label= FR1  
 FT Region 48..56  
 FT /label= CDR1  
 FT Region 57..70  
 FT /label= FR2  
 FT Region 71..86  
 FT /label= CDR2  
 FT Region 87..118  
 FT /label= FR3  
 FT Region 119..132  
 FT /label= CDR3  
 FT Region 133..143  
 FT /label= FR4  
 PN W09412661-A.  
 PD 09-JUN-1994.  
 PR 25-NOV-1993; J01724.  
 PR 28-NOV-1992; JP-341255.  
 PA (KAGA ) CEMO SERO THERAPEUTIC RES INST.  
 PI Kimachi K, Maeda H, Nishiyama K, Tokiyoshi S;  
 DR WPI; 94-200288/24.  
 DR N-PSDB; 064166.  
 PT Feline monoclonal antibody and recombinant antibodies specific  
 for FHV-1 - for detection, treatment and prevention of FHV-1  
 PT infection.  
 PS Disclosure; Page 17-18; 53pp; Japanese.  
 CC The inventors claim a monoclonal antibody against feline herpes  
 CC virus (FHV-1). They also claim a recombinant antibody against FHV-1  
 CC and fragments of VH and VL CDR1, CDR2 and CDR3. The antibodies are  
 CC used in the detection, treatment and prevention of FHV-1. The  
 CC sequences of the CDRs in the VH of the recombinant anti-FHV-1  
 CC antibody are given in R54092. The sequences of the CDRs in the VL of  
 CC the recombinant anti-FHV-1 antibody are given in R54093. These CDR  
 CC sequences are claimed.  
 SQ Sequence 143 AA;

Query Match 81.3%; Score 104; DB 10; Length 143;  
 Best Local Similarity 81.3%; Pred. No. 5.84e-04;  
 Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 71 hiwdddkynpalks 86  
 || |||| |||||  
 Qy 1 HIYDDDKRYNPSLKS 16

RESULT 14

ID R7213 standard; Peptide; 16 AA.  
 AC R7213;  
 DT 23-AUG-1995 (first entry)  
 DE Mouse anti-human IL-6 Ab H chain V region CDR2.  
 KW Primer; PCR; amplify; kappa; light chain; variable region; mouse; human;  
 KW interleukin; antibody; hybridoma; CDR; framework; constant region;  
 KW heavy chain; disorder; antigenicity.  
 OS Synthetic.  
 PN W09428159-A.  
 PD 08-DEC-1994.  
 PF 30-MAY-1994; J00859.  
 PR 31-MAY-1993; JP-129787.  
 PA (CHUS ) CHUGAI SEIYAKU KK.  
 PA (CHUS ) CHUGAI PHARM CO LTD.  
 PI Hirata Y, Sato K, Tsuchiya M;

Mar 18 10:14

US-08-612-929-24.rag

12

DR WPI; 95-022828/03.  
 PT Antibody against IL-6 - useful for the therapy and treatment of  
 PT IL-6 related disorders.  
 PS Claim 8; Page 65; 82pp; Japanese.  
 CC The sequence of the mouse anti-human interleukin-6 (IL-6) antibody heavy  
 CC chain variable region complementarity determining region (CDR) 2. This  
 CC sequence and that of CDR1 and 3 (R77212+4) were used in conjunction with  
 CC the framework regions 1-4 (R77215-8) to construct a chimaeric antibody  
 CC against human interleukin-6 (IL-6). The vectors 075914-7 express  
 CC constructs encoding fragments of a chimaeric antibody to the human IL-6  
 CC comprising (a) a light chain with (i) a variable region containing 3 CDR  
 CC (R77201-3) inserted into several framework regions (FR) (r77204-7) and  
 CC (ii) a human light chain constant region and (b) a heavy chain with (i) a  
 CC variable region containing 3 CDR (R77212-4) inserted into FR (r77215-8)  
 CC and (ii) a human light chain constant region. The FR of the light chain  
 CC may be mouse derived (Q75888) or from the human antibody REI. The heavy  
 CC chain FR may also be mouse derived (Q75889) or from the human antibody  
 CC DAW. The antibodies can be used in the treatment of IL-6 related  
 CC disorders. The antibodies are useful as they have low antigenicity due  
 CC to the use of human derived sequences and low antigenicity mouse derived  
 CC sequences.  
 SQ Sequence 16 AA;

Query Match 71.9%; Score 92; DB 12; Length 16;  
 Best Local Similarity 68.8%; Pred. No. 1.25e-02;  
 Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 1 hiwdddkynpalkg 16  
 || |||| |||||  
 Qy 1 HIYDDDKRYNPSLKS 16

RESULT 15

ID R67658 standard; Protein; 139 AA.  
 AC R67658;  
 DT 23-AUG-1995 (first entry)  
 DE Anti-human IL-6 chimaeric Ab H chain V region in HEL-RVH-SK2a.  
 KW Primer; PCR; amplify; kappa; light chain; variable region; mouse; human;  
 KW interleukin; antibody; hybridoma; CDR; framework; constant region;  
 KW heavy chain; disorder; antigenicity.  
 OS Synthetic.  
 FH Key Location/Qualifiers  
 FT Domain 1..19  
 FT /label= signal peptide  
 FT Domain 20..49  
 FT /label= Framework region 1  
 FT Domain 50..56  
 FT /label= CDR1  
 FT Domain 57..70  
 FT /label= Framework region 2  
 FT Domain 71..86  
 FT /label= CDR2  
 FT Domain 87..118  
 FT /label= Framework region 3  
 FT Domain 119..128  
 FT /label= CDR3  
 FT Domain 129..139  
 FT /label= Framework region 4  
 PN W09428159-A.  
 PD 08-DEC-1994.  
 PF 30-MAY-1994; J00859.  
 PR 31-MAY-1993; JP-129787.  
 PA (CHUS ) CHUGAI SEIYAKU KK.  
 PA (CHUS ) CHUGAI PHARM CO LTD.



Mar 18 10:14

US-08-612-929-24.FRG

13

PI Hirata Y, Sato K, Tauchiya M;  
 DR WPI; 95-022828/03.  
 DR N-PSDB; Q75916.  
 PT Antibody against IL-6 - useful for the therapy and treatment of  
 PT IL-6 related disorders.  
 PS Claim 21; Page 60-61; 82pp; Japanese.  
 CC The sequence of the heavy chain variable region of a chimaeric antibody  
 CC against human interleukin-6 (IL-6). The sequence is found on the plasmid  
 CC HEL-RVH-SK2a. This vector and vectors Q75914, -5 and -7 express  
 CC constructs encoding fragments of a chimaeric antibody to the human IL-6  
 CC comprising (a) a light chain with (i) a variable region containing 3  
 CC complementarity determining regions (CDR) (R77201-3) inserted into  
 CC several framework regions (FR) (r77204-7) and (ii) a human light chain  
 CC constant region and (b) a heavy chain with (i) a variable region  
 CC containing 3 CDR (R77212-4) inserted into an FR (r77215-8) and (ii) a  
 CC human light chain constant region. The CDR region are derived from the  
 CC mouse anti-human IL-6 antibody SK2. The FR of the light chain may be  
 CC mouse derived (Q75888) or from the human antibody REI. The heavy chain FR  
 CC may also be mouse derived (Q75889) or from the human antibody DAM. The  
 CC antibodies can be used in the treatment of IL-6 related disorders. The  
 CC antibodies are useful as they have low antigenicity due to the use of  
 CC human derived sequences and low antigenicity mouse derived sequences.  
 SQ Sequence 139 AA;

Query Match 71.9%; Score 92; DB 13; Length 139;  
 Best Local Similarity 68.8%; Pred. No. 1.25e-02;  
 Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 71 hlwnddkynpalkg 86  
 ||:|||||:|:  
 QY 1 HIYWDKRYNPSLKS 16

Search completed: Tue Mar 18 10:15:44 1997  
 Job time : 11 secs.

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WVLSREH

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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Mar 18 10:16:02 1997; MasPar time 1.99 Seconds

102.353 Million cell updates/sec

Tabular output not generated.

Title: >US-08-612-929-26  
Description: (1-11) from US08612929.pep  
Perfect Score: 104  
Sequence: 1 REYVFWYEDV 11

Scoring table: PAM 150  
Gap 15

Searched: 52205 seqs, 18531385 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: swiss-prot33  
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10

Statistics: Mean 27.173; Variance 49.515; scale 0.549

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	71	68.3	284	2	COX3 LEITA	1.86e-01
2	71	68.3	368	10	YHDX_ECOLI	1.86e-01
3	66	63.5	117	4	HV13 MOUSE	1.09e+00
4	66	63.5	122	4	HV21 MOUSE	1.09e+00
5	66	63.5	123	4	HV19 MOUSE	1.09e+00
6	66	63.5	123	4	HV18 MOUSE	1.09e+00
7	66	63.5	123	4	HV23 MOUSE	1.09e+00
8	66	63.5	123	4	HV24 MOUSE	1.09e+00
9	66	63.5	189	1	APD RAT	1.09e+00
10	66	63.5	570	7	PVTX EMENI	1.09e+00
11	65	62.5	482	6	NF31 NAEFO	1.54e+00
12	64	61.5	49	10	YZOA_BACSU	2.17e+00
13	64	61.5	508	10	YBY9_YEAST	2.17e+00

14	64	61.5	776	5	1SP4 SCHPO	SEXUAL DIFFERENTIATIO	2.17e+00
15	64	61.5	1714	8	SYEP DROME	MULTIFUNCTIONAL AMINO	2.17e+00
16	61	58.7	278	1	ADHR_DROPS	ALCOHOL DEHYDROGENASE	5.93e+00
17	61	58.7	279	1	ADHR_DROMD	ALCOHOL DEHYDROGENASE	5.93e+00
18	61	58.7	279	1	ADHR_DROGU	ALCOHOL DEHYDROGENASE	5.93e+00
19	61	58.7	281	1	ADHR_DROAM	ALCOHOL DEHYDROGENASE	5.93e+00
20	60	57.7	110	7	RBS1 THIFE	RIBULOSE BISPHOSPHATE	8.24e+00
21	60	57.7	370	5	MATK MARPO	PROBABLE INTRON MAFUR	8.24e+00
22	60	57.7	477	1	BGL2_BACSU	PROBABLE BETA-GLUCOSI	8.24e+00
23	60	57.7	519	3	ECTO RAT	ECTO-ATPASE PRECURSOR	8.24e+00
24	60	57.7	4969	8	RNC RABIT	RYANODINE RECEPTOR, C	8.24e+00
25	60	57.7	5032	8	RNCR_HUMAN	RYANODINE RECEPTOR, S	8.24e+00
26	60	57.7	5035	8	RNCR_PIG	RYANODINE RECEPTOR, S	8.24e+00
27	60	57.7	5037	8	RNCR_RABIT	RYANODINE RECEPTOR, S	8.24e+00
28	59	56.7	347	1	CSAR_MOUSE	C5A ANAPHYLATOXIN CHE	1.14e+01
29	59	56.7	402	9	VGLD_PVRV1	GLYCOPROTEIN GP50.	1.14e+01
30	59	56.7	432	5	KGTP_ECOLI	ALPHA-KETOGLUTARATE P	1.14e+01
31	59	56.7	465	1	ARBB_ERWCH	6-PHOSPHO-BETA-GLUCOS	1.14e+01
32	58	55.8	881	4	HELI_HSVB	PROBABLE HELICASE.	1.58e+01
33	58	55.8	881	4	HELI_VZVD	PROBABLE HELICASE.	1.58e+01
34	57	54.8	87	6	NULM_APIME	NADH-UBIQUINONE OXIDO	2.17e+01
35	57	54.8	202	1	ADHR_DROER	ALCOHOL DEHYDROGENASE	2.17e+01
36	57	54.8	269	1	ADHR_DROLE	ALCOHOL DEHYDROGENASE	2.17e+01
37	57	54.8	272	1	ADHR_DROMA	ALCOHOL DEHYDROGENASE	2.17e+01
38	57	54.8	272	1	ADHR_DROTE	ALCOHOL DEHYDROGENASE	2.17e+01
39	57	54.8	273	1	ADHR_DROIM	ALCOHOL DEHYDROGENASE	2.17e+01
40	57	54.8	656	2	CPH1 CANAL	TRANSCRIPTION FACTOR	2.17e+01
41	57	54.8	666	8	ST12_KUJLA	STEL2 PROTEIN.	2.17e+01
42	57	54.8	688	8	ST12_YEAST	STEL2 PROTEIN.	2.17e+01
43	57	54.8	1330	10	YKF5_CAEEL	HYPOTHEICAL 153.4 KD	2.17e+01
44	56	53.8	627	4	HCYD_EURCA	HEMOCYANIN D CHAIN.	2.97e+01
45	56	53.8	823	10	YNS2_CAEEL	HYPOTHEICAL 95.6 KD	2.97e+01

## ALIGNMENTS

RESULT	1	STANDARD;	PRT;	284 AA.
ID	COX3 LEITA			
AC	P14546;			
DT	01-JAN-1990 (REL. 13, CREATED)			
DT	01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)			
DE	01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)			
DE	CYTOCHROME C OXIDASE POLYPEPTIDE III (EC 1.9.3.1).			
OS	LEISHMANIA TARENTOLAE (SAUROLEISHMANIA TARENTOLAE).			
OC	MITOCHONDRION.			
OC	EUKARYOTA; PROTOZOA; SARCOMASTIGOPHORA; MASTIGOPHORA; KINETOPLASTIDA;			
OC	TRYPANOSOMATIDAE.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE; 85079995.			
RA	DE LA CRUZ V.F., NECKELMANN N., SIMPSON L.;			
RL	J. BIOL. CHEM. 259:15136-15147(1984).			
CC	-/- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O +			
CC	4 FERRICYTOCHROME C.			
CC	-/- FUNCTION: SUBUNIT I, II, AND III FORM THE FUNCTIONAL CORE OF			
CC	THE ENZYME COMPLEX.			
DR	PIR; G22848; G22848.			
KW	OXIDOREDUCTASE; MITOCHONDRION; TRANSMEMBRANE; KINETOPLAST.			
SQ	SEQUENCE 284 AA; 34151 MW; 3C38259C CRC32;			

Query Match 68.3%; Score 71; DB 2; Length 284;  
Best Local Similarity 100.0%; Pred. No. 1.86e-01;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Mar 18 10:14

US-08-612-929-26.rsp

3

Db 135 vfywvf 140  
 QY 4 VFWYF 9

## RESULT 2

ID YHDX ECOLI STANDARD; PRT; 368 AA.  
 AC P45767;  
 DT 01-NOV-1995 (REL. 32, CREATED)  
 DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)  
 DE HYPOTHETICAL 40.4 KD PROTEIN IN ACRF-RRND INTERGENIC REGION (0368A).  
 GN YHDX.  
 OS ESCHERICHIA COLI.  
 OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;  
 OC ENTEROBACTERIACEAE.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-K12 / MG1655;  
 RA PLUNKETT G. III;  
 RL SUBMITTED (DEC-1994) TO EMBL/GENBANK/DBJ DATA BANKS.  
 CC -/- FUNCTION: PROBABLY PART OF A BINDING-PROTEIN-DEPENDENT TRANSPORT  
 CC SYSTEM FOR AN AMINO ACID; PROBABLY RESPONSIBLE FOR THE  
 CC TRANSLLOCATION OF THE SUBSTRATE ACROSS THE MEMBRANE.  
 CC -/- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE  
 CC (POTENTIAL).  
 CC -/- SIMILARITY: WITH INTEGRAL MEMBRANE COMPONENTS OF OTHER BINDING-  
 CC PROTEIN-DEPENDENT TRANSPORT SYSTEMS. BELONGS TO THE HISMO  
 CC SUBFAMILY.  
 DR ENBL; U18997; G606210; --.  
 DR ECOGENE; EGI2835; YHDX.  
 DR PROSITE; P500402; BPD TRANSP INN MEMBR.  
 KW HYPOTHETICAL PROTEIN; TRANSPORT; AMINO-ACID TRANSPORT; TRANSMEMBRANE;  
 KW INNER MEMBRANE.  
 SQ SEQUENCE 368 AA; 40395 MW; 6CD2B39D CRC32;

Query Match 68.3%; Score 71; DB 10; Length 368;  
 Best Local Similarity 62.5%; Pred. No. 1.86e-01;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 146 iffwyfav 153  
 QY 4 VFWYFV 11

## RESULT 3

ID HV13 MOUSE STANDARD; PRT; 117 AA.  
 AC P01757;  
 DT 21-JUL-1986 (REL. 01, CREATED)  
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1991 (REL. 20, LAST ANNOTATION UPDATE)  
 DE IG HEAVY CHAIN V REGION (3558).  
 OS MUS MUSCULUS (MOUSE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; RODENTIA.  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE; 80078170.  
 RA SCHILLING J., CLEVINGER B., DAVIE J.M., HOOD L.;  
 RL NATURE 283:35-40(1980).  
 CC -/- THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO BIND DEXTRAN  
 CC DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF WHICH OCCUR IN  
 CC THE D AND J SEGMENTS.  
 CC -/- THIS PROTEIN BINDS DEXTRAN.

Mar 18 10:14

US-08-612-929-26.rsp

4

DR PIR; A26242; MHMSJ5.  
 DR HSSP; P01789; 2FCM.  
 KW IMMUNOGLOBULIN V REGION.  
 FT DISULFID 22 96 BY SIMILARITY.  
 FT NON TER 117 117  
 SQ SEQUENCE 117 AA; 13024 MW; E7548A05 CRC32;

Query Match 63.5%; Score 66; DB 4; Length 117;  
 Best Local Similarity 100.0%; Pred. No. 1.09e+00;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 101 ywyfadv 106  
 QY 6 YWYFV 11

## RESULT 4

ID HV21 MOUSE STANDARD; PRT; 122 AA.  
 AC P01790;  
 DT 21-JUL-1986 (REL. 01, CREATED)  
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DT 21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)  
 DE IG HEAVY CHAIN V REGION (MS11).  
 OS MUS MUSCULUS (MOUSE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; RODENTIA.  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE; 81054880.  
 RA ROBINSON E.A., APPELLA E.;  
 RL PROC. NATL. ACAD. SCI. U.S.A. 77:4909-4913(1980).  
 CC -/- THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT BINDS PHOSPHO-  
 CC RYLCHOLINE.  
 DR PIR; A02070; AVMS75.  
 DR HSSP; P01789; IMCP.  
 KW IMMUNOGLOBULIN V REGION.  
 FT NON TER 122 122  
 SQ SEQUENCE 122 AA; 13652 MW; 4E68C805 CRC32;

Query Match 63.5%; Score 66; DB 4; Length 122;  
 Best Local Similarity 100.0%; Pred. No. 1.09e+00;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 106 ywyfadv 111  
 QY 6 YWYFV 11

## RESULT 5

ID HV19 MOUSE STANDARD; PRT; 123 AA.  
 AC P01788;  
 DT 21-JUL-1986 (REL. 01, CREATED)  
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DT 21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)  
 DE IG HEAVY CHAIN V REGION (H8).  
 OS MUS MUSCULUS (MOUSE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; RODENTIA.  
 RN [1]  
 RP SEQUENCE.  
 RA BARSTAD P.;  
 RL THESIS (1975), CALIFORNIA INSTITUTE OF TECHNOLOGY, U.S.A.  
 CC -/- THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT BINDS PHOSPHO-  
 CC RYLCHOLINE.

Mar 18 10:14

US-08-612-929-26.rsp

5

DR PIR; A02070; AVMS5.  
 DR HSP; P01789; IMCP.  
 KW IMMUNOGLOBULIN V REGION.  
 FT NON TER 123 123  
 SQ SEQUENCE 123 AA; 13805 MW; 705319F1 CRC32;

Query Match 63.5%; DB 4; Length 123;  
 Best Local Similarity 100.0%; Pred. No. 1.09e+00;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 107 ywyfdv 112  
 |||||  
 QY 6 YWYFDV 11

## RESULT 6

ID HV18 MOUSE STANDARD; PRT; 123 AA.  
 AC P01787;  
 DT 21-JUL-1986 (REL. 01, CREATED)  
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DT 21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)  
 DE IG HEAVY CHAIN V REGIONS (TEPC 15, S107, HPCM1, HPCM2, AND HPCM3).  
 OS MUS MUSCULUS (MOUSE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; RODENTIA.  
 RN [1]  
 RP SEQUENCE (TEPC 15).  
 RX MEDLINE; 7622762.  
 RA RUDIKOFF S., POTTER M.;  
 RL PROC. NATL. ACAD. SCI. U.S.A. 73:2109-2112 (1976).  
 [2]  
 RP SEQUENCE FROM N.A. (H107).  
 RX MEDLINE; 80199926.  
 RA EARLY P., HUANG H., DAVIS M., CALAME K., HOOD L.;  
 RL CELL 19:981-992 (1980).  
 [3]  
 RP SEQUENCE (S107).  
 RX MEDLINE; 76110488.  
 RA RUDIKOFF S., BARSTAD P., POTTER M., HOOD L.;  
 RL UNPUBLISHED RESULTS, CITED BY:  
 RL HOOD L., CAMPBELL J.H., EIGIN S.C.R.;  
 RL ANNU. REV. GENET. 9:305-353 (1975).  
 [4]  
 RP SEQUENCE (HPCM1; HPCM2 AND HPCM3).  
 RX MEDLINE; 81197602.  
 RA GEARHART P.J., JOHNSON N.D., DOUGLAS R., HOOD L.;  
 RL NATURE 291:29-34 (1981).  
 CC -/- ALL THOSE SEQUENCE APPEARS TO BE IDENTICAL.  
 CC -/- THESE CHAINS WERE ISOLATED FROM MYELOMA AND HYBRIDOMA PROTEINS  
 CC THAT BIND PHOSPHORYLCHOLINE.  
 DR PIR; A02070; AVMS5.  
 DR HSP; P01789; IMCP.  
 KW IMMUNOGLOBULIN V REGION; HYBRIDOMA.  
 FT NON TER 123 123  
 SQ SEQUENCE 123 AA; 13777 MW; B4F3A2A3 CRC32;

Query Match 63.5%; DB 4; Length 123;  
 Best Local Similarity 100.0%; Pred. No. 1.09e+00;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 107 ywyfdv 112  
 |||||  
 QY 6 YWYFDV 11

Mar 18 10:14

US-08-612-929-26.rsp

6

RESULT 7  
 ID HV23 MOUSE STANDARD; PRT; 123 AA.  
 AC P01792;  
 DT 21-JUL-1986 (REL. 01, CREATED)  
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DT 21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)  
 DE IG HEAVY CHAIN V REGION (HPCG8).  
 OS MUS MUSCULUS (MOUSE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; RODENTIA.  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE; 81197602.  
 RA GEARHART P.J., JOHNSON N.D., DOUGLAS R., HOOD L.;  
 RL NATURE 291:29-34 (1981).  
 CC -/- THIS CHAIN WAS ISOLATED FROM HYBRIDOMA PROTEIN THAT BINDS PHOSPHO-  
 CC RYLCHOLINE.  
 DR PIR; A02070; AVMS5.  
 DR HSP; P01789; IMCP.  
 KW IMMUNOGLOBULIN V REGION; HYBRIDOMA.  
 FT NON TER 123 123  
 SQ SEQUENCE 123 AA; 13879 MW; C4AFD9D0 CRC32;

Query Match 63.5%; DB 4; Length 123;  
 Best Local Similarity 100.0%; Pred. No. 1.09e+00;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 107 ywyfdv 112  
 |||||  
 QY 6 YWYFDV 11

## RESULT 8

ID HV24 MOUSE STANDARD; PRT; 123 AA.  
 AC P01793;  
 DT 21-JUL-1986 (REL. 01, CREATED)  
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DT 21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)  
 DE IG HEAVY CHAIN V REGION (HPCG13).  
 OS MUS MUSCULUS (MOUSE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; RODENTIA.  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE; 81197602.  
 RA GEARHART P.J., JOHNSON N.D., DOUGLAS R., HOOD L.;  
 RL NATURE 291:29-34 (1981).  
 CC -/- THIS CHAIN WAS ISOLATED FROM HYBRIDOMA PROTEIN THAT BINDS PHOSPHO-  
 CC RYLCHOLINE.  
 DR PIR; A02070; AVMS5.  
 DR HSP; P01789; IMCP.  
 KW IMMUNOGLOBULIN V REGION; HYBRIDOMA.  
 FT NON TER 123 123  
 SQ SEQUENCE 123 AA; 13808 MW; 23034AB8 CRC32;

Query Match 63.5%; DB 4; Length 123;  
 Best Local Similarity 100.0%; Pred. No. 1.09e+00;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 107 ywyfdv 112  
 |||||  
 QY 6 YWYFDV 11

Mar 18 10:14 US-08-612-929-26.rsp

CC PERMEASES.  
 DR PIR; S04547; S04547.  
 DR PROSITE; PS00218; AMINO ACID PERMEASE.  
 KW TRANSPORT; AMINO-ACID TRANSPORT; TRANSMEMBRANE; GLYCOPROTEIN.  
 FT DOMAIN 1 44 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 45 64 POTENTIAL.  
 FT TRANSMEM 65 115 POTENTIAL.  
 FT TRANSMEM 121 160 POTENTIAL.  
 FT TRANSMEM 163 211 POTENTIAL.  
 FT TRANSMEM 283 310 POTENTIAL.  
 FT TRANSMEM 318 343 POTENTIAL.  
 FT TRANSMEM 384 414 POTENTIAL.  
 FT TRANSMEM 415 442 POTENTIAL.  
 FT TRANSMEM 473 499 POTENTIAL.  
 FT TRANSMEM 500 525 POTENTIAL.  
 FT DOMAIN 526 570 CYTOPLASMIC (POTENTIAL).  
 FT CARBOHYD 380 380 POTENTIAL.  
 FT CARBOHYD 402 402 POTENTIAL.  
 FT CARBOHYD 416 416 POTENTIAL.  
 SQ SEQUENCE 570 AA; 63101 MW; 25935669 CRC32;

Query Match 63.5%; Score 66; DB 7; Length 570;  
 Best Local Similarity 50.0%; Pred. No. 1.09e+00;  
 Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Db 408 qtfvfywftni 417  
 :||||: ::  
 QY 2 ETVFYWFDV 11

RESULT 11  
 ID NF31 NAEFO STANDARD; PRT; 482 AA.  
 AC P42661;  
 DT 01-NOV-1995 (REL. 32, CREATED)  
 DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)  
 DE VIRULENCE-RELATED PROTEIN NF314 (EC 3.4.16.-).  
 OS NAEGLERIA FOWLERI.  
 OC EUKARYOTA; PROTOZOA; SARCOMASTICOPHORA; SARCODINA; RHIZOPODA; LOBOSA;  
 OC SCHIZOPHYRENA.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=LEE;  
 RX MEDLINE; 92267659.  
 RA HU W.-N., KOPACHIK W., BAND R.N.;  
 RL INFECT. IMMUN. 60:2418-2424(1992).  
 CC -/- FUNCTION: MAY BE REQUIRED BUT IS NOT SUFFICIENT FOR INCREASED  
 CC VIRULENCE.  
 CC -/- INDUCTION: BY GROWTH ON MAMMALIAN CELLS.  
 CC -/- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S10; ALSO KNOWN AS THE  
 CC SERINE CARBOXYPEPTIDASE FAMILY.  
 DR EMBL; M88397; G159720; -.  
 DR PROSITE; PS00131; CARBOXYPEPT\_SER\_SER.  
 DR PROSITE; PS00560; CARBOXYPEPT\_SER\_HIS.  
 KW HYDROLASE; CARBOXYPEPTIDASE.  
 FT ACT\_SITE 163 163 BY SIMILARITY.  
 FT ACT\_SITE 399 399 BY SIMILARITY.  
 FT ACT\_SITE 459 459 BY SIMILARITY.  
 SQ SEQUENCE 482 AA; 53848 MW; A9865400 CRC32;

Query Match 62.5%; Score 65; DB 6; Length 482;  
 Best Local Similarity 57.1%; Pred. No. 1.54e+00;  
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Mar 18 10:14 US-08-612-929-26.rsp

RESULT 9  
 ID APD RAT STANDARD; PRT; 189 AA.  
 AC P23593;  
 DT 01-NOV-1991 (REL. 20, CREATED)  
 DT 01-NOV-1991 (REL. 20, LAST SEQUENCE UPDATE)  
 DT 01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)  
 DE APOLIPOPROTEIN D PRECURSOR.  
 GN APOL.  
 OS RATTUS NORVEGICUS (RAT).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; RODENTIA.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=WISTAR;  
 RX MEDLINE; 90316104.  
 RA SPREYER P., SCHAL H., KUHN G., ROTHE T., UNTERBECK A., OLEK K.,  
 RA MUELLER H.W.;  
 RL EMBL J. 9:2479-2484 (1990).  
 CC -/- FUNCTION: APOL OCCURS IN THE MACROMOLECULAR COMPLEX WITH LECITHIN-  
 CC CHOLESTEROL ACYLTRANSFERASE. IT IS PROBABLY INVOLVED IN THE  
 CC TRANSPORT AND BINDING OF BILIN.  
 CC -/- SUBUNIT: HOMODIMER.  
 CC -/- SIMILARITY: THIS PROTEIN BELONGS TO THE FAMILY OF SMALL  
 CC HYDROPHOBIC MOLECULES TRANSPORT PROTEINS (LIPOCALINS).  
 DR EMBL; X55572; G287650; -.  
 DR PIR; S12556; S12556.  
 DR HSSP; P05090; ZAPD.  
 DR PROSITE; PS00213; LIPOCALIN.  
 KW GLYCOPROTEIN; PLASMA; LIPID-BINDING; TRANSPORT; SIGNAL; LIPOCALIN.  
 FT SIGNAL 1 20  
 FT CHAIN 21 189 APOLIPOPROTEIN D.  
 FT CARBOHYD 65 65 POTENTIAL.  
 FT CARBOHYD 98 98 POTENTIAL.  
 SQ SEQUENCE 189 AA; 21635 MW; A731E791 CRC32;

Query Match 63.5%; Score 66; DB 1; Length 189;  
 Best Local Similarity 55.6%; Pred. No. 1.09e+00;  
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 135 ttfwffhfv 143  
 |:|:|:  
 QY 3 TVFYWFDV 11

RESULT 10  
 ID PUTX EMENI STANDARD; PRT; 570 AA.  
 AC P18696;  
 DT 01-NOV-1990 (REL. 16, CREATED)  
 DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)  
 DT 01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)  
 DE PROLINE-SPECIFIC PERMEASE (PROLINE TRANSPORT PROTEIN).  
 GN PRNB.  
 OS EMERICELLA NIDULANS (ASPERGILLUS NIDULANS).  
 OC EUKARYOTA; FUNGI; ASCOMYCOTINA; PLECTOMYCETES; EUROTIALES.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 89313300.  
 RA SOPHIANPOULOU V., SCAZZOFCCHIO C.;  
 RL MOL. MICROBIOL. 3:705-714(1989).  
 CC -/- FUNCTION: REQUIRED FOR HIGH-AFFINITY PROLINE TRANSPORT.  
 CC -/- INDUCTION: BY L-PROLINE.  
 CC -/- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
 CC -/- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MANY AMINO ACID

Db 45 lfywffe 51  
:||||:  
Qy 4 VFYWFYD 10

RESULT 12  
ID YZOA BACSU STANDARD; PRT; 49 AA.  
AC P40769;  
DT 01-FEB-1995 (REL. 31, CREATED)  
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)  
DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)  
DE HYPOTHETICAL PROTEIN CLONE PSP23 (FRAGMENT).  
GN YZOA.  
OS BACILLUS SUBTILIS.  
OC PROKARYOTA; FIRMICUTES; ENDOSPORE-FORMING RODS AND COCCI; BACILLACEAE.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 89108019.  
RA SMITH H., DE JONG A., BRON S., VENEMA G.;  
RL GENE 70:351-361(1988).  
DR EMBL; M22914; G143698; -.  
DR SUBTILIST; BG11029; YZOA.  
KW HYPOTHETICAL PROTEIN.  
FT NON TER 49 49  
SQ SEQUENCE 49 AA; 5436 MW; 2E63A14A CRC32;

Query Match 61.5%; Score 64; DB 10; Length 49;  
Best Local Similarity 100.0%; Pred. No. 2.17e+00;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 19 fywyf 23  
|||||  
Qy 5 FYWYF 9

RESULT 13  
ID YBY9 YEAST STANDARD; PRT; 508 AA.  
AC P38109;  
DT 01-OCT-1994 (REL. 30, CREATED)  
DT 01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)  
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)  
DE PUTATIVE SERINE CARBOXYPEPTIDASE IN ESRI-IRAI INTERGENIC REGION  
DE (EC 3.4.16.-).  
GN YBR139W OR YBR1015.  
OS SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN-S288C;  
RX MEDLINE; 94378717.  
RA BECAM A.-M., CULLIN C., GRZYBOWSKA E., LACROUTE F., NASR F.,  
RA OZIER-KALOGEROPOULOS O., PALUCHA A., SLONIMSKI P.P., ZAGULSKI M.,  
RA HERBERT C.J.;  
RL YEAST 10:S1-S11(1994).  
RN [2]  
RP DISCUSSION OF SEQUENCE.  
RX MEDLINE; 95042830.  
RA NASR F., BECAM A.-M., GRZYBOWSKA E., ZAGULSKI M., SLONIMSKI P.P.,  
RA HERBERT C.J.;  
RL CURR. GENET. 26:1-7(1994).

CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S10; ALSO KNOWN AS THE  
CC SERINE CARBOXYPEPTIDASE FAMILY.  
DR EMBL; X75891; G496849; -.  
DR EMBL; Z36008; G536436; -.  
RN [1]

DR PIR; S46008; S46008.  
DR PIR; S46581; S46581.  
DR HSP; P08819; IYSC.  
DR PROSITE; PS00131; CARBOXYPEPT SER SER.  
DR PROSITE; PS00560; CARBOXYPEPT SER HIS.  
KW HYPOTHETICAL PROTEIN; HYDROLASE; CARBOXYPEPTIDASE.  
FT ACT SITE 219 219 BY SIMILARITY.  
FT ACT SITE 413 413 BY SIMILARITY.  
FT ACT SITE 474 474 BY SIMILARITY.  
SQ SEQUENCE 508 AA; 57639 MW; 6415CAAB CRC32;

Query Match 61.5%; Score 64; DB 10; Length 508;  
Best Local Similarity 66.7%; Pred. No. 2.17e+00;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 107 fywffe 112  
||||:  
Qy 5 FYWYF 10

RESULT 14  
ID ISP4 SCHPO STANDARD; PRT; 776 AA.  
AC P40900;  
DT 01-FEB-1995 (REL. 31, CREATED)  
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)  
DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)  
DE SEXUAL DIFFERENTIATION PROCESS PROTEIN ISP4.  
GN ISP4.  
OS SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).  
OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 95042833.  
RA SATO S., SUZUKI H., WIDYASTUTI U., HOTTA Y., TABATA S.;  
RL CURR. GENET. 26:31-37(1994).  
CC -1- DEVELOPMENTAL STAGE: TRANSCRIBED SPECIFICALLY DURING SEXUAL  
CC DEVELOPMENT.

DR EMBL; D14061; G218543; -.  
DR PIR; S43741; S43741.  
DR PIR; S45495; S45495.  
SQ SEQUENCE 776 AA; 88256 MW; 9D675742 CRC32;

Query Match 61.5%; Score 64; DB 5; Length 776;  
Best Local Similarity 60.0%; Pred. No. 2.17e+00;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Db 460 evpfywyfslv 469  
||||:  
Qy 2 ETVFYWYFV 11

RESULT 15  
ID SYEP DROME STANDARD; PRT; 1714 AA.  
AC P28668;  
DT 01-DEC-1992 (REL. 24, CREATED)  
DT 01-DEC-1992 (REL. 24, LAST SEQUENCE UPDATE)  
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)  
DE MULTIFUNCTIONAL AMINOACYL-TRNA SYNTHETASE (CONTAINS: GLUTAMYL-TRNA  
DE SYNTHETASE (EC 6.1.1.17) (GLUTAMATE-TRNA LIGASE), AND PROLYL-TRNA  
DE SYNTHETASE (EC 6.1.1.15) (PROLINE-TRNA LIGASE)).  
GN AATS-GLUPRO.  
OS DROSOPHILA MELANOGASTER (FRUIT FLY).  
OC EUKARYOTA; METAZOA; ARTHROPODA; INSECTA; DIPTERA.  
RN [1]

Mar 18 10:14

US-08-612-929-26.fsp

11

RP SEQUENCE FROM N.A.  
 RX MEDLINE: 92097547.  
 RA CERINI C., KERJAN P., ASTIER M., GRATECOS D., MIRANDE M., SEMERIVA M.;  
 RL EMBO J. 10:4267-4277(1991).  
 CC -!- CATALYTIC ACTIVITY: ATP + L-GLUTAMATE + TRNA (GLU) = AMP +  
 CC PYROPHOSPHATE + L-GLUTAMYL-TRNA (GLU).  
 CC -!- CATALYTIC ACTIVITY: ATP + L-PROLINE + TRNA (PRO) = AMP +  
 CC PYROPHOSPHATE + L-PROLYL-TRNA (PRO).  
 CC -!- SUBUNIT: COMPONENT OF THE MULTISYNTHETASE COMPLEX WHICH CONTAINS  
 CC NINE DIFFERENT AA-TRNA SYNTHETASES.  
 CC -!- SIMILARITY: THE N-TERMINAL DOMAIN BELONGS TO CLASS-I AMINOACYL-  
 CC TRNA SYNTHETASES.  
 CC -!- SIMILARITY: THE N-TERMINAL DOMAIN BELONGS TO CLASS-II AMINOACYL-  
 CC TRNA SYNTHETASES.  
 CC -!- SIMILARITY: CONTAINS 6 COPIES OF A DOMAIN THAT WE CALL "WHEP-TRS".  
 DR EMBL; M74104; G157564; -.  
 DR PIR; S18644; S18644.  
 DR HSSP; P00962; LGTR.  
 DR FLYBASE; FBGN005674; AATS-GLUPRO.  
 DR PROSITE; PS00178; AA\_TRNA\_LIGASE\_I.  
 DR PROSITE; PS00179; AA\_TRNA\_LIGASE\_II\_1.  
 DR PROSITE; PS00339; AA\_TRNA\_LIGASE\_II\_2.  
 DR PROSITE; PS00762; WHEP TRS.  
 KW AMINOACYL-TRNA SYNTHASE; PROTEIN BIOSYNTHESIS; LIGASE; ATP-BINDING;  
 KW MULTIFUNCTIONAL ENZYME; REPEAT.  
 FT DOMAIN 170 754 GLUTAMYL-TRNA SYNTHETASE.  
 FT DOMAIN 755 800 WHEP-TRS 1.  
 FT DOMAIN 827 872 WHEP-TRS 2.  
 FT DOMAIN 901 946 WHEP-TRS 3.  
 FT DOMAIN 980 1025 WHEP-TRS 4.  
 FT DOMAIN 1055 1100 WHEP-TRS 5.  
 FT DOMAIN 1129 1173 WHEP-TRS 6.  
 FT DOMAIN 1174 1180 POLY-GLY.  
 FT DOMAIN 1207 1714 PROLYL-TRNA SYNTHETASE.  
 FT SIMILAR 209 220 "HIGH" REGION.  
 FT SIMILAR 438 442 "KMSKS" REGION.  
 FT BINDING 441 441 ATP (BY SIMILARITY).  
 SQ SEQUENCE 1714 AA; 189197 MW; 39A9D8E5 CRC32;

Query Match 61.5%; Score 64; DB 8; Length 1714;  
 Best Local Similarity 50.0%; Pred.No. 2.17e+00;  
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 408 rddqfywfid 417  
 : : : : :  
 Qy 1 RETVFWYFD 10

Search completed: Tue Mar 18 10:16:11 1997  
 Job time : 9 secs.





Mar 18 10:15

US-08-612-929-26 pr

3

QY 1 RETVFWYFDV 11  
|| :|||||

RESULT 2 A30540 #type fragment  
ENTRY Ig heavy chain V region (253.12D3) - mouse (fragment)  
TITLE #formal\_name Mus musculus #common\_name house mouse  
ORGANISM  
DATE 10-Feb-1989 #sequence\_revision 10-Feb-1989 #text\_change 12-Apr-1995  
ACCESSIONS A30540  
REFERENCE A30534  
#authors Claflin, J.L.; Berry, J.  
#journal J. Immunol. (1988) 141:4012-4019  
#title Genetics of the phosphocholine-specific antibody response to Streptococcus pneumoniae. Germ-line but not mutated T15 antibodies are dominantly selected.  
#cross-references MUID:89035545  
#accession A30540  
#status preliminary; not compared with conceptual translation  
#molecule\_type mRNA  
#residues 1-123 #label CIA  
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology  
SUMMARY #length 123 #checksum 8418

Query Match 74.0%; Score 77; DB 5; Length 123;  
Best Local Similarity 100.0%; Pred. No. 1.92e-01;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 106 fywyfdv 112  
:|||||  
QY 5 FYWYFDV 11

RESULT 3 B49038 #type fragment  
ENTRY immunoglobulin lambda light chain variable region - mouse  
TITLE (fragment)  
ORGANISM #formal\_name Mus musculus #common\_name house mouse  
DATE 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 23-Mar-1995  
ACCESSIONS B49038  
REFERENCE A49038  
#authors Weiss, U.; Zobebelein, R.; Rajewsky, K.  
#journal Eur. J. Immunol. (1992) 22:511-517  
#title Accumulation of somatic mutants in the B cell compartment after primary immunization with a T cell-dependent antigen.  
#cross-references MUID:92164733  
#accession B49038  
#status preliminary  
#molecule\_type DNA  
#residues 1-31 #label WEI  
#cross-references NCBIN:85733; NCBIP:85761  
#experimental\_source spleen  
#note sequence extracted from NCB1 backbone  
SUMMARY #length 31 #checksum 9999

Query Match 70.2%; Score 73; DB 12; Length 31;  
Best Local Similarity 85.7%; Pred. No. 6.68e-01;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 25 yywyfdv 31  
:|||||  
QY 5 FYWYFDV 11

Mar 18 10:15

US-08-612-929-26 pr

4

RESULT 4 C49038 #type fragment  
ENTRY immunoglobulin lambda light chain variable region - mouse  
TITLE (fragment)  
ORGANISM #formal\_name Mus musculus #common\_name house mouse  
DATE 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 23-Mar-1995  
ACCESSIONS C49038  
REFERENCE A49038  
#authors Weiss, U.; Zobebelein, R.; Rajewsky, K.  
#journal Eur. J. Immunol. (1992) 22:511-517  
#title Accumulation of somatic mutants in the B cell compartment after primary immunization with a T cell-dependent antigen.  
#cross-references MUID:92164733  
#accession C49038  
#status preliminary  
#molecule\_type DNA  
#residues 1-38 #label WEI  
#cross-references NCBIN:85734; NCBIP:85801  
#experimental\_source spleen  
#note sequence extracted from NCB1 backbone  
SUMMARY #length 38 #checksum 1027

Query Match 70.2%; Score 73; DB 12; Length 38;  
Best Local Similarity 85.7%; Pred. No. 6.68e-01;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 32 yywyfdv 38  
:|||||  
QY 5 FYWYFDV 11

RESULT 5 E49038 #type fragment  
ENTRY immunoglobulin lambda light chain variable region - mouse  
TITLE (fragment)  
ORGANISM #formal\_name Mus musculus #common\_name house mouse  
DATE 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 23-Mar-1995  
ACCESSIONS E49038  
REFERENCE A49038  
#authors Weiss, U.; Zobebelein, R.; Rajewsky, K.  
#journal Eur. J. Immunol. (1992) 22:511-517  
#title Accumulation of somatic mutants in the B cell compartment after primary immunization with a T cell-dependent antigen.  
#cross-references MUID:92164733  
#accession E49038  
#status preliminary  
#molecule\_type DNA  
#residues 1-56 #label WEI  
#cross-references NCBIN:85736; NCBIP:85804  
#experimental\_source spleen  
#note sequence extracted from NCB1 backbone  
SUMMARY #length 56 #checksum 7706

Query Match 70.2%; Score 73; DB 12; Length 56;  
Best Local Similarity 85.7%; Pred. No. 6.68e-01;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 50 yywyfdv 56  
:|||||  
QY 5 FYWYFDV 11

Mar 18 10:15

US-08-612-929-26 rpr

5

RESULT 6

ENTRY D49038 #type fragment  
TITLE immunoglobulin lambda light chain variable region - mouse (fragment)

ORGANISM #formal\_name Mus musculus #common\_name house mouse  
DATE 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 23-Mar-1995

ACCESSIONS D49038

REFERENCE A49038

#authors Weise, U.; Zoebelen, R.; Rajewsky, K.

#journal Eur. J. Immunol. (1992) 22:511-517

#title Accumulation of somatic mutants in the B cell compartment after primary immunization with a T cell-dependent antigen.

#cross-references MUID:92164733

#accession D49038

##status preliminary

##molecule\_type DNA

##residues 1-58 #label WEI

##cross-references NCBI:85735; NCBI:85802

##experimental\_source spleen

##note \_sequence extracted from NCBI backbone

SUMMARY #length 58 #checksum 2946

Query Match 70.2%; Score 73; DB 12; Length 58;

Best Local Similarity 85.7%; Pred. No. 6.68e-01;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 52 ywywfdv 58

:|||||

Qy 5 FYWYFDV 11

RESULT 7

ENTRY F30539 #type fragment

TITLE Ig heavy chain V region (224.4B11) - mouse (fragment)

ORGANISM #formal\_name Mus musculus #common\_name house mouse

DATE 10-Feb-1989 #sequence\_revision 10-Feb-1989 #text\_change 12-Apr-1995

ACCESSIONS F30539

REFERENCE A30534

#authors Claflin, J.L.; Berry, J.

#journal J. Immunol. (1988) 141:4012-4019

#title Genetics of the phosphocholine-specific antibody response to Streptococcus pneumoniae. Germ-line but not mutated T15 antibodies are dominantly selected.

#cross-references MUID:89035545

#accession F30539

##status preliminary; not compared with conceptual translation

##molecule\_type mRNA

##residues 1-124 #label CIA

##note nucleotide sequence is not given

CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology

SUMMARY #length 124 #checksum 689

Query Match 70.2%; Score 73; DB 5; Length 124;

Best Local Similarity 85.7%; Pred. No. 6.68e-01;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 107 ywywfdv 113

:|||||

Qy 5 FYWYFDV 11

Mar 18 10:15

US-08-612-929-26 rpr

6

RESULT 8

ENTRY G30539 #type fragment

TITLE Ig heavy chain V region (224.7E7) - mouse (fragment)

ORGANISM #formal\_name Mus musculus #common\_name house mouse

DATE 10-Feb-1989 #sequence\_revision 10-Feb-1989 #text\_change 12-Apr-1995

ACCESSIONS G30539

REFERENCE A30534

#authors Claflin, J.L.; Berry, J.

#journal J. Immunol. (1988) 141:4012-4019

#title Genetics of the phosphocholine-specific antibody response to Streptococcus pneumoniae. Germ-line but not mutated T15 antibodies are dominantly selected.

#cross-references MUID:89035545

#accession G30539

##status preliminary; not compared with conceptual translation

##molecule\_type mRNA

##residues 1-124 #label CIA

##note nucleotide sequence is not given

CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology

SUMMARY #length 124 #checksum 1542

Query Match 70.2%; Score 73; DB 5; Length 124;

Best Local Similarity 85.7%; Pred. No. 6.68e-01;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 107 ywywfdv 113

:|||||

Qy 5 FYWYFDV 11

RESULT 9

ENTRY H30539 #type fragment

TITLE Ig heavy chain V region (252.5E10) - mouse (fragment)

ORGANISM #formal\_name Mus musculus #common\_name house mouse

DATE 10-Feb-1989 #sequence\_revision 10-Feb-1989 #text\_change 12-Apr-1995

ACCESSIONS H30539

REFERENCE A30534

#authors Claflin, J.L.; Berry, J.

#journal J. Immunol. (1988) 141:4012-4019

#title Genetics of the phosphocholine-specific antibody response to Streptococcus pneumoniae. Germ-line but not mutated T15 antibodies are dominantly selected.

#cross-references MUID:89035545

#accession H30539

##status preliminary; not compared with conceptual translation

##molecule\_type mRNA

##residues 1-124 #label CIA

##note nucleotide sequence is not given

CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology

SUMMARY #length 124 #checksum 923

Query Match 70.2%; Score 73; DB 5; Length 124;

Best Local Similarity 85.7%; Pred. No. 6.68e-01;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 107 ywywfdv 113

:|||||

Qy 5 FYWYFDV 11

RESULT 10

Mar 18 10:15

US-08-612-929-26.rpr

7

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ENTRY      A28782      #type fragment
TITLE      cytochrome-c oxidase (EC 1.9.3.1) chain III - Trypanosoma
            brucei mitochondrion (SGC6) (fragment)
ORGANISM   #formal name mitochondrion Trypanosoma brucei
DATE       28-Aug-1989 #sequence_revision 28-Aug-1989 #text_change
            28-Oct-1994
ACCESSIONS A28782
REFERENCE  A28782
            #authors Feagin, J.E.; Abraham, J.M.; Stuart, K.
            #journal Cell (1988) 53:413-422
            #title Extensive editing of the cytochrome c oxidase III transcript
            in Trypanosoma brucei.
            #cross-references MUID:88210456
            #accession A28782
            ##molecule_type mRNA
            ##residues 1-181 ##label FEa
            ##note the authors translated the codon TGT for residues 131
            and 140 as Arg
GENETICS
            #genome mitochondrion
            #genetic_code SGC6
            #classification #superfamily cytochrome-c oxidase chain III
            #keywords electron transfer; membrane-associated complex;
            mitochondrion; oxidoreductase; transmembrane protein
            #length 181 #checksum 1590
Query Match 68.3%; Score 71; DB 4; Length 181;
Best Local Similarity 100.0%; Pred. No. 1.23e+00;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 32 vfywyf 37
|||||
Qy 4 VFYWF 9

RESULT 11
ENTRY      G22848      #type complete
TITLE      cytochrome-c oxidase (EC 1.9.3.1) chain III - Sauroleishmania
            tarentolae mitochondrion (SGC6)
ORGANISM   #formal name mitochondrion Sauroleishmania tarentolae
DATE       30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change
            28-Oct-1994
ACCESSIONS G22848
REFERENCE  A22848
            #authors de la Cruz, V.F.; Neckelmann, N.; Simpson, L.
            #journal J. Biol. Chem. (1984) 259:15136-15147
            #title Sequences of six genes and several open reading frames in the
            kinetoplast maxicircle DNA of Leishmania tarentolae.
            #cross-references MUID:85079995
            #accession G22848
            ##molecule_type DNA
            ##residues 1-284 ##label DEL
            ##cross-references GB:M10126
GENETICS
            #genome mitochondrion
            #genetic_code SGC6
            #classification #superfamily cytochrome-c oxidase chain III
            #keywords electron transfer; membrane-associated complex;
            mitochondrion; oxidoreductase; transmembrane protein
            #length 284 #molecular-weight 34151 #checksum 2764
Query Match 68.3%; Score 71; DB 4; Length 284;
Best Local Similarity 100.0%; Pred. No. 1.23e+00;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Mar 18 10:15

US-08-612-929-26.rpr

8

```

Db 135 vfywyf 140
|||||
Qy 4 VFYWF 9

RESULT 12
ENTRY      A25877      #type fragment
TITLE      cytochrome-c oxidase (EC 1.9.3.1) chain III - Crithidia
            fasciculata mitochondrion (SGC6) (fragment)
ORGANISM   #formal name mitochondrion Crithidia fasciculata
DATE       19-Jan-1988 #sequence_revision 19-Jan-1988 #text_change
            28-Oct-1994
ACCESSIONS A25877
REFERENCE  A25877
            #authors Sloof, P.; van den Burg, J.; Voogd, A.; Benne, R.
            #journal Nucleic Acids Res. (1987) 15:51-65
            #title The nucleotide sequence of a 3.2 kb segment of mitochondrial
            maxicircle DNA from Crithidia fasciculata containing the
            gene for cytochrome oxidase subunit III, the N-terminal
            part of the apocytochrome b gene and a possible frameshift
            gene; further evidence for the use of unusual initiator
            triplets in trypanosome mitochondria.
            #cross-references MUID:87146364
            #accession A25877
            ##status preliminary; not compared with conceptual translation
            ##molecule_type DNA
            ##residues 1-287 ##label SLO
GENETICS
            #genome mitochondrion
            #genetic_code SGC6
            #classification #superfamily cytochrome-c oxidase chain III
            #keywords electron transfer; membrane-associated complex;
            mitochondrion; oxidoreductase; transmembrane protein
            #length 287 #checksum 9988
Query Match 68.3%; Score 71; DB 4; Length 287;
Best Local Similarity 100.0%; Pred. No. 1.23e+00;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 138 vfywyf 143
|||||
Qy 4 VFYWF 9

RESULT 13
ENTRY      S13687      #type fragment
TITLE      Ig heavy chain V region - mouse (fragment)
ORGANISM   #formal name Mus musculus #common name house mouse
DATE       18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change
            10-Nov-1995
ACCESSIONS S13687
REFERENCE  S13685
            #authors Pennell, C.A.; Mercolino, T.J.; Grdina, T.A.; Arnold, L.W.;
            Haughton, G.; Clarke, S.H.
            #journal Eur. J. Immunol. (1989) 19:1289-1295
            #title Biased immunoglobulin variable region gene expression by Ly-1
            B cells due to clonal selection.
            #cross-references MUID:89338557
            #accession S13687
            ##molecule_type mRNA
            ##residues 1-111 ##label PEN
            ##cross-references EMBL:X53340
            #length 111 #checksum 5825
SUMMARY

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Mar 18 10:15

US-08-612-929-26 rpr

9

Query Match 65.4%; Score 68; DB 12; Length 111;  
Best Local Similarity 60.0%; Pred. No. 3.04e+00;  
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 98 dslgywyfdv 107  
::: |||||  
Qy 2 ETVFYWYFDV 11

RESULT 14  
ENTRY PH0987 #type fragment  
TITLE Ig heavy chain V region (clone 163.47) - mouse (fragment)  
ORGANISM #formal\_name Mus musculus #common\_name house mouse  
DATE 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 11-Apr-1995  
ACCESSIONS PH0987  
REFERENCE PH0971  
#authors Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.  
#journal J. Exp. Med. (1992) 176:761-779  
#title Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cell stimulation in (NZB x NZW)F1 mice.  
#accession PH0987  
#molecule\_type mRNA  
#residues 1-107 #label TIL  
#experimental\_source B cell, strain [NZB x NZW]F1  
#note nucleotide sequence is not given  
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology  
KEYWORDS immunoglobulin  
SUMMARY #length 107 #checksum 8510

Query Match 64.4%; Score 67; DB 5; Length 107;  
Best Local Similarity 85.7%; Pred. No. 4.09e+00;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 100 iywyfdv 106  
:|||||  
Qy 5 FYWYFDV 11

RESULT 15  
ENTRY PH1006 #type fragment  
TITLE Ig heavy chain V region (clone 202.33) - mouse (fragment)  
ORGANISM #formal\_name Mus musculus #common\_name house mouse  
DATE 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 11-Apr-1995  
ACCESSIONS PH1006  
REFERENCE PH0971  
#authors Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.  
#journal J. Exp. Med. (1992) 176:761-779  
#title Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cell stimulation in (NZB x NZW)F1 mice.  
#accession PH1006  
#molecule\_type mRNA  
#residues 1-108 #label TIL  
#experimental\_source B cell, strain [NZB x NZW]F1  
#note nucleotide sequence is not given  
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology  
KEYWORDS immunoglobulin  
SUMMARY #length 108 #checksum 3884

Query Match 64.4%; Score 67; DB 5; Length 108;

Mar 18 10:15

US-08-612-929-26 rpr

10

Best Local Similarity 87.5%; Pred. No. 4.09e+00;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 100 vgywyfdv 107  
| |||||  
Qy 4 VFYWYFDV 11

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